EvolDir

September 1, 2009

Month in Review

Foreword

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.

—— / ——

Conferences

DahlonegaCA SEPEEG Oct16-18

The 2009 SouthEastern Population Ecology and Evolutionary Genetics (SEPEEG) meeting will take place October 16th - 18th at the beautiful Wahsega 4H Center near Dahlonega, GA (http://www.georgia4h.org/-public/ facilities/wahsega/default.htm). Mark your calendars! Keeping with the tradition of SEPEEG, the 2009 meeting will be informal and accommodations will be on the rustic side. Talk and poster submissions are encouraged from undergrads, grad students, post-docs, and faculty. The keynote speaker will be Les Real from the Emory University.

Registration is now open through October 2nd on our official conference website: http://www.sepeeg.com/-, and the low registration fee of $130 can be paid using PayPal.

The meeting organizers are Nicole Gerardo and Todd Schlenke, and the Emory University PBEE Program. Please contact any of us with questions at sepeeg2009@gmail.com. We hope to see you there! Todd

Todd Schlenke Department of Biology Emory University Atlanta, GA 30322 phone: 404-727-0817 fax: 404-727-2880

Todd Schlenke <tschlen@EMORY.EDU>

KansasCity EvolutionaryGenomics Nov13-15

REGISTRATION is now open to attend the 7th Annual “Genes in Ecology, Ecology in Genes” Symposium on November 13, 14, & 15, 2009, in Kansas City.

NEW THIS YEAR: STUDENT TRAVEL FELLOWSHIPS Please visit our website for application information.

The Ecological Genomics Symposium will convene in the historic Muehlebach/Marriott Hotel in downtown Kansas City Friday evening at 6:00 p.m. and conclude on Sunday at noon. For a brochure and complete information regarding poster abstract submission, student travel fellowships, registration and hotel reservations, please visit our Symposium website, www.ecogen.ksu.edu/symp2009 .

Ecological Genomics is a field at the interface of ecology, evolution and genomics that seeks to place the functional significance of genes and genomics into an ecological and evolutionary context.

We have an outstanding lineup of speakers for the 2009 Symposium and we encourage you to attend!

PLENARY SPEAKER:

Jonathan F. Wendel, Iowa State University, “Genes, jeans, and genomes: Exploring the mysteries of polyploidy in cotton"

FEATURED SPEAKERS:

+Andres Aguilar, University of California-Merced, "Genomic differentiation and adaptive divergence in rockfish (genus Sebastes)"

+May R. Berenbaum, University of Illinois at Urbana-Champaign, "Cytochrome P450 genes in plant-insect interactions: War and peace?"

+Jeffrey L. Feder, University of Notre Dame, "Sympatric speciation in Rhagoletis: Islands of speciation or genomic continents of divergence?"

+David C. Queller, Rice University, "The selfish gene at the genetic level: Cooperation and cheating in social amoebas"

+Matthew Rockman, New York University, "Causes of heritable variation in C. elegans"

+Erica Bree Rosenblum, University of Idaho, "The genetics of adaptation: Investigating the functional basis of phenotypic convergence"

+Jay F. Storz, University of Nebraska, "Genetics of high altitude adaptation in vertebrates"

+Chris Toomajian, Kansas State University, "Flowering-time genes as genomic targets of selection in Arabidopsis thaliana"

+Michael J. Wade, Indiana University, "The evolution of conflict and cooperation in genetically and/or ecologically viscous populations"

POSTER ABSTRACTS: Please submit your poster abstract online by Tuesday, October 13, 2009. Abstract submission guidelines are available on the website. Poster sessions will be held on Friday night and Saturday. Poster topics should be related to the field of Ecological Genomics. A LIMITED NUMBER OF SUBMITTED POSTER ABSTRACTS WILL BE SELECTED FOR ORAL PRESENTATIONS.

INFORMATION will be posted on our website, www.ecogen.ksu.edu/symp2009, as details are finalized. Please share this announcement with colleagues and students. If you have questions, please contact us at (785) 532-3482 or dmerrill@ksu.edu.

FUNDING for this symposium is provided by the National Science Foundation and

Targeted Excellence at Kansas State University.

DEADLINES:

9/29/09 Student Travel Fellowship applications are due.

10/13/09 Registration deadline at early bird rates.

10/13/09 Poster Abstracts are due for oral presentation consideration.

10/23/09 Hotel Rooms must be reserved to receive reduced group rate.

10/31/09 Poster Abstracts are due if NOT being considered for oral presentation.

Symposium Organizing Committee:

Michael Herman, Co-Chair, Biology

Loretta Johnson, Co-Chair, Biology

Ted Morgan, Biology

Tim Todd, Plant Pathology

Kun Yan Zhu, Entomology

Lindsey Fallis, Graduate Student Rep, Biology

Doris R. Merrill, dmerrill@k-state.edu

Program Coordinator

ECOLOGICAL GENOMICS INSTITUTE

Kansas State University

Biology, 104 Ackert Hall

Manhattan, KS 66506-4901

(785) 532-3482, ecogen.ksu.edu

Ecological Genomics <dmerrill@ksu.edu>

London EvolutionaryResearchNetwork Sep14 CallForPapers

REMINDER - London Evolutionary Research Network (LERN) 7th Annual Conference 2009 - CALL FOR PAPERS

Deadline: 7 August 2009

The 7th Annual LERN Conference will be held on Monday 14th September 2009, at the Flett Lecture Theatre, Natural History Museum, London, SW7. Mark your diary now!

The LERN conference provides an opportunity for postgraduate students working on any aspect of evolution to present their work to a diverse audience. Last year's programme, available here, demonstrates the broad range of topics showcased at the conference. We welcome applications from institutions beyond London.

The conference spans a full day, with four sessions and two keynote speakers.

Talks are 15 minutes long with five minutes for questions. Posters may also be submitted. Prizes are awarded for the best talks and best poster.

Registration is free, and there will be a drinks reception after the conference.

To apply to present a talk or poster, please complete the form questions below and email to londonev@londonevolution.net <mailto:londonev@londonevolution.net> by 7 AUGUST 2009.

You should receive an email confirming receipt of your application within three days. Please send your application again if you do not!

Further information regarding the conference, including keynote speakers, publicity posters, and timetabling, will be confirmed and circulated in due course.

Please bring the conference to the attention of anyone who may be interested, and contact us for any other conference enquiries on londonev@londonevolution.net.

Name: Institution and Department: Programme and year of study: Abstract (no more than 200 words): Would you prefer to present your work as a talk or a poster?

Gillian Pepper MSc Student - Evolutionary Psychology Brunel Univsersity

Department of Psychology School of Social Sciences Brunel University Uxbridge UB8 3PH UK Mobile: 07951 295 751 Email: ht08ggp1@brunel.ac.uk Personal web page: http://www.scienceandsociety.info Science Policy UK Network: http://network.nature.com/groups/ukpolicy/forum/topics London Evolution Research Network: http://londonevolution.net/ Research and Media Network: http://researchandmedia.ning.com/profile/GillianPepper <

Manchester CommunityGenetics Jan7-8

I am pleased to announce: The 1st Community Genetics Conference "Forward from the Crossroads of Ecology and Evolution" Speaker confirmed - Dr. Marc Johnson, North Carolina State University To be held January 7-8th 2010 at The University of Manchester, Manchester, UK Sponsored by the British Ecological Society Registration £68 Bed and breakfast from £55 per night To register interest please contact: Jennifer Rowntree Jennifer.rowntree@manchester.ac.uk +44-(0)1612755108

Community genetics integrates the fields of ecology and evolution by considering the effects of intra-specific genetic variation on the wider community. The general idea is that species do not live in a stable, abiotic environment. Instead, they interact directly and indirectly with associated species in combination with the abiotic environment, causing effects that can be distinguished at a community level.

jkrowntree@mac.com

MexicoCity DNA Barcode Nov7-13 DeadlineExtended 2

Dear Colleagues,

Due to a server failure over the weekend, we are extending the deadline for abstracts and applications for travel bursaries to the Third International Barcode of Life Conference (www.dnabarcodes2009.org).

The new deadline is midnight, Washington DC time, on Friday, 7 August. We hope to send out the results of the reviews of abstracts and applications on Friday, 14 August.

To ensure that we have not lost any abstracts or travel bursary applications, we are sending messages out to everyone who has submitted an abstract or application. If you tried to submit an abstract or bursary application and you do NOT receive a confirmation email this afternoon, please go to www.dnabarcodes2009.org and resubmit. We apologize for this inconvenience.

Please direct any questions you have concerning your abstract or bursary application to abstract.dnabarcodes2009@si.edu and bol@servimed.com.mx

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 <mailto: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

"Schindel, David" <schindeld@SI.EDU>

NHM London LERN Sep14 DeadlineExtension

***** DEADLINE EXTENSION - AUGUST 28TH 2009 ******

Dear LERN members,

The call for papers for LERN's 7th annual conference is now open.

The 7th Annual LERN Conference will be held on Monday 14th September 2009, at the Flett Lecture Theatre, Natural History Museum, London, SW7. Mark your diary now!

The LERN conference provides an opportunity for postgraduate students working on any aspect of evolution to present their work to a diverse audience. We welcome applications from institutions beyond London.

The conference spans a full day, with four sessions and two keynote speakers.

Talks are 15 minutes long with five minutes for questions. Posters may also be submitted. Prizes are awarded for the best talks and best poster.

Registration is free, and there will be a drinks reception after the conference.

To apply to present a talk or poster, please complete the form questions below and email to londonev@londonevolution.net <mailto:londonev@londonevolution.net <mailto:londonev@londonevolution.net> > by 28th AUGUST 2009.

You should receive an email confirming receipt of your application within three days. Please send your application again if you do not!

Further information regarding the conference, including keynote speakers, publicity posters, and timetabling, will be confirmed and circulated in due course.

Please bring the conference to the attention of anyone who may be interested, and contact us for any other conference enquiries on londonev@ <mailto:londonev@londonevolution.net <mailto:londonev@londonevolution.net> > londonevolution.net <mailto:londonev@londonevolution.net <mailto:londonev@londonevolution.net> > .

See the website at www.londonevolution.net <javascript:void(0);/*1247568066693*/> for more details and last year's program ______

Name:

Institution and Department:

Programme and year of study:

Abstract (no more than 200 words):

Would you prefer to present your work as a talk or a poster?

Gillian Pepper MSc Student - Evolutionary Psychology Brunel Univsersity

Department of Psychology School of Social Sciences Brunel University Uxbridge UB8 3PH UK Mobile: 07951 295 751 Email: ht08ggp1@brunel.ac.uk <mailto:ht08ggp1@brunel.ac.uk> Personal web page: http://www.scienceandsociety.info < http://www.scienceandsociety.info/ > Science Policy UK Network: http://network.nature.com/groups/ukpolicy/forum/topics < http://network.nature.com/groups/ukpolicy/forum/topics > London Evolution Research Network: http://londonevolution.net/ Research and Media Network: http://researchandmedia.ning.com/profile/GillianPepper < http://researchandmedia.ning.com/profile/GillianPepper >

Gillian Pepper <ht08ggp1@brunel.ac.uk>

NHM London LERN Sep14 Register

Dear LERN members,

The 7th Annual LERN Conference will be held on Monday 14th September 2009, at the Flett Lecture Theatre, Natural History Museum, London, SW7. Mark your diary now!

The LERN conference provides an opportunity for postgraduate students working on any aspect of evolution to present their work to a diverse audience. We welcome applications from institutions beyond London.

The conference spans a full day, with four sessions and two keynote speakers.

* Refreshments will be provided free of charge and there will be a wine reception at the end of the conference.

If you would like to attend, please register by providing your name and affiliation. Registration is free and the deadline is September 13th 2009.

Kind Regards,

The LERN Committee

Gillian Pepper MSc Student - Evolutionary Psychology Brunel Univsersity

Department of Psychology School of Social Sciences Brunel University Uxbridge UB8 3PH UK Mobile: 07951 295 751 Email: ht08ggp1@brunel.ac.uk <mailto:ht08ggp1@brunel.ac.uk> Personal web page: http://www.scienceandsociety.info < http://www.scienceandsociety.info/ > Science Policy UK Network: http://network.nature.com/groups/ukpolicy/forum/topics < http://network.nature.com/groups/ukpolicy/forum/topics > London Evolution Research Network: http://londonevolution.net/ Research and Media Network: http://researchandmedia.ning.com/profile/GillianPepper < http://researchandmedia.ning.com/profile/GillianPepper >

Gillian Pepper <ht08ggp1@brunel.ac.uk>

Novosibirsk Bioinformatics Jun20-27

Dear colleagues,

The Institute of Cytology and Genetics of the Siberian Branch of the Russian Academy of Sciences will be hosting the International Conference on Bioinformatics of Genome Regulation and Structure/Systems Biology (BGRS\SB-2010) in Novosibirsk, Russia, from 20-27 June 2010. This Conference is the seventh in the series since the first BGRS event held in 1998.

As one of the key disciplines in modern biology, bioinformatics is a rapidly developing science. Consequently, each of the past BGRS events was focused on the most important topics of that time. To keep this tradition going, BGRS\SB-2010 will be centered on bioinformatics and systems biology.

Systems biology largely focuses on the study of the organization and operation of the biological systems at various levels: molecular genetic entities, cells, tissues, organs and organisms on the basis of information encoded in their genomes.

Systems biology strongly depends on high-performance experimental technologies:

* sequencing of genomic DNA, analysis of its between-population and evolutionary variation;

* study of the expression of genes and gene complexes using biochips-based modalities;

* structural and functional analysis of proteins and metabolites using mass spectrometric methods;

* study of the structural and functional organization of biological objects (macromolecules, chromosomes, cells, tissues, organs, organisms) using modern microscopic methods;

* construction of artificial molecular genetic systems using genetic engineering techniques.

In systems biology, bioinformatics methods play by far the most important role. With them, the researcher can:

* accumulate and integrate experimental information in databases;

* bring this information to computer analysis;

* perform mathematical modeling of the structural and functional organization of living systems;

* predict new properties of living systems;

* design new rounds of experimental research.

Systems biology follows in the steps of physics where no experiment or its interpretation is possible until profound theoretical and computer-aided analyses of the systems and processes being studied are made.

Consequently, BGRS\SB-2010 will have special focus on research efforts that are based on integration of experimental and computer-based/theoretical approaches.

The following are the particular studies, in which bioinformatics and systems biology meet and which are of special interest to the Conference:

* genomics;

* chromosomics;

* transcriptomics;

* proteomics;

* metabolomics;

* reconstruction and modeling of gene networks;

* cell biology;

* physiological genetics;

* developmental biology;

* evolutionary biology;

* synthetic biology;

* medical biology and pharmacology;

* biotechnology.

The results of the most recent research in these fields will be presented. The Conference program will include plenary papers, session papers and round tables. As previously, we are hoping to hear from those who wish to step down as Session Chairs and about their suggestions for the sessions they wish to chair. The Session Chairs will be offered special privileges at the Conference.

You are very welcome to participate in the 7th International Conference on Bioinformatics of Genome Regulation and Structure/Systems Biology - BGRS\SB-2010.

The Conference's official site is

< http://www.bionet.nsc.ru/meeting/bgrs2010/-index.html > http://www.bionet.nsc.ru/-meeting/bgrs2010/index.html The email address is bgrs_sb2010@bionet.nsc.ru <mailto:%20bgrs_sb2010@bionet.nsc.ru>

Best regards,

Organizing Committee BGRS\SB-2010.

bgrs_sb2010 <bgrs_sb2010@bionet.nsc.ru>

QueenMaryU Darwin in Humanities

https://eshop.qmul.ac.uk/events/-eventdetails.asp?eventidS Darwin published The Origin 150 years ago. From that point on he, and many others, have applied evolutionary theory to behaviour. And from that point on controversy has never been far away. Darwin's own work contributed to the rise of Comparative Psychology in the late nineteenth century, which in turn impacted upon Behaviourism. The 1970s saw the rise of Sociobiology, and much criticism of attempts to apply evolutionary biology to human concerns. Initially these criticisms were grounded in Marxist ideology and set limits to the remit of biological science: human properties required a different framework. More recently the humanities and social sciences have taken a similar view but with a post-modern twist, actively eschewing scientific, and especially biological understanding, and in so doing forsaking prediction. In spite of this history of ideological criticism, what might be termed the Human Evolutionary Behavioural Sciences (HEBS) have diversified into Evolutionary Psychology, Human Behavioural Ecology and Cultural Evolution, and in so doing have flourished. In this meeting we hope to showcase new and exciting work from within HEBS, and look at where efforts should be focused in the future. It is our contention that the humanities and social sciences cannot ignore the central place of evolution as a theoretical framework for understanding human affairs.

This symposium celebrates 200 years of Darwin's birth and 150 years since the publication of The Origin. It also coincides with the launch of a new undergraduate degree in Psychology at the School of Biological & Chemical Sciences (Queen Mary University of London, http://www.sbcs.qmul.ac.uk/index.html) which is underpinned by an evolutionary framework. We acknowledge the generous support of the European Human Behaviour & Evolution Association (EHBEA), The Galton Institute and the School of Biological & Chemical Sciences (QMUL).

Price: EHBEA and Galton Institute members - £20 Non-members - £25

SPEAKERS: Alex Bentley (Durham); Mhairi Gibson (Bristol); Dominic Johnson (Edinburgh); Stephen Lycett (Kent); Alex Mesoudi (QMUL); Daniel Nettle (Newcastle); Ian Penton-Voak (Bristol) and Rebecca Sear (London School of Economics).

https://eshop.qmul.ac.uk/events/-eventdetails.asp?eventidS

Alan McElligott <a.g.mcelligott@qmul.ac.uk>

Seattle SICB EvolutionMigr Jan3-7

We are sending out a call for abstracts in a session complementing our symposium, Integrative Migration Biology. This symposium will be held at the 2010 Society for Integrative and Comparative Biology (SICB) meeting, Jan. 3-7, Seattle, WA. We would especially like to extend this invitation to students and post-docs, but welcome abstracts from all researchers currently studying animal migration. As a student or post-doc, this would give you a wonderful opportunity to interact with some of the top researchers in the field of animal migration. We welcome submissions for both contributed papers and posters, and encourage students to apply for SICB's Charlotte Mangum Student Support Program. Please check out the SICB meeting page at http://-www.sicb.org/meetings/2010/index.php3 for more information.

Billions of animals migrate each year, and they can have enormous effects on the communities and ecosystems they inhabit. We wish to bring together researchers from all over the world who are attempting to integrate ecology, evolution, behavior, physiology, and theory in order to understand the phenomenon of migration. In order to migrate, organisms themselves must integrate many aspects of behavior, physiology, genetics, and morphology. Migration is therefore an excellent system in which to study adaptation and the interplay between various ecological and evolutionary levels of analysis. Traditionally, however, researchers have tended to focus on one narrow aspect of migratory behavior to the exclusion of all else. More recently, biologists have begun to examine multiple aspects of migration in order to better understand this important life history strategy. The primary goal of this symposium is to bring these researchers together with students and post-docs who are just staring their research programs in order to foster discussion and collaboration and further the development of integrative migration biology research.

This symposium and the complementary session(s) are designed to provide a venue for researchers from around the globe to discuss the past, present, and future of migration research. The list of symposium speakers and preliminary titles include:

1. Melissa Bowlin (Lund University), Isabelle-Anne Bisson (Princeton University), & Martin Wikelski (Max Planck Institute for Ornithology). “Integrative migration biology: Past, present, and an exciting future.”

2. Marilyn Ramenofsky (University of California Davis). “Endocrine and metabolic parameters coincide with daily fueling and flight cycles of captive migrants.”

3. Anders Hedenström (Lund University). “Testing migration theory: the utility of inegrative approaches using field experiments and wind tunnels”

4. Chris Guglielmo (University of Western Ontario). TBA

5. Susanne Åkesson (Lund University). “Endogenous migration programs, migratory fattening and orientation in passerine birds”.

6. Kasper Thorup (University of Copenhagen). “Understanding the migratory orientation program in birds: extending laboratory studies to studying free-flying migrants in a natural setting”.

7. Tom Kunz (Boston University). TBA

8. Nir Sapir (The Hebrew University of Jerusalem). “The effect of weather on migrating bee-eaters studied by radio-telemetry and numeric atmospheric model”

9. Judy Shamoun-Baranes (Amsterdam University). “Integrating measurements and models to study the influence of weather on migration”.

10. Peter Marra (Migratory Bird Center, Smithsonian Institution). “Seasonal interactions and carry-over effects - understanding migration in the context of the annual cycle”.

11. David Wilcove (Princeton University). TBA

Additional information will be posted on our symposium website, which can be found here: http://-sicb.org/meetings/2010/symposia/index.php3 once we have finalized some additional details. If you have questions about the symposium or the meeting, please contact us at melissabowlin at gmail dot com or ibisson at princeton dot edu.

Funding for this symposium was provided by MIGRATE, an NSF-funded Research Coordination Network, and SICB.

Note: in order to ensure that your talk or poster will be placed in the correct session, be sure to put our symposium, Integrative Migration Biology' into the field following the statement, “I would like to be in a session complementing a regular symposium” on the abstract submission form on SICB's meeting webpage.

We hope to see you in Seattle!

Isabelle-Anne Bisson, Research Associate Dept. Ecology and Evolutionary Biology Princeton University, Princeton NJ 08544 P: (609) 258-7925 F: (609) 258-7892 ibisson@princeton.edu http://-www.isabellebisson.com/ ibisson@Princeton.EDU ibisson@Princeton.EDU

UCaliforniaSanDiego Drosophila Oct29-Nov1

Annual Drosophila Species Workshop

The Ninth Annual Drosophila Species Workshop will be held October 29- November 1, 2009 at UCSD, La Jolla, California. Registration of $350 includes instruction and materials, welcome Mexican food reception, Banquet and Keynote address, and field collecting trip and lunch.

The workshop program, schedule, instructors and information for applying to attend can be found on the stock center website at https://stockcenter.ucsd.edu/info/-welcome.php Therese Ann Markow, Professor Amylin Chair in Life Sciences Section of Ecology Behavior and Evolution Division of Biological Sciences Muir Biology Building 2215 9500 Gilman Drive University of California at San Diego La Jolla, CA 92093-0116

Email: tmarkow at ucsd.edu Phone: (858) 246 0095 Laboratory: (858) 246 0402 FAX:(858) 534-7108

http://biology.ucsd.edu/labs/markow/ http://-/stockcenter.ucsd.edu Therese Markow <tmarkow@ucsd.edu>

UChicago DarwinAnniversaries Oct29-31

The University of Chicago Celebrates the Darwin Anniversaries, October 29-31, 2009

Distinguished biologists, historians, and philosophers will gather in fall of next academic year to celebrate the Darwin anniversaries at University of Chicago. For the schedule of speakers and registration go to: < http://darwin-chicago.uchicago.edu >http://darwin-chicago.uchicago.edu.

Jerry Coyne <j-coyne@uchicago.edu>

ULiverpool ParkerTribute Sep15

It is Geoff Parker's formal retirement year. To mark the auspicious occasion, we're going to have a symposium (and party) for him. The day in question is Tuesday 15th September. The place is the School of Biological Sciences, University of Liverpool. We have talks from 10am from his past collaborators, colleagues and students (list at the bottom of this email), and then for those minded to stay, a party in the evening. The day is free (and we throw in lunch and wine after, courtesy of Cell press and TREE) and is open to all. The evening reception is £20. Full details at: http://tinyurl.com/Geoffdayhomepage Please register at: http://tinyurl.com/GeoffPday (this allows us to actually cater for people for lunch and dinner, registration is absolutely essential for the evening party so we can book in advance)

For enquiries, please email g.hurst@liv.ac.uk<mailto:g.hurst@liv.ac.uk>

Greg

Speakers:

Charles Godfray (Oxford): "Selfish genes and mosquito control - applied Parkerology"

Tim Birkhead (Sheffield): "Undergraduate sex: flies and birds".

Leigh Simmons (UWA): "Sperm competition: the Parkerian paradigm"

Matt Gage (UEA): "Empirical tests of Parkerian sperm competition theory"

Nick Royle (Exeter): "Personality & parental care: Does behavioural consistency reduce sexual conflict over parental investment?"

Bill Sutherland (Cambridge): "Applying the Parker insights to conservation science"

Tommaso Pizzari (Oxford): "Chickens: the pursuit of truth and happiness".

Steve Ramm (Liverpool):"Of Mice and Molecules: Interdisciplinary Sperm Competition Games"

Kate Lessells (NIOO): "Parkerian influences, a summary"

(Prof) Greg Hurst School of Biological Sciences University of Liverpool Crown Street Liverpool L69 7ZB UK

0151 7954520 (t)

G.Hurst@liverpool.ac.uk G.Hurst@liverpool.ac.uk

UStAndrews ComparativeGenomics Aug18

Dear Evoldir,

* * * * * * * * * * * * * * *

Comparative Genomics One-day International Conference Date: 18th August 2009, 9:30 am Location: Bute Building, University of St Andrews, UK

* * * * * * * * * * * * * * *

This is a one day event - A day of exciting talks on comparative genomics from an array of international speakers.

Thousands of genome sequences are now available, and the amount of data on genomes continues to increase. This presents enormous opportunities to make discoveries of biological and medical interest, but also requires new approaches.

Confirmed speakers:

o Prof MARK BLAXTER, University of Edinburgh. “Comparative Nematode Genomics”. o Prof GEOFF BARTON, University of Dundee. “A tale of three small RNAs”. o Prof DANNIE DURAND, Carnegie Mellon University. “The Evolution of Multidomain Families”. o Prof NEIL HALL, University of Liverpool. “Fast forward Genetics using second generation sequencing”. o Dr MATTHEW HEGARTY, Aberystwyth University. “Genomic mergers: the consequences of hybridisation and polyploidy in Senecio”. o Prof IAN KORF, University of California Davis Genome Center. “Intron mediated enhancement”. o Prof ALAN ARCHIBALD FRSE, Roslin Institute. “Comparative farm animal genomics - from synteny to synergy”. o Dr ZEMIN NING, Wellcome Trust Sanger Institute. “Cancer genome assemblies and variation detection between normal and tumor human cells”. o Prof ZIHENG YANG FRS, University College London. “Population genomics and human-chimpanzee speciation”. o Prof ANDY WATERS, University of Glasgow, “Translation of Translation: Comparative genomics yields practical insights into sexual development in malaria parasites”.

More information can be found at http://www.sbforum.org/events.php?e_idp Registration details:

Early registration is encouraged. Registration fees are GBP 40; students can register for a reduced fee of GBP 20.

** Please register on-line at: http://www.sbforum.org/eregister.php?e_idp The event is preceded by a conference dinner, at a subsidized price for conference delegates. Please book in advance. http://www.sbforum.org/events.php?e_idv The conference itself is followed by a networking buffet dinner, included in the registration fee.

Poster submission:

Delegates are welcome to submit an abstract on any aspect of comparative genomics. The poster abstract deadline has been extended to Thursday 13th August.

* * * * * * * * * * * * * * *

We look forward to seeing you on Tuesday 18th August.

Best regards,

Daniel

– Daniel Barker http://bio.st-andrews.ac.uk/staff/db60.htm The University of St Andrews is a charity registered in Scotland : No SC013532

db60@st-andrews.ac.uk db60@st-andrews.ac.uk

UStAndrews ComparativeGenomics Aug18 2

Dear Evoldir,

Apologies for repetition. Some URLs got damaged in transit. I'm re-sending, with simpler URLs.

* * * * * * * * * * * * * * *

Comparative Genomics One-day International Conference Date: 18th August 2009, 9:30 am Location: Bute Building, University of St Andrews, UK

* * * * * * * * * * * * * * *

This is a one day event - A day of exciting talks on comparative genomics from an array of international speakers.

Thousands of genome sequences are now available, and the amount of data on genomes continues to increase. This presents enormous opportunities to make discoveries of biological and medical interest, but also requires new approaches.

Confirmed speakers:

o Prof MARK BLAXTER, University of Edinburgh. "Comparative Nematode Genomics". o Prof GEOFF BARTON, University of Dundee. "A tale of three small RNAs". o Prof DANNIE DURAND, Carnegie Mellon University. "The Evolution of Multidomain Families". o Prof NEIL HALL, University of Liverpool. "Fast forward Genetics using second generation sequencing". o Dr MATTHEW HEGARTY, Aberystwyth University. "Genomic mergers: the consequences of hybridisation and polyploidy in Senecio". o Prof IAN KORF, University of California Davis Genome Center. "Intron mediated enhancement". o Prof ALAN ARCHIBALD FRSE, Roslin Institute. "Comparative farm animal genomics - from synteny to synergy". o Dr ZEMIN NING, Wellcome Trust Sanger Institute. "Cancer genome assemblies and variation detection between normal and tumor human cells". o Prof ZIHENG YANG FRS, University College London. "Population genomics and human-chimpanzee speciation". o Prof ANDY WATERS, University of Glasgow, "Translation of Translation: Comparative genomics yields practical insights into sexual development in malaria parasites".

More information can be found at http://www.sbforum.org/events.php - scroll down to "Comparative Genomics one-day International Conference".

Registration details:

Early registration is encouraged. Registration fees are GBP 40; students can register for a reduced fee of GBP 20.

** Please register on-line via: http://www.sbforum.org/events.php The event is preceded by a Conference Dinner, at a subsidized price for conference delegates. Please book in advance: http://www.sbforum.org/events.php The conference itself is followed by a networking buffet dinner, included in the registration fee.

Poster submission:

Delegates are welcome to submit an abstract on any aspect of comparative genomics. The poster abstract deadline has been extended to Thursday 13th August.

* * * * * * * * * * * * * * *

We look forward to seeing you on Tuesday 18th August.

Best regards,

Daniel

– Daniel Barker http://bio.st-andrews.ac.uk/staff/db60.htm The University of St Andrews is a charity registered in Scotland : No SC013532

db60@st-andrews.ac.uk db60@st-andrews.ac.uk

GradStudentPositions

Antarctica ComparativePhylogenetics

A PhD research scholarship (includes stipend and fees) is currently available at the University of Adelaide, School of Earth and Environmental Sciences, Adelaide, South Australia. Information about the school, and in particular the Ecology and Evolutionary Biology Unit can be found at http://ees.adelaide.edu.au/disciplines/eeb/. The candidate must hold either Australian or New Zealand residency status.

Project Description: The project will contribute to an Australian Antarctic Division - funded project (AAD 2355). Specifically, the project examines comparative phylogenetic and phylogeographic data for terrestrial invertebrates (Collembola, Acari, nematodes, tardigrades and rotifers) to explore presence and distribution of cryptic species (biodiversity exploration), patterns of colonisation, and recent gene flow from Australian, New Zealand, and British Antarctic territories. Coupled with this will be a co-phylogeny of the endosymbiotic bacteria (e.g. Wolbachia, Rickettsia, Spiroplasma) that have been widely identified among invertebrates. These are likely to have either been affected by the long-term habitat fragmentation or may be of a more recent origin in the Antarctic region. The project has collaborations with the British Antarctic Survey, UK (Peter Convey and Chester Sands), Brigham Young University, US (Byron Adams), Massey and Waikato Universities, NZ (Murray Potter and Ian Hogg). Further information can be obtained from the web site [http://www.scieng.flinders.edu.au/biology/people/academic/stevens_m/], or by informal email [Mark.Stevens@samuseum.sa.gov.au].

The expected starting date is November 2009 or as soon as a suitable candidate is identified. The first Antarctic field-trip (to Davis and Mawson Bases, Australian Antarctic Territory) will be in December 2009.

Candidate Experience: Candidates for this position should have a strong interest in invertebrate systematics and evolution and demonstrate experience in molecular methods including knowledge of phylogenetic and phylogeographic analyses. A knowledge of invertebrate sampling techniques will be a benefit. Fieldwork in Antarctica is a critical component that requires passing a complete medical.

To apply: Please send a cover letter, curriculum vitae, a statement of research experience that explains your background and specific interests in the project, and names and contact information of at least two scientists available for reference.

Please email your application as a pdf or Word (.doc) document to:

Dr. Mark I. Stevens Email: Mark.Stevens@samuseum.sa.gov.au

Dr. Mark I. Stevens South Australian Museum North Terrace, Adelaide SA 5000 GPO Box 234 Science Centre, Morgan Thomas Lane (off Kintore Ave) [courier address] +61 8 82077685 0466672727 +61 8 82077222 Mark.Stevens@samuseum.sa.gov.au http://www.samuseum.sa.gov.au and

Senior Lecturer (Affiliate) University of Adelaide School of Earth and Environmental Sciences Adelaide Faculty of Sciences SA 5000 Australia http://ees.adelaide.edu.au/disciplines/eeb/ and

Honorary Academic Associate School of Biological Sciences Flinders University of South Australia Adelaide, SA 5001 Australia http://www.scieng.flinders.edu.au/biology/people/academic/stevens_m/ "Stevens, Mark (SAM)" <Mark.Stevens@samuseum.sa.gov.au>

ETH Zurich HostParasiteEvolution

ETH Zurich, Institute of Integrative Biology (IBZ) The Experimental Ecology Group (Paul Schmid-Hempel) is seeking to fill a Ph.D. Position (Evolutionary ecology of host-parasite systems) to work on questions of host-parasite interactions using Bombus spp. and theirparasites as the study system. In particular, the project would investigate the natural diversity of host species and their infections (of Crithidia bombi in particular). Our questions ultimately relate to the co-evolutionary dynamics of the host interactions with parasites, the epidemic processes in natural populations, or the spread and effect of infectious parasites in ecological communities of host species. We work with molecular tools but the project would focus on ecological questions. In particular, little is known about the occurrence, distribution and correlates of parasitism in the diverse sets of Bombus species. The project aims at gathering this knowledge and using it to test some concepts of ecological theory and host-parasite coevolution. Problems of species invasion might be a particular topic in this context. Although the prime motivation is questions of basic importance, the project is embedded in a larger set of studies conducted at ETH addressing the significance of ecological and genetic variation in natural systems with respect to disease, climatic change and environmental degradation.

The ideal candidate likes to work with this system, has an interest at the crossroads of ecology, genetics and evolution and a background in any of the relevant fields. Salaryand other conditions in accordance with local regulations. The normal duration of aPhD at ETH is 3 years. Special conditions for acceptance into the PhD program ofETH may apply; a degree equivalent to a M.Sc. is normally required. Preferred starting date autumn 2009 or shortly thereafter. Please send applications, with CV, names of referees, and short statement of your interests in this position to Prof. Paul Schmid-Hempel, preferably by email (psh@env.ethz.ch). Screening of applications will start 31 August 2009 or until post is filled. For more information, you may check our web page (www.eco.ethz.ch).

Prof. Paul Schmid-Hempel ETH Zurich Institute of Integrative Biology (IBZ) Experimental Ecology ETH-Zentrum CHN K11 CH-8091 Zurich

ph: + 41 44 633 6048 / 6033 fax: +41 44 632 1271 psh@env.ethz.ch www.eco.ethz.ch paul.schmid-hempel@env.ethz.ch paul.schmid-hempel@env.ethz.ch

---

Finland PopulationGenetics

The Finnish graduate school in population genetics

The graduate school in population genetics is funded by the Department of Education and the Academy of Finland. The school builds a doctoral program and trains graduate students in the broad area of population genetics. The students take formal courses and carry out research work and complete a doctoral thesis in about four years.

The students entering the school should join a research project led by one of the supervisors that are members of the school. The topics covered by different projects include evolutionary genetics, bioinformatics, genetic epidemiology, gene mapping, plant and animal breeding, conservation genetics, molecular anthropology and archaeology, and risks associated with GMO. The working place depends on the research group and the supervisor (http://cc.oulu.fi/~biolwww/PopGenSchool/)

The salary is set by the Department of Education which finances the graduate school, but the local university (research group) can pay a somewhat higher salary that includes some teaching duties.

The school announces seven positions for PhD students, starting at the beginning of 2010. The positions are maximally for four years. The application should include (when applicable):

1. CV 2. a list of publications 3. a training plan for PhD studies (what type of formal training, courses etc you would like to have) 4. a short description of a career plan (why this type of training) 5. a plan for PhD research (a research plan or a good description of the direction the student wants to take), max 2 pages 6. contact information of two referees

The applications should be sent (as a single document) to Outi Savolainen electronically (Outi.Savolainen@oulu.fi) or by regular mail Dept of Biology, Box 3000, FIN-90014 University of Oulu, Finland). The deadline for the applications is 15 September 2009. For additional information, please contact Outi Savolainen or directly the project leader you would like to work with.

Outi Savolainen <Outi.Savolainen@oulu.fi>

KansasStateU PlantPopgenBioinformatics

A Ph.D. graduate research assistant position is available in the laboratory of Chris Toomajian (sites.google.com/site/toomajianlab) to pursue projects in plant population genetics and functional genomics. Looking for a student with a bachelor's or master's degree in bioinformatics, biology, or a related quantitative discipline such as computational biology, computer science, or statistics. Applicants should have some computer programming experience and a working knowledge of molecular evolution or population genetics, ideally with some coursework in statistics. Prior work on a project combining these fields is advantageous. The student's projects will likely involve the statistical and population genetic analysis of DNA sequence and polymorphism data-sets. This may include collaborations with molecular biologists, bioinformaticians, and statistical geneticists. Please contact me for further information about potential projects. Research will emphasize bioinformatics. Additional wet-lab or bioinformatics components may be added depending on shared interests and funding opportunities.

The expected starting date is flexible, anywhere between January and August 2010, though earlier start dates are preferred.

To apply: For all email correspondence, please use 'Grad student recruitment' as your subject. Send a letter describing your interests and qualifications for the position, specifying how your skills match the position requirements, your CV, and contact information for 3 academic/professional references. Please include your GPA and GRE scores (if available) in your application. The selected student is expected to enroll either in the Interdepartmental Genetics program (www.oznet.ksu.edu/genetics) or the Department of Plant Pathology (www.plantpath.k-state.edu). Further information about policies and entrance requirements pertaining to university admission are found at the Kansas State University Graduate School website (www.k-state.edu/grad/). Current stipends for Ph.D. students in either program are $22,300. The KSU Department of Plant Pathology is a diverse and nurturing graduate training environment, and little or no teaching assistant duties are required for the degree. The lab also participates in K-State's Ecological Genomics Institute, a vibrant community composed of faculty, post-docs, and graduate students from a number of disciplines.

For more information contact: Chris Toomajian (785) 532-0879 or toomajia@ksu.edu

Christopher Toomajian Assistant Professor Kansas State University Department of Plant Pathology 4024 Throckmorton Plant Sciences Center Manhattan, KS 66506 office: (785) 532-0879 fax: (785) 532-5692 toomajia@ksu.edu http://sites.google.com/site/-toomajianlab/ iChat A/V: christoomajian@AIM

Chris Toomajian <toomajia@k-state.edu>

Naples EvolutionaryEcol

Positions on offer International Ph.D. Program 2009/2010

6 Ph.D. fellowships are available to carry out interdisciplinary training in Biological Sciences at the Stazione Zoologica 'Anton Dohrn' Naples Italy, under Open University (UK) supervision.

Applications are invited from suitably qualified postgraduate candidates (see details on www.szn.it)

The closing date for applications is 15 September 2009

Gabriele Procaccini

Ph.D. in Marine Ecology Group of Evolutionary Ecology of Marine Organisms (P.I.) Functional and Evolutionary Ecology Lab

Stazione Zoologica Anton Dohrn Villa Comunale 80121 - Napoli (Italy)

E-mail: gpro@szn.it Tel. ++39 081 5833363 Fax. ++39 081 7641355 http://www.szn.it/ Gabriele Procaccini <gpro@szn.it>

RuhrU DaphniaEvolutionaryGenomics

Ruhr-University Bochum/Germany

PhD position in Daphnia evolutionary genomics application deadline: 10/ Sept. 2009

A PhD position is available in the Department of Animal Ecology, Evolution and Biodiversity at the Ruhr-University of Bochum in the field of evolutionary genomics. At our department we combine traditional evolutionary and ecological biology with molecular genetic, genomic and bioinformatic approaches to address questions from molecule to ecosystem levels.

The current project focuses on the analysis of genes and pathways involved in predator-induced defences in the model crustacean Daphnia pulex. A variety of different molecular genetic and bioinformatic approaches shall be utilized to study regulatory pathways. In particular, microarray and real-time PCR analyses will be applied to identify and investigate pathways related to differential gene expression. This work will contribute to the annotation of functional regions in the Daphnia genome.

Candidates should have a diploma or MSc in Biology, Zoology or related disciplines. They should have a background in evolutionary/functional genomics, molecular biology and bioinformatics (e.g. be familiar with a script or programming language). The earliest starting date for the position is October 15th 2009. Salary: TVL E13/2. Funding is available for two years with an extension of 1 year.

For more information contact Prof. Dr. Ralph Tollrian at (tollrian@rub.de). To apply, send a CV, copies of relevant degrees, a cover letter with a short description of your research interests and email contact information for two references to the above email address. Review of applications will begin September 10th. and continue until the position is filled.

Ruhr-Universitat Bochum is committed to promoting the careers of women and therefore actively welcomes applications from female candidates. As an equal opportunities employer, we also encourage applications from suitably qualified disabled candidates and other groups.

Prof Ralph Tollrian Ruhr-Universitat Bochum Evolutionsokologie und Biodiversitat der Tiere Universitatsstr. 150 /Gebaude ND05 D-44780 Bochum phone: +49 (0)234-3224998; 3224563 fax: +49 (0)234-3214114 email: tollrian@rub.de

Ralph Tollrian <tollrian@rub.de>

TexasTechU PlantPopulationGenetics

A Ph.D. Graduate Research Assistant position is available in the Department of Plant and Soil Science at Texas Tech University to investigate plant molecular ecology, field ecology, and/or microbial molecular ecology. The research program focuses on molecular and field ecology of natural populations of orchids and their fungal associates.

REQUIREMENTS

1. An M.S. degree in an ecology-based discipline in Plant or Biological Sciences, or a closely related field.

2. Background in techniques and data analysis methods in molecular biology, i.e., DNA extraction, selecting suitable markers, PCR, molecular data analyses, sequencing, constructing and interpreting phylogenies, etc., for application toward plant population genetics and mycorrhizal diversity studies.

3. A fellowship award is possible for American citizens or green card holders if the application is processed and accepted in time for Spring 2010 as start date.

SALARY and BENEFITS

Competitive salary. Varies with status (i.e., assistantship vs. fellowship).

APPLICATION Please submit:

1. Letter of application describing interests and qualifications. The applicant should specifically address how their skills match the position description and requirements;

1. Curriculum Vitae; and

1. Names, complete address, phone, and e-mail information for at least three references to:

Dr. Jyotsna Sharma Department of Plant and Soil Science Texas Tech University PO Box 42122; Lubbock, TX 79409 jyotsna.sharma@ttu.edu<mailto:jyotsna.sharma@ttu.edu>

“Sharma, Jyotsna” <jyotsna.sharma@ttu.edu>

UAlgarve Bioinformatics

GRADUATE AND POSTDOCTORAL PROPOSALS* Selection of candidates for a grant proposal to submit to the Portuguese Foundation for Science and Technology (FCT).

The Centre for Marine Science (CCMAR - http://-ccmar.ualg.pt/) at the University of the Algarve, Portugal (http://www.ualg.pt) seeks Ph.D. or Postdoctoral candidates for the implementation of bioinformatic tools to analyse high-throughput transcriptomic data generated by next generation sequencing platforms (Roche/Illumina/Solexa). The experimental data will be derived from Polar eukaryotic phytoplankton communities dominated by diatoms, and the colonial algae Phaeocystis from the Southern and Arctic Oceans. Examples of the questions we seek to answer involve comparisons of community transcriptional profiles from different oceanographic regions, the effects of UVR, and responses of communities to predicted global change scenarios.

Applicants should hold a Ph.D. or M.Sc. in biology or bioinformatics, and have a good publication record in the field. The successful applicant will have a working knowledge of relational databasing, a cross-platfrom scripting language (Python/Perl/Java), and new generation sequencing analysis methods and tools. The successful applicant will also have the opportunity to become involved in molecular biology projects investigating transcriptional responses, molecular phylogenetics, and other areas of phytoplankton research in a new and dynamic group at CCMAR.

A postdoctoral position (open to all nationalities) would be available for a minimum of 3 years with the researcher receiving an untaxed salary of 1495 euros/month. A Ph.D. candidate position (Portuguese nationals only) would be available for 4 years with standard a FCT stipend. The prospective start date for postdoctoral and Ph.D. positions is January 2010.

Applications should be submitted before 20th August 2009 to Gareth Pearson (gpearson@ualg.pt) or Cymon

J. Cox (cymon@ualg.pt). Applicants should send a covering letter detailing their research interests, a current C.V., and the email addresses for 3 professional referees. Informal enquires are welcome to the same address.

CCMAR is located on the Gambelas campus, 4km from Faro, the captial city of the Algarve and close to Faro International Airport (FAO). (http://www.ualg.pt/index.php?option=com_google_maps&Itemid#11&lang=en)

(* all Ph.D. and postdoctoral positions must be proposed to and approved by the Portuguese Foundation for Science and Technology)

Gareth Pearson (Research Associate) MAREE-Marine Ecology and Evolution (http://ccmar.ualg.pt/maree/-) CCMAR - Centre of Marine Sciences, and CIMAR -Laboratório Associado Faculdade de Ciências do Mar e Ambiente, Universidade do Algarve

Mailing address: F.C.M.A., Univ. Algarve, Gambelas, 8005-139 Faro, Portugal Fax: +351 289 800 069 Phone: +351 289 800 928 E-mail: gpearson@ualg.pt

gpearson@ualg.pt

UColorado 2 EvolutionaryDynamics

The newly formed Safran Lab in the Department of Ecology and Evolutionary Biology, University of Colorado, Boulder is seeking to admit 2 - 3 highly motivated Ph.D. students for the Fall 2010. We are an integrative group of researchers with collaborative projects centered on ecological and evolutionary dynamics related to sexual selection, the interactions between morphological-physiological-behavioral variation, and relationships between within- and among-population dynamics. Students receive full Departmental funding via teaching assistantships, with other potential funding sources currently pending. Students may pursue independent research in related topics or develop their own projects within the framework of current international research on Holarctic-distributed barn swallows. Projects in our lab center on both field-based experiments and lab-based analyses (antioxidants, hormones, DNA). For more information, please contact Becca at: rebecca.safran@colorado.edu and check out our lab web page http://www.colorado.edu/-eeb/facultysites/safran/Home.html . With 12 new faculty members in the Department of Ecology and Evolution at the University of Colorado in Boulder, we are an exciting place for enthusiastic and dedicated graduate students!

–

Rebecca J. Safran Assistant Professor Department of Ecology and Evolutionary Biology N395 Ramaley Hall University of Colorado, Boulder UCB 334 Boulder, Colorado 80309 Phone: 303-735-1495 E-mail: rebecca.safran@colorado.edu http://www.colorado.edu/-eeb/facultysites/safran/Home.html Rebecca J Safran <Rebecca.Safran@Colorado.EDU>

UExeter SystemsBiol

A PhD studentship is available to study response dynamics and evolution in signalling networks regulating bacterial chemotaxis. Details of the project and how to apply can be found at:

http://biosciences.exeter.ac.uk/postgraduate/phd/-studentships/responsedynamics/ This studentship will be based at the Streatham Campus, Exeter and is open to international applicants as well as UK/EU applicants.

Best Regards,

Orkun S. Soyer, PhD Lecturer in Systems Biology Engineering, Mathematics and Physical Sciences University of Exeter http://people.exeter.ac.uk/oss203/ “Soyer, O.S” <O.S.Soyer@exeter.ac.uk>

UFreiburg ReproductiveIsolation

Ph.D. positions in Evolutionary Biology

University of Freiburg, Germany

Dept. of Evolutionary Biology and Animal Ecology

Application deadline:

30. September 2009

Start of the position

Between 1.11. 2009 and 1.1. 2010

A PhD position (BAT IIa/E 13 (50%) ˜ 1100) is available within the research group of PD Dr. H. Martin Schaefer at the University of Freiburg. The project will focus on the contemporary evolution of reproductive isolation among blackcap populations (Sylvia atricapilla) that differ in migratory orientation. The project will investigate the rapid evolution of isolating barriers in sympatry, hybrid-speciation and compare different models that analyse speciation with ongoing gene flow. The project will be carried out in close collaboration with Dr. Segelbacher, Department of wildlife ecology, University of Freiburg. Field work will take place in southern Germany (for more information, see http://www.biologie.uni-freiburg.de/data/bio1/schaefer/index.html).

To study genetic and ecomorphological adaptations the Ph.D. candidate will capture blackcaps upon spring arrival on the breeding grounds and before departure in autumn at different sites in southern Germany. The PhD project includes independent field work, genetic analyses in the lab (nuclear markers and candidate genes) as well as modelling the evolution of population divergence. In addition to the data gathered throughout the project a dataset of >600 birds from the last years is available for analysing the contemporary evolution of reproductive isolation.

The successful candidate should have a strong background in evolutionary biology, behavioural ecology, genetics and advanced statistical analyses. Further experience in working with birds will be beneficial. A Diplom/M.Sc. degree in Biology or a related subject will be required. A driving licence and the availability of an own car would be useful for getting to field sites. We expect the candidate to have good communication skills and the ability to work independently as well as in a team. Application should include a cover letter, C.V., list of publications, a statement of research interests, a copy of the last degree, and names and email-addresses of two references within a single PDF. The closing date for applications will be 30. September 2009. Applications in English or German are sent preferentially by e-mail. We especially encourage women to apply. Physically handicapped persons will be given preference in case of equal qualifications. Interviews will be held in mid-October.

PD Dr. H. Martin Schaefer Dept. of Animal Ecology and Evolutionary Biology Faculty of Biology University of Freiburg 79104 Freiburg Germany Tel: ++49-761 203 2531 Fax ++49 761 203 2544 http://www.biologie.uni-freiburg.de/data/bio1/schaefer/

Martin Schaefer <martin.schaefer@biologie.uni-freiburg.de>

UIllinois DiseaseEvolution

The National Institute of Allergy & Infectious Diseases (NIAID), Division of Intramural Research (DIR), Laboratory of Clinical Infectious Diseases (LCID) is seeking an outstanding Bioinformatician to participate in clinical and translational infectious diseases research.

The LCID conducts clinical and basic studies of human infectious and immunologic diseases, with a focus on the comprehensive understanding of and management of patients and their diseases. The major theme of the LCID continues to be the pathogenesis, pathophysiology, treatment and prevention of infectious diseases.

The LCID seeks a Master's level Bioinformatician to fill a technical support position. Projects will include clinical genomics studies correlating patient outcome with genomic plasticity and will study the role of copy number variation, single nuclear polymorphisms and transcriptional signatures of humans as well as fungal pathogens. The ideal candidate has demonstrated experience in computer programming and high dimensional data analysis. As a technician, you will be responsible for organizing and coordinating study specimen preparation and analysis of data in collaboration with statistical geneticist collaborators. Individuals desiring to pursue advanced studies including a PhD are encouraged and flexible work schedules and independent projects are available to facilitate such advanced studies. Salary is dependent on qualifications and experience.

Interested candidates may contact Dr. John E. Bennett JBENNETT@niaid.nih.gov or Dr. Steven M. Holland at smh@nih.gov for additional information about the position. To apply for the position, candidates must submit a curriculum vitae, bibliography, three letters of reference, a detailed statement of research interests, and up to 3 selected reprints to: Steven M. Holland, LCID/DIR/NIAID, c/o Ericka Thomas, 9000 Rockville Pike, Bldg 10, Room 11N234, MSC 1888, Bethesda, MD 20892-1888 by November 15, 2009.

Peter R. Williamson, MD/PhD Professor of Medicine, Pathology, Microbiology and Immunology University of Illinois at Chicago School of Medicine Section of Infectious Diseases Rm 888, Bld 910, m/c 735 808 S. Wood St. Chicago, IL 60612 tel: (312) 996-6070 fax: (312) 413-1657

Peter Williamson <prw@uic.edu>

ULausanne EvolutionaryGenomics

PHD IN FUNCTIONAL EVOLUTIONARY GENOMICS

Center for Integrative Genomics, University of Lausanne, Switzerland

A PhD student position (~4 years) is available in the evolutionary genomics group of Henrik Kaessmann in the framework of major new projects funded by the European Research Council.

We are seeking talented and highly motivated applicants (preferably with some experience/background in molecular evolution), who have strong programming skills (or the willingness and drive to acquire them) and an interest in evolutionary genome analyses using bioinformatics approaches. A MSc degree or equivalent is required.

Our group has been interested in a range of topics related to the functional evolution of genomes from primates (e.g., emergence of new genes and their functions) and other mammals (e.g., the origin and evolution of mammalian sex chromosomes). In the framework of a new major line of projects funded by the European Research Council, a large amount of qualitative and quantitative transcriptome data will be produced for a unique collection of tissues from representative mammals by the wet lab unit of the group using next generation sequencing technologies (RNA-Seq). The PhD student will perform integrated evolutionary/bioinformatics analyses based on these data and available mammalian genomes. The specific project will be developed together with the candidate.

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

For more information on the group and our institute more generally, please refer to our website: http://www.unil.ch/cig/page7858_en.html Please submit a CV, statement of research interest, and names of three references to: Henrik Kaessmann (Henrik.Kaessmann@unil.ch).

– Henrik Kaessmann, Ph.D. Associate Professor Center for Integrative Genomics University of Lausanne, Switzerland E-mail: Henrik.Kaessmann@unil.ch Phone: +41 (0)21 692 3960

Some recent publications from the lab:

Henrichsen, C., Vinckenbosch, N., Zöllner, S., Chaignat, E., Pradervand, S., Frédéric Schütz, Ruedi, M., *Kaessmann, H. and *Reymond, A. (2009) Segmental copy number variation shapes tissue transcriptomes. Nature Genet. 41: 429-9.

Potrzebowski, L., Vinckenbosch, N., Marques, A. C., Chalmel, F., Jegou, B. & Kaessmann, H. (2008) Chromosomal Gene Movements Reflect the Recent Origin and Biology of Therian Sex Chromosomes. PLoS Biol. 6: e80.

Brawand, D., Wahli, W. & Kaessmann, H. (2008) Loss of egg yolk genes in mammals and the origin of lactation and placentation. PLoS Biol. 6: e63.

Rosso, L., Marques, A. C., Weier, M., Lambert, N., Lambot, M.-A., Vanderhaeghen, P. & Kaessmann, H. (2008) Birth and Rapid Subcellular Adaptation of a Hominoid-Specific CDC14 Protein. PLoS Biol. 6: e140.

Vinckenbosch, N., Dupanloup, I. & Kaessmann, H. (2006) Evolutionary fate of retroposed gene copies in the human genome. Proc. Natl. Acad. Sci. U. S. A. 103: 3220-3225.

Marques, A., Dupanloup, I., Vinckenbosch, N., Reymond, A. & Kaessmann, H. (2005) Emergence of young human genes after a burst of retroposition in primates. PLoS Biol. 3: e357.

Burki, F. & Kaessmann, H. (2004) Birth and adaptive evolution of a hominoid gene supporting high neurotransmitter flux. Nature Genet. 10: 1061-1063.

Henrik.Kaessmann@unil.ch Henrik.Kaessmann@unil.ch

UMassachusetts Lowell CaribbeanBarcodes

A PhD graduate research position is available in the laboratory of Dr. Rick Hochberg, Department of Biology, University of Massachusetts Lowell, starting in January 2010.

Description: The PhD student will contribute to an NSF-funded project that focuses on the biodiversity of Caribbean meiofauna. Specifically, the student will obtain molecular barcodes (COI) to gain estimates of species richness and cryptic diversity in marine Gastrotricha - a phylum of microscopic invertebrates that are abundant in coastal sediments. In particular, the genus Tetranchyroderma contains some of the most geographically widespread and morphologically diverse marine gastrotrichs. Most morphospecies are easily identified by the structure of their cuticle, providing a unique opportunty to correlate taxonomic characters with individual DNA tags. The specific objectives of the doctoral research are to 1) generate mitochondrial COI sequences for the development of DNA barcodes of Tetranchyroderma; 2) determine if molecular operational taxonomic units (MOTUs) are concordant with the morphospecies concept for Tetranchyroderma, i.e., mtDNA and morphological monophyly are supported, and 3) assist in the development of a database of haplotypes with links to digital vouchers and GPS information.

The expected starting date is January, 2010 (spring semester). The first Caribbean trip will be in June or July, 2010.

Candidate Experience: Candidates for this position should have a strong interest in invertebrate systematics and evolution and demonstrate experience in molecular methods including knowledge of bioinformatics. SCUBA certification is beneficial but not required. Fieldwork on select Caribbean islands will occur for 2-3 weeks every summer for three years beginning in 2010; a US passport is necessary. Fluency in Spanish is extremely valuable.

To apply: The selected student is expected to enroll in either the 1) University of Massachusetts School of Marine Sciences (http://www.umassmarine.net/-admissions/) or the Department of Biological Sciences at the University of Massachusetts Lowell (http://www.uml.edu/College/arts_sciences/Biology/-Programs_of_Study/graduate.html) The candidate will have the option of obtaining a PhD in Marine Science and Technology (University of Massachusetts) or Biochemistry (UML), respectively, depending on his/her academic interests. Additional information about policies and entrance requirements pertaining to university admission are found at: http://www.uml.edu/grad/ Opportunities for teaching at the undergraduate level are available (as teaching assistantships). Current stipends for Ph.D. research graduate students are $20,000.

Please send a cover letter, curriculum vitae, a statement of research experience that explains your background and specific interests in the project, and names and contact information of at least two scientists available for reference.

Please send your application as a pdf or Word (.doc) document to: Dr. Rick Hochberg University of Massachusetts Lowell Department of Biological Sciences One University Avenue Lowell, MA 01854 USA Phone: 978.934.2885 EMail: rick_hochberg@uml.edu

rick_hochberg@uml.edu

UNewSouthWales Biodiversity

PhD or M Phil Positions in Genes, Maths & Biodiversity

A/Prof W Sherwin Evolution & Ecology Research Centre, BEES, UNSW, Sydney AUSTRALIA. http://www.bees.unsw.edu.au/school/staff/sherwin/-sherwinresearch.html

These projects integrate mathematical and biological expertise, at an exciting time when biologists are increasingly realizing the power of mathematics to make forecasts, as other scientists have done before them. The projects centre on making forecasts for management of biodiversity.

Project 1: Forecasting demography of bottlenose dolphins With partners from Murdoch University we are studying ecology, threats, and genetics of Bunbury (WA) bottlenose dolphins. The PhD student at UNSW will use these data in existing or novel programs, to evaluate population viability with different management and threats. There would be field-trips to Bunbury.

Project 2: Mathematics of forecasting and managing biodiversity. We have used information theory to produce new biodiversity theory (Molecular Ecology 15:2857). The PhD would further develop this theory and apply it to a wide range of existing datasets in genetic and community biodiversity.

Project 3: Resilience of small populations to periods of selection A consortium of mathematicians and biologists at UNSW has produced new theory about the way that small endangered populations might rapidly recover their responsiveness to selection. This PhD position will follow up this theoretical work by carrying out experiments in model populations of flies. There could be an additional stipend supplement for this project.

Project 4: Conservation of Little Penguins in New South Wales: With Dr J Sinclair. To assess the viability of an endangered population of Little Penguins in Sydney Harbour under a range of threats and management strategies, by conducting a genetic and demographic analysis on NSW penguin populations to input into a population forecasting model. There could be an additional stipend supplement for this project.

Other projects: It is possible to negotiate other projects in this general area of research. Note that projects which are theoretical or use existing data in Sherwin's group, are much quicker to start because they can commence without application for external funding of research expenses!

PROCEDURE: (1) DISCUSS: Email letter with CV, academic record, and details of two academic referees, to A/Prof Bill Sherwin (W.Sherwin@unsw.edu.au). For further information phone: +61-2-9385-2119.

(2) PhD M/Phil CANDIDACY APPLICATION: Requirements for PhD are BSc (Hons 1), MSc, or equivalent. For MPhil, requirement is BSc. Degree should be in maths, physics, computing, molecular sciences, population genetics or ecology. Solid research and communication skills. Full NSW driver license desirable. For exact timing and details http://www.grs.unsw.edu.au/

(3a) PhD SCHOLARSHIP APPLICATION - LOCAL: Citizens or permanent residents of Australia/NZ, apply for APA and UPA at UNSW. Applications due Sep/Oct, for study commencing in First Session in the following year. For exact timing and details see http://www.grs.unsw.edu.au/scholarships/local.html (3b) PhD SCHOLARSHIP APPLICATION - INTERNATIONAL: NON-citizens or permanent residents of Australia/NZ, apply for IPRS and UIPA at UNSW. Applications are due Aug, for study commencing in First Session in the following year. For exact timing and details see http://www.grs.unsw.edu.au/scholarships/internationalschols.html (3c) M Phil SCHOLARSHIP APPLICATION. Local and international students can apply for a $4000 stipend form the EERC, UNSW. International students can apply for a tuition fee waiver scholarship, provided that they can formally guarantee the remainder of their own stipend http://www.grs.unsw.edu.au/scholarships/internationalschols.html http://www.eerc.unsw.edu.au/GradProgram.html

Associate Professor WB Sherwin

Co-coordinator, Genetics Plan

Evolution & Ecology Research Centre

Deputy Head of School, Biological Earth and Environmental Science, University of New South Wales, Sydney NSW 2052 Australia

W.Sherwin@unsw.edu.au

PH:61-2-9385-2119 FX: 61-2-9385-1558 < http://www.bees.unsw.edu.au/school/staff/sherwin/sherwinwilliam.html > http://www.bees.unsw.edu.au/school/staff/sherwin/sherwinwilliam.html CRICOS provider code 00098G

w.sherwin@unsw.edu.au

— / —

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

---

UTuebingen AncientMycobacterium

PhD position in Ancient Mycobacterium tuberculosis genome project

We are seeking a PhD candidate with research experience in the areas of Molecular Biology, Genetics and Egyptology. The graduate student will be working on the main research theme in Identification of Bacterial and Protozoan DNAin Mummies. We offer a stimulating research environment in a lively and social institute in Tuebingen at the Institute for Tropical Medicine with active interaction with several other research groups. Previous experience with Ancient DNAwill be an advantage but not a prerequisite. The proposed start date will be from 1st Sep. The graduate student will be paid a stipend of 1000 Euros per month.

Interested candidates, please write to Prof. Dr.Juergen Kun (juergen.kun@uni-tuebingen.de) Institute for Tropical Medicine Universityof Tuebingen Wilhelmstr. 27 72074 Tuebingen

Dr.Velavan TP Institute for Tropical Medicine Wilhelmstr 27 72074 Tuebingen Germany Office:+49-7071-2982195 Mobile : +49-176-24199950 Email: velavanp@yahoo.com

Velavan <velavanp@yahoo.com>

UTurku 9 BiologicalInteractions

Biological interactions graduate school announces 9 new PhD-positions

The Biological Interactions Graduate School (BIOINT) is a national graduate school in Finland which includes representatives from 11 different universities and research institutes. The participants in the graduate school excel in basic research in areas of evolutionary biology, genetics, molecular biology, physiology, ecology and their applications. The aim of the school is especially to train graduates with multidisciplinary expertise spanning traditional fields in the biological and environmental sciences, as well as to encourage application of the obtained knowledge for solving local and global environmental problems. Three Centers of Excellences (CoE in Evolutionary research, Jyväskylä), CoE in Evolutionary genetics and physiology (Turku and Helsinki) and CoE in Virology (Helsinki and Jyväskylä) offer their excellent working environments to the benefit of the school.

BIOINT is accepting applications for 5 four-year and 4 two-year graduate student positions, as well as from project leaders with projects suitable for PhD students in the graduate school.

More information about the school and the application procedure can be found at http://www.sci.utu.fi/biovuo/en/ First round applications should be sent to Thomas Lilley by email (tmlill@utu.fi) or mail (Laboratory of Animal Physiology, Department of Biology, 20014 University of Turku) by 15.9.2009.

Thomas Lilley Coordinator

Masters Degree Programme in Environmental Sciences (or) Biological Interactions Graduate School Department of Biology Laboratory of Animal Physiology FI-20014 University of Turku FINLAND

tel. +358 2 333 5787 fax. +358 2 333 6575 e-mail: tmlill@utu.fi www.sci.utu.fi/envsci/ www.sci.utu.fi/biovuo/ Thomas Lilley <tmlill@utu.fi>

Jobs

Bonn Germany ArthropodEvolution

The Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Bonn (< http://www.zfmk.de/ > http://www.zfmk.de), seeks to fill the position of a researcher in the Department of Arthropods (succession of Dr. M. Schmitt). We anticipate that funds will be available by December 2009. We look for a PhD scientist who has his/her focus on systematics of insects and has a substantial publication record in taxonomic, phylogenetic and other biosystematic research. We expect him/her to work in these fields from a sound theoretical basis and to be able to apply an array of appropriate modern methods. He/she should be able to combine collection-based work with modern phylogenetic and/or ecological approaches. We also expect him/her to integrate into ongoing research projects and teaching programmes of the University of Bonn and to be successful in acquiring external funding.

The successful candidate will be active in research projects and as curator will have the responsibility for the substantial collections of Coleoptera housed in the ZFMK. He/she will also be involved in the self-administration of the institute and eventually will head the arthropod department.

Initially, the successful candidate can be employed for a period of five years. Pending on his/her performance during this time, the candidate may obtain subsequent tenure. According to German law, applications by women and by disabled scientists will be given priority in case of superior or equal qualification. Depending on occupational qualification and experience salary corresponds to grade TV-L/13 - 15 in the German Public Service scheme.

ZFMK is a fellow institute of the Wissenschaftsgemeinschaft Gottfried Wilhelm Leibniz (WGL: = Science Community G.W. Leibniz) and works in close cooperation with the University of Bonn. It holds internationally important scientific collections, libraries, a scanning electron microscope, and bioacoustic, histological and molecular laboratories.

Interested applicants should send a CV, a complete publication record, a comment on teaching experience and research funding, certificates for university degrees and selected publications in hard copy to the following address:

Prof. Dr. J.W. Wägele, Director, Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, D-53113 Bonn, Germany, by September 15. E-mail inquiries: < <mailto:w.waegele.zfmk@uni-bonn.de> w.waegele.zfmk@uni-bonn.de>.

Prof. Dr. J. Wolfgang Waegele Direktor Zoologisches Forschungsmuseum Alexander Koenig und Lehrstuhl für Spezielle Zoologie Rheinische Friedrich-Wilhelms-Universität Bonn Adenauerallee 160 53113 Bonn, Germany

w.waegele.zfmk@uni-bonn.de Tel.: 0049 (0) 228 9122 200 Fax: 0049 (0) 2289122 202 < http://www.zfmk.de > http://www.zfmk.de

Werden Sie Mitglied der Alexander Koenig Gesellschaft! (http://www.zfmk.de/web/Foerderer/-Freunde/index.de.html)

“W. Waegele” <w.waegele.zfmk@uni-bonn.de>

BowdoinCollege 1semester

The Bowdoin College Biology Department seeks applicants for a one semester visiting faculty position at the assistant professor level, with expertise in evolution. The visiting faculty member will teach a course in evolution, including a weekly laboratory, along with a lab instructor.

Review of applications will begin September 30, 2009. Bowdoin College is now accepting electronic submissions. Please visit https://careers.bowdoin.edu to submit letter of application, curriculum vitae, statement of teaching and research interests and expertise and the names of three references who will provide letters of recommendation.

A highly selective liberal arts college on the Maine coast with a diverse student body made up of 28% students of color, 3% International students and approximately 15% first generation college students, Bowdoin College is committed to equality and diversity and is an equal opportunity employer. We encourage inquiries from candidates who will enrich and contribute to the cultural, socio-economic, and ethnic diversity of our college. Bowdoin College does not discriminate on the basis of age, race, creed, color, religion, marital status, gender, sexual orientation, veteran status, national origin, or disability status in employment, or in our education programs. Please visit http://www.bowdoin.edu for further information.

mpalopol@bowdoin.edu mpalopol@bowdoin.edu

BritishAntarcticSurvey Phylogeneticist

Full details: http://www.antarctica.ac.uk/-employment/vacancies/job.php?JobID=3D460 The British Antarctic Survey (BAS), part of the Natural Environment Research Council, aims to undertake a world-class programme of scientific research, and to sustain for the UK an active and influential regional presence and a leadership role in Antarctic affairs.

This role requires contribution to understanding of the biodiversity and biological evolution of Antarctica and the Southern Ocean by carrying out phylogenetic and population genetic analysis within the Evolutionary History of the Polar Regions workpackage. Also, to carry out molecular laboratory work including extraction, amplification and sequencing of DNA.In addition, the candidate will need to carry out a full range of cladistic analytical techniques and interpretation. The job will provide important phylogenetic input a multidisciplinary study of the controls of evolutionary processes in the polar regions.

Qualifications: PhD in molecular biology, cladistic studies or equivalent experience.

Duration: Open-ended

Salary: Salary will be in the range of £26,180 to £29,410 per annum, pro-rata. We offer a generous benefits package including a final salary pension scheme, free car parking, flexible working hours and 30 days annual leave.

On-line application forms and further information are available on our website at www.antarctica.ac.uk/-employment These are also available from the Personnel Section, British Antarctic Survey, High Cross, Madingley Road, Cambridge, CB3 0ET. Tel: (01223) 221508.

Please quote reference: BAS 44/09 Closing date for receipt of application forms is 6th September 2009 Interviews are scheduled to be held 1 October 2009.

chester.sands@gmail.com

EdinburghU ResAssoc SwordtailEvolution

RA position in evolutionary/behavioural genetics Institute of Evolutionary Biology, Edinburgh University

A Research Associate is sought to work on a project studying the genetics of behavioural interactions in green swordtails (Xiphophorus helleri). The successful candidate will assist in the establishment and day to day management, of fish population. You will be involved in collecting data from trials of fish behaviour and some microsatellite genotyping. A strong interest in Evolutionary Biology and/or animal behaviour is essential and the ideal candidate will have completed an undergraduate degree relevant to these fields. Experience in animal husbandry (particularly with fish) and molecular techniques would be advantageous but is not essential as full training will be given. The job is initially for a 2 year period with possible extensions up to 5 years.

More information and full details of application procedures are available at http://-www.jobs.ed.ac.uk/vacancies/index.cfm?fuseaction=-vacancies.detail&vacancy_ref=3011324 For informal inquiries e-mail Alastair.Wilson@ed.ac.uk

Alastair.Wilson@ed.ac.uk Alastair.Wilson@ed.ac.uk

FloridaStateU LabTech AmphibianPhylogenetics

Scientific Aide / Laboratory Technician Amphibian Phylogenetics, Phylogeography, and Genomics Florida State University

Genomic technologies are emerging which will allow sequencing and genotyping of amphibian species on an unprecedented scale. A scientific aide / laboratory technician position is available in the Moriarty Lemmon Lab, where current and next-generation sequencing technologies are used to elucidate the phylogenetic relationships and biogeographic patterns of amphibians and to understand the genetic basis of reproductive behaviors in frogs.

The Scientific Aide will assist the principal investigator and laboratory personnel in performing molecular research on empirical projects and in developing technical advances for genomic applications. In addition he/she will provide technical and administrative support for running the laboratory.

Minimum qualifications include a bachelor's degree in Biology, a related field, or equivalent combination of education and/or experience. Demonstrated laboratory experience is also necessary. Additional desirable qualifications include a master's degree and experience in molecular biology. Salary will be $26,000 - $30,000 plus benefits. Starting date flexible, although September-October 2009 preferred.

Please direct inquiries to by 20 August 2009 to Dr. Emily Moriarty Lemmon at chorusfrog@bio.fsu.edu http://www.bio.fsu.edu/chorusfrog/index.html , including a cover letter and CV. Interviewing will begin after this date. Three letters of recommendation will later be requested from promising candidates.

Emily Moriarty Lemmon Department of Biological Science Florida State University 319 Stadium Drive, P.O. Box 3064295 Tallahassee, FL 32306-4295 Phone: 850-645-9170 http://www.bio.fsu.edu/chorusfrog/index.html http://www.bio.fsu.edu/faculty-moriarty-lemmon.php Chorusfrog@bio.fsu.edu Chorusfrog@bio.fsu.edu

GeorgetownU EEB LabAssistantProfessor

Dear Colleagues,

The Department of Biology of Georgetown University invites applications for a full-time Laboratory Assistant Professor with a flexible start date during the Fall semester of 2009.

We seek an enthusiastic science educator to actively collaborate with faculty in the development and deployment of our ecology, evolution and behavior (EEB) curriculum. We especially encourage applications from science educators able to develop and offer inquiry-based, active learning pedagogy. The successful candidate will have primary responsibility for the laboratory component, and contribute to lecture activities, of one semester of Foundations in Biology (BIOL 104). Duties in the alternate semester are to provide laboratory and instructional support to upper-level undergraduate EEB courses. Applicants should have enthusiasm for science education and a PhD in biology with an emphasis in EEB or a Masters degree in science and/or science education.

Applicants should possess excellent writing and speaking skills; be well organized and able to carry out position duties independently; have the ability to provide individual and group instruction with an awareness of diverse learning styles; be able to train and manage undergraduate and graduate TAs; and be able to teach effectively in lecture, field and laboratory contexts. This is a nine month position with the possibility to teach in our summer school for additional compensation. Applicants should send a brief cover letter summarizing their qualifications, a curriculum vitae, and names and contact information of three references.

Learn more about the Department of Biology at http:// biology.georgetown.edu.

Applications should be mailed to Laboratory Assistant Professor Search, Department of Biology, P.O. Box 571229, Georgetown University, Washington, DC 20057-1229 or sent via email as pdf files to Mr. Jamie Kidder (jmk245@georgetown.edu). Potential applicants can contact Dr. Matthew B. Hamilton (hamiltm1@georgetown.edu) with questions. Review of applications will begin August 31, 2009 and continue until the position is filled.

Georgetown University is committed to workplace diversity as an Affirmative-Action, Equal-Opportunity Employer.

hamiltm1@georgetown.edu

GeorgiaTech Teaching

Biology Teaching Faculty in Ecology and Molecular Cellular Biology

The School of Biology at Georgia Tech seeks two broadly-trained PhDs in Biology for full-time positions beginning in January 2010. Candidates should have experience teaching undergraduate biology courses and an interest in innovative instruction in the undergraduate curriculum. One position will require expertise in some combination of ecology, mathematical modeling, and biostatistics. In addition to teaching 2 full courses per semester and contributing to curriculum innovation, this academic professional will also be responsible for academic advising of undergraduate biology majors. The other position will involve teaching, lab development, and supervision of teaching assistants in freshman biology courses, and will require expertise in at least one of: molecular biology, cell biology, microbiology, genetics, plant or animal physiology. This academic professional may also teach upper-level biology courses dependent upon their expertise, but their primary responsibility will be towards student success in the freshman biology program.

Salary will be commensurate with experience and qualifications. These 12-month positions are non-tenure track. The application should include a curriculum vitae, a statement of teaching philosophy and summary of experiences sent to: aps@biology.gatech.edu. Review of applications will begin immediately and continue until both positions are filled. Georgia Tech is an affirmative action, equal opportunity employer and requires compliance with the Immigration Control and Reform Act of 1986. http://www.biology.gatech.edu Michael A D Goodisman

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

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

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

LeicesterU ResTech

Research Technician

Department of Genetics, University of Leicester

Salary Grade 5 - £19,645 to £23,449 p.a. Fixed Term Contract available immediately until 31st July 2014

Ref: MBP00029

Sex, genomes, history: molecular, evolutionary and cultural effects on human genetic diversity

A research technician post is available as part of a Wellcome-Trust- funded project to investigate the long- and short-term evolution of sequences on the sex chromosomes, the effects of sex-specific population processes, and the implications for understanding human population histories. Experience of molecular biology techniques, especially PCR is essential as well as experience of mammalian cell culture.

For further information and to apply on-line, please see http://www.jobs.ac.uk/jobs/YD192/-Research_Technician/r or contact Mark Jobling

Closing Date: 18 August 2009

Prof Mark A. Jobling Wellcome Trust Senior Research Fellow in Basic Biomedical Science Department of Genetics Room G5, Adrian Building University of Leicester University Road Leicester LE1 7RH UK

tel.: +44 (0)116 252 3427 fax: +44 (0)116 252 3378 email: maj4@le.ac.uk web: http://www.le.ac.uk/-genetics/maj4/maj4.html Times Higher Education University of the Year 2008-9

maj4@leicester.ac.uk maj4@leicester.ac.uk

OregonStateU USDA LabManager ShellfishGenomics

LAB MANAGER POSITION in shellfish genetics, genomics, and breeding.

I have a vacancy for a full-time, permanent, GS7/8/9 LABORATORY MANAGER/TECHNICIAN with the USDA Agricultural Research Service. The position is best suited for someone with a Masters degree who is familiar with a wide range of molecular genetics techniques (DNA and RNA extraction, PCR, reverse transcription, quantitative real-time PCR, microsatellite markers, AFLP markers, RFLP markers, gel electrophoresis, DNA cloning and sequencing); equipment (ABI 3730XL sequencer, ABI 7500 RT-PCR, Biomek FX pipetting robot, gel image analysis etc.); and data management and analysis methods. Duties include conducting research under the supervision of the PI (me); working closely with and training graduate students, postdocs, and other technicians; performing routine maintenance and calibrations on lab equipment; and maintaining inventories of reagents, buffers, etc. Most of the work is lab-based, but occasional field work and sample collection duties are also required.

The research in the lab focuses on genetic improvement of cultured shellfish, mainly oysters, using QTL mapping, gene expression assays, population genetics, and parentage analysis.

The position in located at the Hatfield Marine Science Center in Newport, Oregon which is about 1 hour west of Corvallis on Yaquina Bay. Newport is a small but vibrant coastal community with a mixed economy based on tourism, fishing, and scientific research. It rains a lot in the winter here. This is a permanent position with the federal government, and as such is only open to US citizens by law. Ideally, the chosen candidate would be seeking a long-term situation.

The position has not been formally announced yet by the Human Resources folks, so please email me directly. I will compile a list for direct contact when the position is officially available and provide details about how to apply.

Mark Camara <Mark.Camara@oregonstate.edu>

OregonStateU USDA LabManager ShellfishGenomics 2

Sorry for the re-post. This position has now been officially announced, and this message includes that announcement and instructions on how to apply below.

LAB MANAGER POSITION in shellfish genetics, genomics, and breeding.

I am recruiting to fill a vacancy for a full-time, permanent, GS7/8/9 LABORATORY MANAGER/TECHNICIAN with the Agricultural Research Service. The position is best suited for someone with a Masters degree who is familiar with a wide range of molecular genetics techniques (DNA and RNA extraction, PCR, reverse transcription, quantitative real-time PCR, microsatellite markers, AFLP markers, RFLP markers, gel electrophoresis, DNA cloning and sequencing); equipment (ABI 3730XL sequencer, ABI 7500 RT-PCR, Biomek FX pipetting robot, gel image analysis etc.); and data management and analysis methods. Duties include conducting research under the supervision of the PI (me); working closely with and training graduate students, postdocs, and other technicians; performing routine maintenance and calibrations on lab equipment; and maintaining inventories of reagents, buffers, etc. Most of the work is lab-based, but occasional field work and sample collection duties are also required.

The research in the lab focuses on genetic improvement of cultured shellfish, mainly oysters, using QTL mapping, gene expression assays, population genetics, and parentage analysis.

The position in located at the Hatfield Marine Science Center in Newport, Oregon which is about 1 hour west of Corvallis on Yaquina Bay. Newport is a small but vibrant coastal community with a mixed economy based on tourism, fishing, and scientific research. It rains a lot in the winter here. This is a permanent position with the federal government, and as such is only open to US citizens by law. Ideally, the chosen candidate would be seeking a long-term situation.

The formal position announcement and instructions on how to apply are included below.

Mark D. Camara USDA/ARS Shellfish Genetics OSU - Hatfield Marine Science Center 2030 SE Marine Science Dr. Newport, OR 97365

Office: 541-867-0296 Fax: 541-867-0138 Mobile: 541-961-8243 Mailto: Mark.Camara@oregonstate.edu

Agricultural Research Service Department: Department Of Agriculture Agency: Agricultural Research Service Sub Agency: Horticultural Crops Research

Job Announcement Number: ARS-X8W-0084

Overview

<https://recruiter.usajobs.opm.gov/sourcing/-?jobID=66305957&jsd=jobsearch%2Eusajobs%2Eopm%2Egov&hd=www%2Eusajobs%2Egov&TabNum=7
Detailed Version

Biological Science Laboratory Technician (Molecular Biology) Salary Range: 35,752.00 - 56,849.00 USD per year Open Period: Wednesday, December 12, 2007 to Monday, January 14, 2008 Series & Grade: GS-0404-07/09 Position Information: Full-Time Permanent

Promotion Potential: GS-09 Duty Locations: 1 vacancy - Newport, OR

Who May Be Considered:

Applications will be accepted from United States citizens and nationals.

Job Summary:

Find Solutions to Agricultural Problems that Affect Americans Every Day, >From Field to Table

Provides technical assistance for a research program studying shellfish genetics and selective breeding. Primary responsibilities are to perform molecular biology laboratory procedures such as DNA/RNA extractions, PCR and reverse PCR, agarose gel electrophoresis, DNA sequencing, tissue collection and archiving, etc. and overall laboratory management.

U.S. citizenship is required and must be verified prior to entrance on duty.

Duties

Major Duties:

Provides technical assistance for a research program studying shellfish genetics and selective breeding. Plans, organizes, coordinates and conducts technical aspects of laboratory operations. Responsibilities emphasize molecular aspects such as marker development, high-throughput genotyping and gene expression analyses which include performing molecular biology laboratory procedures such as DNA/RNA extractions, PCR and reverse PCR, agarose gel electrophoresis, DNA sequencing, molecular cloning and analyses tissue collection and archiving. Operates a variety of laboratory equipment including autoclaves, centrifuges, homogenizers, spectrophotometers, thermal cyclers including a real-time PCR thermal cycler, automated DNA sequencers, and robotic liquid handling systems. Responsible for sample collection, sorting, preparation, analyses, and verification from lab or/and field environment; uses computer software for recording, tabulating, and maintaining data, methods, and procedures used in data collection. Assists with data analyses, report preparation and presentation. Maintains inventory of chemicals, prepares solutions and reagents for use in the laboratory, and safely disposes of waste material, both chemical and biological according to established laboratory procedures.

Qualifications:

— / —

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

---

OxfordUniversity WTCHG 4 Bioinformaticians

Bioinformatics Research Associate (3x) and Research Scientist (1x) positions

Oxford University

Wellcome Trust Centre for Human Genetics

http://www.nature.com/naturejobs/science/jobs/107224-Bioinformatics-Research-Scientist http://www.nature.com/naturejobs/science/jobs/107223-Bioinformatics-Research-Associate The WTCHG is seeking up to four new members of staff to join the High- Throughput Sequence Analysis group in the Bioinformatics and Statistical Genetics Core at the Wellcome Trust Centre for Human Genetics. The post-holders will join a team of bioinformaticians and statistical geneticists supporting the WTCHG high-throughput sequencing (HTS) facility, which is responsible for analyzing HTS data and developing statistical methods, algorithms and tools to do so. Currently the facility comprises 4 Illumina GA-II and two Roche FLX sequencers. The WTCHG has been awarded MRC Sequencing Hub status, which will increase the sequencing capacity further.

The post-holders will work as part of a team responsible for the analysis of the data produced by the facility for a large variety of projects, and for conducting longer-term research and software development aimed at increasing our understanding of the sequencing process and broadening its utility in the context of scientific investigations. The balance between these two roles will in part depend on the applicant's interests. Appointments will be for three years initially.

Computational Biology Research Scientist in High-Throughput Genomics. Ref: H5-09-033-GL

University grade 8 £36,532 to a discretionary £47,666

Applicants for this role should ideally have a PhD, and have experience in computational biology, particularly the development of algorithms, statistical methods, software and databases in the context of HTS. However, we also encourage applications from exceptional candidates without a PhD and/or applicants with related demonstrable and relevant experience. Excellent computational and communication skills are essential, and experience with software engineering is highly desirable. This role also includes line management of junior staff and students, so line management experience is important.

Bioinformatics Research Associate in High-Throughput Genomics, up to 3 posts. Ref: H5-09-032-GL

University grade 7 £28,839 to a discretionary £38,757

For these posts we are looking for applicants who ideally have a PhD, and have experience in computational biology / bioinformatics, the analysis of HTS data and/or in the development of software, tools and databases to support HTS. However, we also encourage applications from exceptional candidates without a PhD and/or applicants with related demonstrable and relevant experience. The ability to communicate effectively with people from a variety of technical backgrounds is essential for these posts.

One of these positions will be dedicated to work on analysis of next generation sequencing data, and development of bioinformatics tools and statistical algorithms as part of the Oxford Biomedical Research Centre's translational genetics programme. This is an exciting opportunity to be involved in several large collaborative research projects evaluating the clinical applications of next generation sequencing using whole genome de novo and re-sequencing approaches in humans and pathogens.

Informal enquiries should be made to Dr Gerton Lunter (gerton.lunter@well.ox.ac.uk).

To apply please submit your CV and a cover letter demonstrating how you meet the criteria to personnel@well.ox.ac.uk. Please ensure you quote the appropriate job reference on both your CV and cover letter. The closing date for all these roles is August 31. Any applications received after this date will not be shortlisted.

gerton.lunter@dpag.ox.ac.uk gerton.lunter@dpag.ox.ac.uk

PennsylvaniaStateU EvolutionWebDesigner

Job: Website Designer/Developer Institution: Pennsylvania State University Location: University Park, PA, USA Start date: immediately (or negotiable)

A full-time position for Website Designer/Developer is available immediately in a research laboratory supervised by Prof. Blair Hedges in the Department of Biology at The Pennsylvania State University (http://evo.bio.psu.edu/hedgeslab/). The successful candidate for this position will be responsible for the design and development of science and natural history web sites (e.g., www.timetree.org), some of which will include integration with databases. Other duties will include creation of figures for research publications. Requires a Bachelor of Science degree (or equivalent), preferably in graphic design, and preferably with 2+ years of work experience. Graphics design and programming (hand-coding) skills are required. The candidate must be proficient in Photoshop, Illustrator, and Dreamweaver; and be a functional (not necessarily advanced) user of PHP, HTML, MySQL (or PostgreSQL), CSS, and JavaScript. Past website experience should include design and layout. The ideal candidate will know how to balance creativity and aesthetics with simplicity and functionality in website design. Salary is competitive and commensurate with experience. Excellent benefits. Screening of applicants to begin immediately and continue until position is filled. To apply, email a cover letter describing experience (also provide URLs of websites designed) and professional goals, and a curriculum vitae/resume with contact information for three referees to Prof. Hedges at sbh1@psu.edu. This is a fixed-term appointment funded for one year from date of hire with an excellent possibility of re-funding. Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

sbh1@psu.edu sbh1@psu.edu

RoyalBotanicGardens Kew ChromosomeEvolution

Research Cytogeneticist

Genetics Section, Jodrell Laboratory, Royal Botanic Gardens, Kew, UK

Ref: 529

A post has become available for a research cytogeneticist to work in the Genetics Section of the Jodrell Laboratory (Royal Botanic Gardens, Kew, UK). The post is for three years. The successful candidate will undertake scientific research for publication, focusing studies on genome size and chromosome evolution, using the techniques of traditional and molecular cytogenetics, Feulgen microdensitometry, flow cytometry, DNA sequencing etc. Other responsibilities include training staff and visitors in plant cytological techniques and managing the day to day running of the cytogenetics laboratory. Salary per year: 21,391

Closing date: 12 pm Friday 28th August

For further information and to apply please go to: http://www.kew.org/aboutus/jobs/ref_ResearchGeneticist529.htm Dr Ilia Leitch Jodrell Laboratory Royal Botanic Gardens, Kew Richmond, Surrey TW9 3AB UK

Tel: + 44 (0)208 332 5329 Fax: + 44 (0)208 332 5310

I.Leitch@kew.org

TexasAMU EvolutionaryIchthyology

Texas A&M University- College Station, Texas

Assistant Professor and Curator of Ichthyology: evolutionary biology, systematics, genetics, ecology, or conservation biology

The Department of Wildlife and Fisheries Sciences seeks an Assistant Professor and Curator of Ichthyology. Candidates must have a doctorate and demonstrate capacity for excellence in research in evolutionary biology, systematics, genetics, ecology, or conservation biology. The position is tenure-track with a 12-month annual appointment. The successful candidate will teach Ichthyology, a graduate course in their specialty, and contribute occasionally to a course in vertebrate zoology. The successful candidate will be Curator of the TCWC fish collection, consisting of 630,000 specimens (wfsc.tamu.edu/TCWC). Many opportunities exist for interdisciplinary collaborations among departments and programs including Ecology and Evolutionary Biology (eeb.tamu.edu), Genetics (gene.tamu.edu) and Renewable Natural Resources. Applicants may address their ability to contribute to the mission of the university^{1}s diversity plan (diversity.tamu.edu/plan/index.asp). To apply: Submit electronically a CV, statements of teaching, research, and curation, plus contact information for three references to: Dr. Kirk O. Winemiller, Ichthyologist Search Committee Chair, kwinemiller@tamu.edu. Review of applications will begin October 5, 2009.

The Texas A&M University System is an Equal Opportunity Employer committed to building a diverse faculty, staff, and student body reflecting the population and educational needs of Texas and the Nation.

More detailed information at http://-wfsc.tamu.edu/news_items/api.html Mariana Mateos <mmateos@neo.tamu.edu>

Trinidad FieldTech EvolutionaryEcol

Field technician position in tropical stream evolutionary ecology

Temporary field technicians are needed for work in a multi- disciplinary, multi-investigator study of evolutionary stream ecology in Trinidad, led by professor David Reznick at the University of California and funded by the Foundations for Integrative Biological Research program of the National Science Foundation. The research project is aimed at integrating multiple biological fields for the study of the interactions between ecological and evolutionary processes. The position will include some labor intensive monthly censuses of fish populations (guppies and killifish) as well as monitoring of ecosystem processes and community structure (aquatic invertebrate sampling, nutrient chemistry, etc) in montane streams.

The position requires to spend a 3-month stay in Trinidad, with possibility of extension for an entire year. Starting dates are flexible, starting as early as September 2009. Successful applicants will earn stipend of $500/month and have their traveling expenses, accommodation and insurance covered.

Applicants should send an updated CV and two references to Andrés López-Sepulcre (andresls@ucr.edu) and David Reznick (gupy@ucr.edu).

Andres Lopez-Sepulcre <lopezsepulcre@gmail.com>

UConcepcion VertebrateSystematics

The Department of Zoology at the University of Concepción, Chile, invites applications for a position of Assistant Professor in Vertebrate Systematic and Diversity.

We seek innovative applicants with a strong record in research, who have proven their ability to develop and apply novel concepts in systematic and diversity studies of vertebrates. The successful candidate is expected to develop an independent research program, gather external funding, and teach at the graduate and undergraduate levels.

The candidate should be available to begin in October 1th, 2009. Applications should include a curriculum vitae and a letter of intention. Hard copies of all documents should be sent, together with names and addresses of two potential referees, to Dirección de Personal, Universidad de Concepción. Casilla 160-C, Concepción. Chile, by 10th September, 2009. The digital copy of application material should be submitted as a single PDF file to pvictori@udec.cl.

For further information, please contact Dr. Pedro F. Victoriano at pvictori@udec.cl

Sincerely

Pedro F. Victoriano

Pedro Victoriano <pvictori@udec.cl>

UEdinburgh ChairOfNaturalHistory

School of Biological Sciences, University of Edinburgh Chair of Natural History

The School of Biological Sciences at the University of Edinburgh, Edinburgh, Scotland is seeking to fill the Chair of Natural History. The successful applicant will be a member of the Institute of Evolutionary Biology (IEB) and/or the Institute of Immunology and Infection Research (IIIR), which have developed strong cross-disciplinary research links and host the Wellcome Centre in development for Immunology, Infection and Evolution. This offers a unique interdisciplinary research environment. Applicants with research programmes at the interface between evolutionary and infectious disease biology would thus be particularly welcomed. Full details of the position can be found on the University Website under Vacancy No. 3011197(http://www.jobs.ed.ac.uk/-vacancies/index.cfm?fuseaction=vacancies.index). The closing date is 30th September 2009. Informal inquiries can be addressed to Prof. Brian Charlesworth, Head of IEB (Brian.Charlesworth@ed.ac.uk), or Prof. David Gray Head of IIIR (d.gray@ed.ac.uk).

Brian Charlesworth <brian.charlesworth@ed.ac.uk>

UJyvaskyla Finland EvolBiol

Professorship in Evolution University of Jyväskylä, Finland

The professorship belongs to the Department of Biological and Environmental Science in the Faculty of Mathematics and Science. The appointment is effective starting 1 December 2009 or as soon as possible thereafter. The main research areas in the department are evolutionary and conservation biology, aquatic sciences, molecular recognition, and environmental science and technology. The current teaching staff of the department is 39 (15 professors, 3 lecturers, 13 senior assistants, and 8 assistants). Moreover, there are about 100 researchers and senior researchers in the department. The professorship in ecology belongs to the ecology and evolutionary biology section in the department. The section has, in addition to this professorship, three permanent professorships (evolutionary ecology, applied ecology, and evolutionary genetics), two lecturers and five senior assistants. The Centre of Excellence in Evolutionary Research nominated by the Academy of Finland highlights the achievements of the section. The research profile of the section comprises high-level evolutionary research and conservation biology research integrated with evolutionary aspects. The nominee is expected to further strengthen this profile. The nominee is presumed to develop research, teaching and research training in ecology. The successful candidate is expected to: - have an excellent research-profile within ecology, with a relevant background in theoretical ecology, behavioral ecology, evolutionary ecology, population ecology, community ecology, macroecology or ecological biogeography, at the level of international excellence, documented both by publications in the best international ecology journals and in general high-impact journals; - have competence to advance research and teaching in ecology at high international level, documented by research plan and teaching portfolio; - have experience in directing externally funded research programs in ecology; - attract substantial funding from international and Finnish sources; - strengthen links and develop new synergies with relevant research groups worldwide, with other Finnish universities and research institutions; - have wide experience in educating undergraduate, graduate and PhD students, and postdoctoral researchers in skills relevant to ecology; - have a good track record in teaching and good teaching skills; - show activity in science communication and dissemination. The University statutes stipulate that a professor is expected to follow scientific development in his or her field, conduct and supervise research, and direct and develop teaching in his or her field of responsibility. (S)he is also required to supervise the work for examinations, essays, and theses, and carry out other duties as laid down in the statutes. The appointment will be within University Salary System 1 bands 8-11 (basic salary 4,176.45 - 6,091.80 per month) depending on the qualifications and experience of the nominee. An additional salary payment as a proportion of the basic band salary (up to a maximum of 46,3 %) will be paid according to personal performance.

For more information: http://www.jyu.fi/science/en/-faculty/current/jobs/

Mikko Mönkkönen <mikko.monkkonen@bytl.jyu.fi>

UmeaU EvolutionaryAdaptations

At the Department of Ecology and Environmental Science of Umeå University, Sweden, a position in spatial ecology is announced.

Possible directions for the position include ecological processes in heterogeneous habitats, ecological dynamics and coupling between habitats and systems, effects of local and regional processes on the distribution of populations, evolutionary adaptations to local abiotic and biotic environments. The position may have an empirical or theoretical direction or a combination of both.

The Department of Ecology and Environmental Science constitutes around 150 staff members and includes a wide range of research fields such as biogeochemistry, evolutionary ecology, evolutionary genetics, landscape ecology, paleolimnology and population and community ecology. The department offers seven different study programs and a wide range of independent courses for approximately 500 full-time students. Also Master's programs in Ecology, Experimental Plant Science and Geoecology are offered.

The position is open for an outstanding scientist with a strong research track record. Ability to collaborate with researchers of the different research groups at the department is a major asset.

For further information about the position, please see http://www8.umu.se/umu/aktuellt/arkiv/-lediga_tjanster/312-570-573-09.html#eng or contact Professor Lennart Persson, phone +46 90 786 6316, e-mail lennart.persson@emg.umu.se.

folmer.bokma@emg.umu.se
folmer.bokma@emg.umu.se

UMuenster MolGenomeEvolution

Junior Professorship (W1) in Molecular or Genome Evolution

The Faculty of Biology, University of Münster, Germany, seeks an Evolutionary Biologist working on Molecular and/or Experimental Evolution at the Junior Professor (W1)-level, (equivalent to a non-tenure track assistant professorship or Lecturer). The position, located at the Institute of Evolution and Biodiversity (IEB, ieb.uni-muenster.de), is funded by the Volkswagen-Foundation âInitiative Strengthening Evolutionary Biologyâ in Germany and starts on October 1st, 2009. Continuation after the initial three years is possible for another three years and depends on external review. Candidates are expected to lead an independent junior group with a strong research program. Particularly welcome are applicants working on one or more of the following subjects:

â experimental evolution in short generation organisms â molecular evolution of key genes â population and comparative genomics using experimental and/or computational approaches

The successful candidate must have a PhD or doctorate in a biological or related discipline. Postdoctoral experience and a strong publication record are expected. The position includes teaching at the undergraduate (Bachelor) and graduate (Master) level in the field of evolutionary biology. To promote exchange of students, all teaching at the graduate level will be in English.

The IEB is equipped with a central molecular genetic laboratory, greenhouses, climate chambers and computational facilities. Base funding for consumable and personnel will be provided, nevertheless the candidate is expected to participate in ongoing collaborative funding efforts of the Faculty of Biology and encouraged to acquire additional extramural funding.

The University of Münster seeks to increase the proportion of female staff members in the faculty and therefore encourages interested female candidates to apply.

Handicapped candidates with equivalent qualifications will be given preference.

To apply for this position, please send a Curriculum Vitae in English, including a publication list, a summary of scientific achievements, teaching experience, acquired funding and a description of research plans not later than Sept 15th, 2009. Please also provide a pdf to dekanat.bio@uni-muenster.de. Send hardcopies to: Dekan des Fachbereichs Biologie, Westfälische Wilhelms-Universität, Schlossplatz 4, D-48149 Münster, Germany.

For further details see: http://ieb.uni-muenster.de/ Prof. Erich Bornberg-Bauer PhD, Institute for

Evolution and Biodiversity School of Biol.Sciences, University of Muenster, Huefferstr.1 D48149 Germany Tel/Fax: +49(0)251-83-21630/24668 web: www.uni-muenster.de/evolution/ebb/ "E. Bornberg" <ebb@uni-muenster.de>

UNebraskaLincoln ArthropodHostInteractions

Position: Molecular arthropod/host interactions - Assistant Professor

The University of Nebraska-Lincoln (UNL), through the Institute of Agriculture and Natural Resources, seeks applications to fill a 9- month, tenure-track research (80%) and teaching (20%) position at the Assistant Professor rank in the Department of Entomology. An individual with expertise and interests in arthropod-host interactions as the molecular level is sought. The successful candidate will be expected to develop a nationally recognized program in stress biology with an emphasis on hypothesis driven research addressing the molecular basis of arthropod interactions with plant or animal hosts. Collaboration with relevant faculty across the university to expand and strengthen the molecular life sciences in expected.

Description: Research: The successful candidate will be expected to develop a nationally recognized research program as evidence by publication of results in peer reviewed journals, competiveness for external funding, and recruitment and successful supervision of graduate students. Applicants should be well versed in one or more of these areas: molecular biology, functional or structural genomics, and insect biochemistry related to signaling pathways modulating responses to biotic or abiotic stressors.

Teaching: Teaching responsibilities include a strong commitment to undergraduate and graduate teaching, teaching insect physiology or one or more classes in the area of specialization, participation in graduate seminars, and contributing to curriculum development in Entomology. Opportunities exist for engaging in undergraduate research and mentoring, distance education, and outreach to public or K-12 audiences. There is an expectation that all faculty will participate in student recruitment activities

Qualifications: PhD in Entomology or related field with emphasis in the molecular investigations of arthropod interactions with plant or animal hosts as it related to stress biology required. Must show experience and commitment to research and teaching, have strong communication skills, ability to bring in extramural funding, and an interest and desire to work cooperatively on multi-disciplinary projects.

Salary/Benefits: Salary is competitive and commensurate with qualifications and experience. The University of Nebraska offers a benefits package that makes available group life, health, and disability insurance and family coverage programs to the employee; TIAA/CREF and/or Fidelity Investment Fund retirement plans; excellent vacation and sick leave plans; and staff and dependent tuition remission.

Application: Go to http://employment.unl.edu. Search for requisition #090448. Complete the faculty/academic administrative information form. Attach a letter of application and curriculum vitae. In the 'other' category include two personal statements - one describing your research focus/interest and one describing your teaching expertise/ experience. Arrange for three letters of reference to be emailed by October 1, 2009 to: Marilyn Weidner, mweidner1@unl.edu. For questions about the position contact the Search Co-Chairs, Dr. Blair Siegfried, 202 Entomology Hall, Lincoln, NE 68583, 402-472-8714, bsiegfried1@unl.edu or Dr. Tiffany Heng-Moss, 202 Entomology Hall, Lincoln, NE 68583, 402-472-8708, thengmoss2@unl.edu. Screening of applicants will begin on October 1, 2009, and continue until the position has been filled or the search is closed.

The University of Nebraska has an active National Science Foundation ADVANCE gender equity program and is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers. It is the policy of the University of Nebraska-Lincoln not to discriminate based on gender, age, disability, race, color, religion, marital status, veteran's status, national or ethnic origin, or sexual orientation. AA/EEO details may be secured by contacting 128 Canfield Administration Building, P.O. Box 880437, Lincoln, NE 68588-0437, or by telephoning 402-472-3417. Employment eligibility verification is required for all new hires pursuant to the Immigration and Control Act of 1986.

Institute of Agriculture and Natural Resources, University of Nebraska- Lincoln

The Institute of Agriculture and Natural Resources (established in 1973 by the Nebraska State Legislature to give added emphasis to agriculture and the management of natural resources in Nebraska) serves the people of Nebraska in the four-fold mission of teaching, research, extension and service. Commonly referred to as “IANR,” the Institute is administered by the Vice Chancellor for Agriculture and Natural Resources and has faculty and staff located throughout the

— / —

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

UNebraska Omaha ResTech Bioinformatics

A Research Technician in bioinformatics is available in the laboratory of Dr. Guoqing Lu, in the Department of Biology at the University of Nebraska at Omaha.

The successful candidate will be responsible for computer programming and database development and participate in the development and maintenance of web site and tools. A bachelor?s degree in bioinformatics, computer sciences, biology or a relating field, with some working experience, is desirable. Candidates in the progress toward their bachelor can however, be considered. Salary and benefits will be commensurate with experience and in accordance with NIH guidelines. Visit the website http://www.flugenome.org for detailed information about this project. To learn more about us, please visit the website http://bioinfo-srv1.awh.unomaha.edu/glu.

Send curriculum vitae, cover letter, and contact information of three references to e-mail: glu3@mail.unomaha.edu, and include Technician Application in the Subject line. Review of applications will begin immediately and continue until the position is filled.

Many thanks,

Guoqing Lu

Assistant Professor in Bioinformatics Department of Biology University of Nebraska at Omaha Omaha, NE 68182-0040 Tel: 1-402-5543195 Fax: 1-402-5543532

Guoqing Lu <glu3@mail.unomaha.edu>

UNorthCarolina ChapelHill ResTech BehavEvolEcol

Animal Care/Research Technician in Behavioral and Evolutionary Ecology

University of North Carolina, Chapel Hill

I am seeking a full time technician to coordinate research projects and oversee the care of a large spadefoot toad colony. The successful applicant will carry out day-to-day animal care, maintain a large database, supervise undergraduates, and carry out research projects involving behavioral observations and fitness measures of toads. Details of my research program can be found at: http://bio.unc.edu/Faculty/KPfennig/ The position requires someone who is detail-oriented, extremely well organized, independent, and capable of working with a diverse research team. Experience working with live animals and a background in ecology, evolution, behavior, or organismal biology (with a B.S. in Biology or its equivalent) is required. Prior research experience, experience handling amphibians, and supervisory experience is preferred. Starting salary ranges from $22-29K depending on experience.

To apply, please email me a resume/CV and a cover letter describing your qualifications and interest in the post. Please also arrange for three letters of reference to be sent to me via e-mail.

Review of applications will begin immediately and continue until the position is filled.

Dr. Karin Pfennig University of North Carolina, Chapel Hill Dept. of Biology, CB#3280 Chapel Hill, NC 27599-3280 (919) 843-5590 E-mail: kpfennig@email.unc.edu

UNorthCarolina ChapelHill ResTech ViralEvolution

Research Technician in Virus Experimental Evolution

Professors Christina Burch and David Pfennig

University of North Carolina, Chapel Hill

We are seeking a full time research technician to assist in collaborative laboratory projects related to the role of resource competition in generating diversity within and divergence between co-occurring virus populations. The position is expected to last 1-2 years, and is therefore ideal for recent graduates seeking additional experience prior to graduate school.

The successful candidate will have a BA/BS degree, prior independent research experience, some background in evolution and genetics, good organizational skills, and the ability to work well as part of a research team. We are looking for someone who can work independently, but we will provide training. Experience working with microbes and using molecular methods like PCR is also desirable. Salary will range from $25-30K depending on experience.

To apply, please email a CV, a cover letter describing your qualifications and interests, and the names and contact information for three references to Dr. Christina Burch, cburch@bio.unc.edu. Additional information about the project can be found at: http://-www.unc.edu/~cburch/lab .

Review of applications will begin August 15h and continue until a successful candidate is identified.

Christina Burch University of North Carolina Department of Biology CB# 3280 Chapel Hill, NC 27599 919-843-2691

http://www.unc.edu/~cburch/lab

CBurch@bio.unc.edu CBurch@bio.unc.edu

UNotreDame EvolutionaryBioinformatics

The Department of Computer Science and Engineering at the University of Notre Dame invites applications for positions at the rank of Assistant or Associate Professor. Exceptional candidates in all areas of specialization will be considered, and the area of bioinformatics is an especially high priority for us this year, including research focusing on comparative and evolutionary genomics.

The Department offers a PhD degree as well as accredited undergraduate Computer Science and Computer Engineering degrees. There are approximately seventy-five students in the PhD program and over one hundred majors in the undergraduate programs. Our faculty are engaged in cutting-edge and highly visible research in algorithms, bioinformatics and computational biology, computer architecture and nanotechnology, computer security, data mining / machine learning, computer vision / image analysis, and networks / systems. The Gates Foundation recently awarded a $20 million grant to Biology and CSE faculty in the bioinformatics area, and the Semiconductor Research Corporation (SRC) together with the state of Indiana and the city of South Bend recently announced the Midwest Institute for Nanoelectronics Discovery, a research consortium led by Notre Dame, has received $25 million in new funding.

The University of Notre Dame is a private, Catholic university with a doctoral research extensive Carnegie classification, and it is consistently ranked in USN&WR as a top-twenty national university. The South Bend area has a vibrant and diverse economy with affordable housing and excellent school systems, and is within easy driving distance of Chicago and Lake Michigan. Screening of applications is on-going. Applicants should send (pdf format preferred) a CV, statement of teaching and research interests, and contact information for three professional references to: facultysearch AT cse.nd.edu

The University of Notre Dame is an Equal Opportunity, Affirmative Action Employer.

Ginny Watterson Computer Science & Engineering University of Notre Dame 384 Fitzpatrick Notre Dame, IN 46556 (574)631-8321 (574)631-9260/FAX vjohns@cse.nd.edu

Ginny Watterson <vjohns@cse.nd.edu>

UNotreDame ResTech PopGenetics

JOB: RESEARCH TECHNICIAN POSITION

A research technician position is available in the lab led by Beth Archie in the Biology Department at the University of Notre Dame. The Archie Lab uses population genetic tools to understand the genetic and disease-related causes and consequences of animal social behavior. Our current research systems are wild elephants and baboons living in Amboseli National Park, Kenya. For more information about the Archie Lab, see our web page at http://www.nd.edu/~earchie/ . The successful applicant will conduct population genetics research in the lab and be involved in laboratory management (ordering supplies, working with students). A Bachelorâs degree in biology, or a related discipline, is required.

Experience with basic genetics techniques (e.g., DNA extraction, PCR, gel electrophoresis) is essential; experience with research in population genetics and/or phylogenetics is especially useful. Notre Dame has strong research programs in ecology, evolution and infectious disease in a Biology Department with collegial and interactive faculty and students. The department houses state-of-the-art genomics and imaging cores, more information on departmental and other college faculty and facilities can be found at http://biology.nd.edu and http://science.nd.edu . The position can begin as early as October 2009 and will be open until filled. Salary is commensurate with experience. Interested applicants should apply online at http://hr.nd.edu/-employment/job_opportunities.shtml under job number 09293. Please submit a CV, cover letter, and contact information for two references, including the applicantâs relationship to the reference, their phone number, email address, and mailing address. Please contact Beth Archie at earchie@nd.edu for informal inquiries.

Beth Archie Clare Booth Luce Assistant Professor University of Notre Dameâ Department of Biological Sciencesâ 107 Galvin Life Science Centerâ Notre Dame, IN 46556 Phone: (574) 631-0178 Email: earchie@nd.edu

Elizabeth Archie <Elizabeth.A.Archie.2@nd.edu>

UOklahoma LabTech EvolutionaryEcology

Please distribute the following job advertisement:

Laboratory Technician (Lab/Research Technician III)

University of Oklahoma Biological Station, Kingston, Oklahoma

The laboratory of Dr. Brian Langerhans is seeking a highly motivated individual with strong organizational skills to serve as laboratory technician, overseeing and implementing a range of activities centered on studying the evolutionary ecology of fishes. The position is a 12-month, full-time position with benefits.

The ideal candidate will have a B.S. or M.S. (or equivalent years of experience) in a biological science or related field, prior experience working in a research laboratory, familiarity with computer software for data entry and organization, knowledge of scientific principles, and a basic understanding of ecological and evolutionary concepts.

Salary will be commensurate with education and experience, and can range from $11.00 - $13.40 per hour, plus benefits.

Primary duties include general lab maintenance, live-fish care, imaging, specimen handling and preparation, tissue sampling, specimen cataloging, data entry and manipulation, digital archival and creation of biotic databases, DNA extraction, PCR amplification, and sequencing of genes. After initial training regarding procedures and techniques, the technician should be capable of effectively performing most tasks independently within a couple of months on the job. A driver's license is required, as travel to OU main campus in Norman, OK and field sites will occasionally occur.

The Biological Station is situated on Lake Texoma in a rural, lake-side environment. A fully-furnished rental apartment (only ~5 years old) is available on site for $390 per month. A signed lease is required for rental, and no pets are allowed.

To apply, send the following materials to Dr. Brian Langerhans (langerhans@ou.edu): 1) a cover letter indicating why you are interested in the position, 2) a resume or CV, and 3) contact information for three references. Review of applications will begin immediately. Please contact Brian Langerhans (langerhans@ou.edu, 903-870-6383) with any questions. Position to start approximately September, 2009.

For more information on the Langerhans Lab, the Biological Station, and on-site housing, please visit these websites:

http://faculty-staff.ou.edu/L/Randall.B.Langerhans-1 http://www.ou.edu/uobs http://www.ou.edu/uobs/-research_housing.html

Dr. R. Brian Langerhans University of Oklahoma Biological Station Ph: 903-870-6383 Fax: 580-564-2479 E-mail: langerhans@ou.edu Web: http:/-/faculty-staff.ou.edu/L/Randall.B.Langerhans-1 langerhans@ou.edu langerhans@ou.edu

---

UPennsylvania LabTech MicrobeEvolution

Job: Laboratory Technician Department of Biology, University of Pennsylvania

A laboratory technician position is available in the evolution of infectious microbes lab led by Dustin Brisson at the University of Pennsylvania. The main focus of the projects involves the bacterial cause of Lyme disease, Borrelia burgdorferi. All projects is the lab intellectually integrate multiple scales of biological complexity (i.e. molecular-level, organism-level, and population-level) using laboratory, field, and computational studies.

The position requires a highly motivated, enthusiastic, and enquiring individual with a background in evolutionary biology or ecology. Strong molecular genetic skills are highly advantageous. Duties of the successful candidate may include molecular biology, field collections, animal husbandry and will contribute to formulation of experiments, performance of experiments, data collection and data analysis.

A Bachelor's degree in biology (or a related science) OR 2 years of experience or equivalent combination of education and experience is required.

The University of Pennsylvania has a strong group of evolutionary biologists and ecologists in the biology department that frequently interact with each other and with an accomplished group of microbiologists in the Medical and Veterinary schools.

The positions are available as early as September 2010. Starting dates are flexible and I will wait for outstanding candidates. Salary is commensurate with experience.

Applications must be submitted through the human resources department at the University of Pennsylvania (https://jobs.hr.upenn.edu/ — search ref# 090827157). Please include relevant documents including reference contacts and a CV.

Informal enquiries can be submitted to:

Dustin Brisson Department of Biology University of Pennsylvania Leidy Laboratories, 326 433 South University Avenue Philadelphia PA 19104-6018 http://www.bio.upenn.edu/faculty/brisson/ http://brisson.bio.upenn.edu/ dbrisson@sas.upenn.edu V:(215) 746-1731

dbrisson@sas.upenn.edu dbrisson@sas.upenn.edu

USouthernCalifornia LabTech MouseEvolutionaryGenetics

Research Lab Specialist

The Dean Lab in the Department of Molecular and Computational Biology at the University of Southern California is currently seeking a research lab specialist to help study population and evolutionary genetics.

Responsibilities include:

Collecting molecular data (purification, amplification, cloning, sequencing of DNA/RNA, mass spec proteomics, etc.) Maintaining and supervising mouse colonies and experimental procedures (prior mousing skills desirable, but not necessary). Includes field work. Ordering lab supplies and maintaining general lab functions. Supervising and training undergraduates in the laboratory Analyzing data (computer programming skills - e.g. Python or Perl - desirable)

Annual salary=$38,000-$50,000 depending on experience

Qualifications:

Bachelors degree in Biology or a related field with extensive laboratory research experience. Knowledge of evolutionary genetics, genomics, bioinformatics, proteomics, and molecular biological techniques. Above all, must have outstanding problem-solving skills, good organizational abilities, keen attention to detail, and a burning internal motivation to study fascinating topics in biology.

To apply: send a <1 page cover letter summarizing research experience, a CV, and the names of three references to matthew.dean@usc.edu Review of applications immediately. For more information, email Dr. Matt Dean at above email address or visit http://college.usc.edu/cf/faculty-and-staff/faculty.cfm?pid=1027430 Gloria Gamboa CIR Recruiter (213) 740-3449 phone (213) 740-8784 fax http://www.usc.edu/jobs Gloria Gamboa <GGamboa@caps.usc.edu>

UToronto Bioinformatics

BioInformatician: Metagenome Sequence AnaLysis

The Department of Chemical Engineering and Applied Chemistry at the University of Toronto (Toronto, Ontario, Canada) has 1-2 openings for full-time Bioinformaticians to conduct research on computational biology of environmental metagenomes for bioenergy and biodegradation of existing and emerging contaminants. This role presents a unique opportunity to conduct basic research that will have a clear and immediate impact on Canadaâs green economy.

Project Objective The objective of BEEM (Bioproducts and Enzymes from Environmental Metagenomes) is to develop microbial cultures and enzymes to biodegrade contaminants and generate value-added products from waste. Our multidisciplinary team, consisting of biologists, engineers, industry leaders, and policy experts, will ensure that the technologies developed in this research will be quickly commercialized for industrial and field applications. Essential position responsibilities

Primary Function

â Development of methods for integrating independently developed algorithms into computational pipeline development to support analysis of metagenome sequence; â Maintaining sequence databases of the various metagenome to facilitate annotation and mapping the metabolic pathways; and â Development of tools for disseminating the results of sequence analysis to the public.

Communication

â Prepare written progress reports; â Prepare manuscripts for peer-reviewed publications; â Prepare and present posters and platform presentations at conferences; â Present seminars to both internal (project team) and external audiences; and â Train new personnel as needed. Supervisors: Drs. Elisabeth Tillier, Radhakrishnan Mahadevan, and Elizabeth Edwards

Education/experience

Essential Qualifications

Â M.S. in engineering, computer science, or a related discipline or B.S. with experience Â Expert knowledge of sequence analysis and annotation tools (BLAST, Perl, scripting) Â Verbal and written communication skills in English Â Ability to multitask and prioritize concurrent duties

Assets

Â Experience with developing and maintaining web applications or as web master (Apache, PHP), database administration (Oracle) Â Experience with Unix System Administration/Set-up Â Basic knowledge of microbial metabolism

Work style

Â Personable Â Collaborative Â Willing to share knowledge and assist colleagues as needed Â Flexible Â Self-motivated Â Dedicated.

How to apply Please email a cover letter and 2-page resume to Melanie Duhamel (mel.duhamel@utoronto.ca). We thank all applicants for their interest; however, only those considered for an interview will be contacted.

Elisabeth Tillier, PhD Canada Research Chair in Analytical Genomics Assistant Professor, Dept. of Medical Biophysics, University of Toronto Scientist, Cancer Genomics & Proteomics, Ontario Cancer Institute, University Health Network Toronto Medical Discoveries Tower (MaRS) room 5-354 101 College St. Toronto, Ontario M5G 1L7 Canada

Phone 416 581 7534 Fax 416 581 7581 email: e.tillier@utoronto.ca URL: http://www.uhnres.utoronto.ca/tillier/ Elisabeth Tillier <e.tillier@utoronto.ca>

VanderbiltU 2 Bioinformatics

Bioinformatics Engineer II

Functional Genomics Shared Resource (FGSR), Vanderbilt University Medical Center

One Bioinformatics Engineer II position is available immediately to join the Vanderbilt Microarray Shared Resource (VMSR, http://array.mc.vanderbilt.edu/). The VMSR is currently under expansion and in the transition to Functional Genomics Shared Resource (FGSR). The successful candidate is expected to join the Informatics Group which includes bioinformatics engineers and post-doctoral fellows and is under the leadership of Dr. Zhongming Zhao, Chief Bioinformatics Officer in Vanderbilt-Ingram Cancer Center. The position is supported by the Vanderbilt-Ingram Cancer Center.

Job Responsibilities: 1. Data process and transfer and computer support for the Vanderbilt Microarray Shared Resource (VMSR). 1a. Data process, quality control, data transfer, basic analysis and some advanced analysis for microarrays. 1b. Provide software and hardware installation and maintenance for the various computers in the VMSR.

2. Database development and software design 2a. Develop web-based tools to access data contained in the databases maintained by the VMSR. 2b Develop software tools to automate the transfer of data from internal databases. 2c. Develop custom software to assist users in data analysis to present information for publication and grant submission.

3. Web development 3a. Assist with design and maintenance of web-based resources including web pages. 3b. Develop web pages for online submission of sample

information and handling.

4. Provide training and educational support to users of shared resource lab 4a. Develop manuals and detailed documentation for training sessions. 4b. Develop and lead monthly training to the resource users on the various informatic and analysis software packages supported by the area.

5. Serve as a leader to ensure objectives are met 5a. Provide bioinformatics leadership for the lab core, staff, and students. 5b. Instruct in methods and procedures using effective teaching techniques. 5c. Handle employee problems. 5d. Hire, terminate and discipline according to institutional policies.

6. Actively identify and participate in training, education, and development activities to improve own knowledge and performance to sustain and enhance professional development

Requirements a. Experience in processing and analyzing high-throughput genomic datasets derived from microarray and some other high throughput technologies as well as familiarity with available third party software packages useful to analyzing these data. b. Effective communication skills are required. c. Those candidates having significant experience in basic quality control and analysis as well as advanced analysis of data generated by Affymetrix, Agilent, and NimbleGen arrays are strongly encouraged to apply.

Applicants should send a CV and reference to: Zhongming Zhao (zhongming.zhao@vanderbilt.edu), Chief Bioinformatics Officer, Vanderbilt-Ingram Cancer Center. Please specify the position “Bioinformatics Engineer II in FGSR” in the application.

– Zhongming Zhao, Ph.D. Associate Professor, Departments of Biomedical Informatics, Psychiatry, and Cancer Biology Vanderbilt University Medical Center Phone: 615-343-9158 Fax: 615-936-8545

zhongming.zhao@Vanderbilt.Edu zhongming.zhao@Vanderbilt.Edu

YaleU ResAssist MolSystematics

The DNA Analysis Facility at Yale University (http://research.yale.edu/dna_analysis/) is hiring a Full-Time permanent Research Assistant to work as part of a team within a high throughput DNA Analysis Core offering Capillary electrophoresis of Sanger Sequencing and Fragment Analysis of AFLP and microsatellites samples.

Our lab is located within the YIBS Molecular Systematics and Conservations Genetics Laboratory (http://www.yale.edu/caccone/ecosave/index.html) therefore we have daily interactions with undergraduates, graduate students, posts docs and visiting staff members that have ongoing research projects and use our facility to carry out their aims. You will interact with these scientists on a daily basis, attend weekly lab meetings and seminars.

New Haven, Connecticut (http://www.cityofnewhaven.com/) is a vibrant and culturally diverse city located on Long Island sound. The dramatic seasonal changes of the northeast climate accommodate year round outdoor activities from hiking, biking and rock climbing to snowboarding and skiing.

All applicants should apply through the link at http://www.yale.edu/hronline/stars/application/external/index.html , STARS Req. # 7848BR

and send resume to the Lab PI: adalgisa.caccone@yale.edu

Type of Employment Full Time Duration Type Regular Salary Grade (Min/Max) C Work Week Non Standard Work Week Work Hours (Other than Standard) 10:00-6:00 Monday-Friday Work Location Central Campus Worksite Address ESC 140 Position General Purpose Work as part of a team within a high-volume DNA Analysis Core facility to provide customized service to researchers at Yale and the broader scientific community. Assist in preparing, processing, and reviewing data. Ensure timely billing for both Yale and external customers. Essential Duties 1. Assist with all day-to-day operations of DNA Core Facility sample processing. Approximately120,000 sequencing and 45,000 Fragment Analysis samples are analyzed per year. 2. Use web-based Laboratory Information Management System to process and manage orders. 3. Use FTP servers to transport data to and from computers. 4. Follow established protocols to prepare and process samples for Sequencing and Fragment Analysis using a combination of microliter pipettes and/or a robotic liquid handling system. 5. Operate and maintain laboratory equipment including routine maintenance of AB 3730xl DNA Sequencer, robotic liquid handling system and Thermal Cyclers. 6. Order and maintain stock solutions and lab supplies. 7. Effectively communicate and interact with facility users, in person, over the phone and through email to answer routine questions regarding setting up new user accounts, sample submission and preparation and purchasing details. 8. Use a variety of software applications to analyze and review data for quality control and troubleshooting purposes using a variety of software including: a. For Sequencing . i. Sequencher, Codon Code Aligner, FinchTV and other sequence editing and alignment programs. b. For Fragment Analysis. i. GeneMarker and GeneMapper. 9. Assist with data review and generation of monthly invoices for internal and external customers, filing of paperwork and light office duties. Education and Experience 1. Six years of related work experience, four of them in the same job family at the next lower level, and high school level education; or four years of related work experience and an Associate's Degree; or little or no work experience and a Bachelor's Degree in a related field; or an equivalent combination of experience and education. Additional Education and Experience 1. Educational emphasis in biology, genetics, or biochemistry preferred. Candidates with Prior experience in Automated Sanger Sequencing, Microsatelite Analysis and/ or Population Genetics, will be given immediate consideration. Skills & Abilities 1. Experience with automated Sanger Sequencing, Microsatellite Analysis, and/or Population Genteics. 2. Experience in standard molecular biology and general laboratory techniques. 3. Able to effectively communicate with scientists of various levels of training; from Principal Investigators to Undergraduates. 4. Follow established molecular biology protocols for DNA preparation and analysis. 5. Work independently as well as part of a team. 6. Familiarity with MAC, PC, and common software packages such as MS Office and Adobe. Background Check Requirements All external candidates for employment will be subject to pre-employment screening. All offers are contingent on successful completion of a background check.

Carol Mariani <carol.mariani@yale.edu>

YeshivaU SystemsComputationalBiol

Department of Systems and Computation Biology Albert Einstein College of Medicine of Yeshiva University

Multiple Tenure Track Faculty Positions

The Albert Einstein College of Medicine, one of the leading medical schools in New York City, is seeking to fill multiple tenure track faculty positions in the newly formed Department of Systems and Computational Biology. Established in April 2008, the main goal of the new department is to advance our understanding of living systems by developing theoretical, computational and experimental approaches to study complex biological systems.

The College has 750 medical students, 325 graduate students and 360 post-doctoral fellows in training and boasts a strong research faculty covering broad areas of experimental biology, offering outstanding opportunities for collaborative interactions. The 200,000 square foot Center for Genetic and Translational Medicine at Einstein, which opened in late 2007, locates computational, systems and experimental scientists in physical proximity to foster interdisciplinary communication and collaboration. Highly competitive start-up packages are available.

We seek outstanding scientists with broad experience and demonstrated collaborative interactions with experimental or clinical investigators. Candidates should have strength in a physical, mathematical or computational field at the Ph.D. or equivalent level. Experience applying these skills to a biological or biomedical area (demonstrated through publications or support) is also required. Areas of interest include, but are not limited to: Modeling cellular processes, such as signaling, transcriptional regulation and immune response; Pathway analysis; Genetic networks; Functional proteomics and genomics; Evolution of structure and function; Computational neuroscience; Mathematical and computational modeling of complex traits and diseases.

Applicants should send a letter of interest, C.V., statement of research and teaching interests, and names of three referees, in electronic format to:

Systems and Computational Biology Search Committee Albert Einstein College of Medicine Jack and Pearl Resnick Campus 1300 Morris Park Ave. Price Center, Rm. 153 Bronx, New York 10461 E-mail Address: SysBio@aecom.yu.edu Subject line should be: SCB Faculty Search

Careers <careers@aecom.yu.edu>

Other

Arabidopsis field densities

Hi all,

I am looking for citations - or personal knowledge - of the population densities for colonizing versus established populations of Arabidopsis thaliana. Any help is much appreciated.

Thank you,

Kerri Crawford email to: kcrawford@rice.edu

Bioportal computational resource

Dear EvolDir members,

Bioportal http://www.bioportal.uio.no/ at the University of Oslo is a computational resource for bioinformatics and statistical analyses.

The service is freely available for all academic users. The service uses 300 dedicated cores in a Linux cluster and presently has these programs available:

ADSCREENING AIR-APPENDER AIR-IDENTIFIER AIR-REMOVER AUTODOCK4 BLAST DALTON DIRAC FAMHAP FRISCH GARLI GAUSSIAN LAMARC MAFFT MCMCPHASE MELTPROFILE MODELTEST MRBAYES MR-MODELTEST NEWBLER NPMLE OPENBUGS PAUP PFAM PHASE PHRED PHREDPHRAP PHYLOBAYES PHYML PPSCL PROTTEST PSCL R RAXML SIMWALK2 STRUCTURE SUNNYSNP SUNNYSNPP1 TRANSSEQ TREEFINDER UNPHASED

Applying for access: When applying for access (http://www.bioportal.uio.no/) please provide your affiliation and academic e-mail address.

A few applications are restricted to users with a valid license (such as PAUP). Please provide license information when applying for access to such programs.

Limitations of use: Bioportal is best suited for large or parallel tasks (applications are not interactive). Each job submitted to the Bioportal is currently restricted to 1000 hours. Files and processed data are removed after 4 months or earlier - ensure you save your files on your own resources.

Citation: For the Bioportal to remain a free resource we are reliant on being cited: Therefore results from analysis performed on the Bioportal should be cited properly and the full reference sent to kamran@bio.uio.no.

Bioinformatics courses: Please contact us if you want to use Bioportal as computing resource for regular University courses or workshops.

You can find tutorial information about the Bioportal here: http:// hpc.uio.no/index.php/OSCG:Tutorial/

Best wishes, Kamran Shalchian-Tabrizi

Associate Professor Microbial Evolution Research Group (MERG) Bioportal bioinformatics services

Department of Biology University of Oslo P.O. 1066 Blindern N-0316 Oslo Norway t: +47 228 57 302 m: +47 410 45 328 e-mail: kamran@bio.uio.no

MERG: http://www.merg.uio.no/people/kamran.html Bioportal: http://www.bioportal.uio.no kamran@ulrik.uio.no

Bottleneck and inbreeding accumulation

Dear EvolDir,

I would like to know if anyone knows of a way to calculate or simulate the accumulation of inbreeding through a bottleneck.

I am dealing with a wild population that passed through a bottleneck about 5 generations ago. I have detailed population census data from the lowest point of the bottleneck through the recovery up to the current population. I can also provide approximate ancestral population sizes at intervals before the bottleneck occurred.

I have pedigree data for the recovering population so am able to calculate the inbreeding coefficients of the recovered population, but these are based on the assumption that the founding individuals all had an inbreeding coefficient of zero, which is unlikely given the bottleneck.

Any suggestions gratefully received.

Many thanks, Claire Raisin

cr200@kent.ac.uk

Claire Raisin MSc, Durrell Institute of Conservation & Ecology, University of Kent.

Claire Raisin <claireraisin@hotmail.com>

Bovini GenomicDNAsamples

Myself and colleagues Dr Tracey Coffey and Dr. Stephanie Widdison are in need of genomic DNA samples from undomesticated members of the tribe Bovini (buffalo, bison and other bovine-type species).

If anyone can help with this please could you email either myself or one of my colleagues at one of the following addresses:

nicola.pickup@bbsrc.ac.uk

stephanie.widdison@bbsrc.ac.uk

tracey.coffey@bbsrc.ac.uk

Many thanks in advance.

Nikki Pickup

Dr. Nicola Pickup Postdoctoral research assistant Bovine Post-genomics group Institute for Animal Health Compton RG20 7NN

01635 578411 Extension 2596

“nicola pickup (IAH-C)” <nicola.pickup@bbsrc.ac.uk>

Calculating D

Dear EvolDir members,

I am working on estimating the level of linkage disequilibrium in wild deer population, and I am looking for a software program that calculates Lewontin’s D’ for each pair of loci from unphased microsatellite genotypes. Since my samples are unrelated, I do not have haplotype phase information, which is making it difficult for me to find a program that can run my data. I would really appreciate any suggestions you have.

Thank you for your help in advance.

Tomomi Matsumoto

MSc Candidate Department of Biological Sciences University of Alberta Edmonton, Alberta Canada T6G 2E9

tmatsumo@ualberta.ca

Calculating multiallele Fst

I am the maintainer of a forward-time population genetics simulation environment simuPOP. This program has a Fst estimator based on Weir and Cockerham 1984. However, because simuPOP simulates large populations and the WC84 algorithm is designed to *estimate* Fst of a population from a random sample, I am trying to implement an *observed* Fst statistic using observed and expected heterozygosities of a population. The problem is that although the diallelic case is well documented in population genetics textbooks, I could not find a reliable reference on how to calculate H_obs (step 8 of http://www.uwyo.edu/dbmcd/popecol/Maylects/FST.html) if there are more than two alleles at a locus.

Thank you very much.

Bo Peng, Ph.D. Instructor Department of Epidemiology The University of Texas M. D. Anderson Cancer Center

“Peng,Bo” <bpeng@mdanderson.org>

Calculating multiallele Fst answers

Dear EvolDir,

I asked a question about how to calculate multi-allele Fst under a forward-time simulation settings and received many helpful comments. Because other people may be interested in this problem, I am posting some of the comments here for future references.

Background (Original question):

I am the maintainer of a forward-time population genetics simulation environment simuPOP. This program has a Fst estimator based on Weir and Cockerham 1984. However, because simuPOP simulates large populations and the WC84 algorithm is designed to *estimate* Fst of a population from a random sample, I am trying to implement an *observed* Fst statistic using observed and expected heterozygosities of a population. The problem is that although the diallelic case is well documented in population genetics textbooks, I could not find a reliable reference on how to calculate H_obs (step 8 of http://www.uwyo.edu/dbmcd/popecol/Maylects/FST.html) if there are more than two alleles at a locus.

Clarification:

Several people pointed out that the calculation of H_obs is easy because it is merely the frequency of heterozygotes in the population. However, my question was actually how to handle different heterozygotes (A1A2, A1A3, A2A3 etc) in the calculation of F_st using expected and observed heterozygote frequencies. Although a combined H_obs could be used, it is possible that Fst based on different heterozygotes could be estimated separately, and be combined in some way. It turned out that I was heading the wrong way. I should not have calculated H_obs (and H_exp) in the first place.

Answer 1:

Fst cannot be estimated if there are more than two alleles at a locus. Maybe you want to use Gst (Nei 1973)? There are also Rst (Slatkin 1995) and more recently Dest (Jost 2008). Feel free to take a look at my Dest estimator at http://www.ngcrawford.com/django/jost/ - Nick

Answer 2:

In my (perhaps fuzzy) understanding the difference between W&C’s theta (Fst) and Gst is the difference between the estimate of the parameter (the mean of Fst over many realizations of evolution) and realized (˜observed) value. Nei wrote a short paper on this issue (http://www.jstor.org/pss/2408586).

I recollect that there are published methods for calculating Gst at multiallelic loci (some relevant papers come up if you use google scholar (gst multiallelic). I hope this helps

Richard

Answer 3:

You need to use Gst, the k allele analog of Fst. Nei was the one who originally described Gst. See:

Nei M. 1973. Analysis of gene diversity in subdivided populations. Proceedings of the National Academy of Sciences USA 70:3321-3323.

NEI, M., 1977 F-statistics and analysis of gene diversity in subdivided populations. Ann. Hum. Genet. 41: 225-233.

Takahata N, and NEI M. 1984. FsT AND GST STATISTICS IN THE FINITE ISLAND MODEL. Genetics 107: 501-504.

You might also see this paper: http://

www.amjbot.org/cgi/content/full/89/3/460 Matt

Summary Answer:

It turned out that Gst is equivalent to the Wright's Fst in the diallic case so it can be considered as an extension to Wright's Fst in the multi-allele, multi-locus cases. As Nei pointed out (Nei 1986, Evolution, Vol 40, No. 3), Gst calculates the fixation index for existing populations for which genotype frequencies are available, and Fst (Weir and Cockerham 1984) treats existing populations as samples of infinite many populations derived from the same ancestral population. In the estimation of Fst of large simulated populations where genotype frequencies are known, Gst appears to be more appropriate.

However, the calculation and interpretation of Fst are still controversial, after 60+ years of study. :-) New statistics are available (Slatkin's Rst and Jost's Dest), Weir has extended his Fst estimator (Wier and Hill 2002, Annu. Rev. Genet. 36:721-50), and there are different ways to calculate Gst (Culley et al, American J of Botany, 2002, 89, 460-465). For the sake of time, I have only implemented the original Nei 1973 version of Gst in simuPOP. New statistics could be added later.

Further discussion:

To test the new Gst statistics, I have written a short simuPOP script to calculate Fst and Gst for a large evolving population, and for small samples drawn from this population. The script is posted on the simuPOP online cookbook: http://simupop.sourceforge.net/cookbook/pmwiki.php/Cookbook/PopStructure . Briefly speaking, three randomly initialized subpopulations (sizek) are evolved separately for 400 generations. For every 20 generations, Fst and Gst are calculated for the whole population, and for a random sample

— / —

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

Celebrating Darwin

Originally from, ... From: "Phil Terry" <pterry@readingodyssey.com> Date: August 25, 2009 7:53:07 AM PDT Subject: Join E.O. Wilson, Sean Carroll... celebrating Darwin? Reply-To: pterry@readingodyssey.com

I'm writing with a special request regarding a campaign that a ragtag group of volunteers on Facebook has created - along with support from E.O. Wilson, Sean Carroll and media partners like National Geographic. The campaign is Darwin150 and our goal is to gather millions online to celebrate the 150th anniversary of the publication of Darwin's "On the Origin of Species."

While acknowledging that you don't know us, we would like to ask for your help.

1. Help us get to 1 million members on Facebook We already have over 250,000 members on our Darwin Facebook group, and want to get to 1 million members by November 24th to show the breadth and depth of support for evolutionary theory and the significance of Darwin's great book.

Even if you don't use Facebook yourself, please pass this e-mail to your students, postdocs, fellow faculty and others and ask them to join our group on Facebook.

The link to join our Facebook group is here: http://www.facebook.com/group.php?gid=53320310123 2. Join our lecture series

We have designed a free lecture series, available live via webcast and teleconference, on the following dates:

- Wednesday, September 16. "The World before Darwin", Prof. Everett Mendelsohn, Harvard, 8PM EST - Wednesday, October 7, "Variation", Prof. Weiner, Columbia, 8PM EST - Wednesday, November 4, "Natural Selection" Prof. Sean Carroll, University of Wisconsin, 8PM EST - Tuesday, November 24 - "Frontiers of Biology", E.O. Wilson et al, Harvard, 1PM EST

We'd love to have you and your classes join us for any or all of these lectures.

To register to join the lecture, click on the links above or visit this page for more details: http://www.darwin150.com/events 3. Consider hosting an event at your university

St. Louis University, for example, is organizing an auditorium for each of the lecture dates above and inviting all students to come to listen to each lecture together.

We'd love for you to consider doing the same.

The event on November 24, the actual publication anniversary, is at 1PM on the Tuesday before Thanksgiving, which may be a perfect time to gather students to celebrate this momentous occasion.

Would you like to consider hosting an event at your school to bring students and faculty together to participate in one or more of these lectures?

[ ] Yes, please get in touch with more details [ ] Maybe, please get in touch with more details

Again, the link to the lecture series is here: http://www.darwin150.com/events Thanks to our sponsors for helping to make this campaign possible: National Geographic, Harvard Museum of Comparative Zoology, Citrix Online and their HiDef teleconferencing division, Campaign Monitor and our advisor, Harvard Professor John Dowling.

And thanks to you for taking a moment to read and consider this invitation from our volunteer - and ragtag - Darwin150 campaign. For all the details about our project, go to www.Darwin150.org . Best,

Phil Terry Creator, Darwin150 Campaign Founder, Reading Odyssey pterry@readingodyssey.com http://www.facebook.com/group.php?gid=53320310123 http://www.Darwin150.com P.S. Scientists who have participated in our campaign, helped us design the series or lent us their name/support for our efforts this year include:

- Dr. George Amato, American Museum of Natural History - Professor Baker, Columbia; Director, Coral Research Lab - Professor Sean B. Carroll, University of Wisconsin - Professor Rodolfo Dirzo at Stanford - Professor John Dowling at Harvard - Dr. John Durant, MIT Museum - Professor Marc Hauser at Harvard - Professor Jonathan Losos at Harvard - Professor Everett Mendelsohn at Harvard - Professor Olsen, Lamont-Doherty Earth Observatory, Columbia University - Dr. Ploegh, Whitehead Institute, MIT - Professor Peter Raven at Washington University, President Missouri Botanical Garden - Professor Maryellen Ruvolo at Harvard - John Rennie, Editor-in-Chief, Scientific American - Professor Laurie Santos at Yale - Professor Jonathan Weiner, Columbia (author "Beak of the Finch") - Professor E.O. Wilson, Harvard This email was sent to bjswalla@u.washington.edu. You can instantly unsubscribe from these emails by clicking here.

Forwarded to the EvolDir by, "J. R. Stone" <jstoner@mcmaster.ca>

Darwin was first

Some recent posts here have discussed the search for the first evolutionary tree depiction. Joel Parker, in a post titled "Darwin was not first!!," suggested it was Lamarck (1809) and Peter Gogarten suggested Pallas (1766). Augier (1801) also has been mentioned. However the development of evolutionary theory was stepwise, so deciding on the first tree depends on your definition of evolution. Lamarck made significant contributions, but he did not have it right. Because Darwin was the first to propose the model of evolution we all consider to be correct (genetics aside), it is not unreasonable to consider his evolutionary trees–including his 1837 notebook tree and 1859 published tree–to be the first evolutionary trees in the modern sense of the word "evolution."

Blair Hedges

sbh1@psu.edu sbh1@psu.edu

ESEB accomodation

Cheap accommodation for ESEB

I have booked a room in the residence hall for ESEB but will not be staying there. If you would like to stay in this room (description below), please contact me. The fee is 100 euros for 6 nights (Aug. 24-30). (I paid 165 euros.)

Please contact me at: a.agrawal@utoronto.ca Aneil

>>>>Info on residence hall & room:

Address: Hall of Residence Borsellino Via Paolo Borsellino 42 V 10138 Torino Tel.: +39 011 4308758

How to reach the Hall of Residence: > From Porta Nuova railway station: Bus number 68 towards Frejus for 5 stops, get off at Palagiustizia stop and walk along Via Borsellino. As an alternative, tram number 9 towards Stampalia for 5 stops, get off at Palagiustizia stop and walk along Via Borsellino. > From Porta Susa railway station: Bus number 56 towards Di Vittorio for 10 stops, get off at Monginevro Est stop and walk along Via Borsellino.

View the map of the area: http://www.edisu.piemonte.it/cms/images/stories/mappe_residenze/mappa_borsellino.pdf Each room has a private bathroom with shower, a refrigerator, internet connection and a phone for entrance calls. No air conditioning.

Note, that all the university residences are open 24h/24h Check-in: 17:00h Check-out: 10:00h

For more information please click on: http://www.edisu.piemonte.it/ http://-

www.edisu.piemonte.it/cms/residenza-borsellino.html or contact: accommodation.eseb2009@eds.unito.it

There is no wireless connection. However, internet with cable connection is possible 24h/24h and is free of charge. Please, remember to bring your own cable (RJ45).

PLEASE NOTE: Breakfast (25th of August - 30th of August) usually consists of foods that may contain traces of PEANUTS, NUTS, SOYA. Ask onsite for details to our breakfast staff.

Aneil Agrawal <a.agrawal@utoronto.ca>

Estimating Ne answers

Hi all, Thanks to those of you who replied to my quesitons. Peter Beerli's book chapter (see below) was quite helpful and I recommend checking it out.

Here is my orignial query:

I am using Peter Beerli's MIGRATE program to estimate Ne for a number of populations for which I have microsatellite data. So far, I am getting reasonable Ne estimates (I assume microsat mutation rates between 10ˆ-4 and 10ˆ-3). I would like to get some feedback on how to properly interpret these coalescent-based estimates. Specifically, I am wondering how the estimates might be biased if:

(1) the assumption of migration-drift equilibrium is violated (2) the assumption of constant population size has been violated (fluctuating pop size or declines) (3) the organisms have overlapping generations (which is the case with my study organism)

Also, I have used ONeSAMP and LDNe to get estimates of Ne from the linkage-disequilibrium method. In general, the estimates I am getting from MIGRATE are about an order of magnitude larger than the LD-based estimates. Since the estimates from MIGRATE are "long-term" estimates and the LD estimates are "contemporary," does this difference provide evidence in support of population declines? Based on other analyses, I have reason to believe my study populations have undergone decline.

Thanks for any input or suggestions you can provide!

Ivan

Here are the replies:

Dear Ivan,

> (2) In a recent book chapter (*) I explored the issue of violation of > assumption (concerning effects on population size) in MIGRATE a little. It turned out that the estimates are long-term averages > heavily influenced by the recent past. In terms of coalescent events this may be no surprise because many lineage > pairs give information recent coalescences and so seem to influence the results more than the > distant past. Do not forget that recent past the coalescence framework may be still far in the past for some other > estimators.

> (1) If migration happened only during a short time in the past, MIGRATE > will fit an average migration rate but you may want to see whether the data supports such bursts in the past by > using the migration event options in the program.

> (3) I assume all your populations have the same life history/generation > time schedule and so even if there is a bias in the estimates (although the coalescence seems rather robust to these) your comparison > would be unproblematic.

> > You do not say how you did your analysis or whether your populations are > connected by migration or not, if they are then you should analyze them > together and not as single (independent) populations.

> Peter

> * P. Beerli. How to use migrate or why are Markov chain Monte Carlo > programs difficult to use? In G. Bertorelle, M. W. Bruford, H. C. Hauïe, A. Rizzoli, and C. Vernesi, > editors, Population Genetics for Animal Conservation, volume 17 of Conservation Biology, pages 42"79. > Cambridge University Press,

Cambridge UK, 2009.

Some of the problems you are thinking about are dealt with by the Lamarc program, which incorporates growth parameters. Also, use other software to estimate growth, isolantion-with-migration, and compare with your Migrate results. If your data has quite a straight-forward pattern all methods should give you similar results, and if they don't that is also interesting.

> Also, my experience is that Peter Beerli himself is very approachable and helpful if you want to ask specific questions about Migrate -n. > Ramos-Orsins et al. have written a few papers about how different key tests are affected by population size change. > Best,

Magdalena

Hi Ivan,

> I don't know if you've yet found a solution to your inquiry, but the > software BottleSim and information

provided in the companion paper might > provide some insight for your purposes (see > http://chkuo.name/software.html).

> Best wishes,

> Fred Janzen

Ivan C. Phillipsen Department of Zoology Oregon State University 3029 Cordley Hall Corvallis, OR 97331-2914 Email: philliiv@science.oregonstate.edu Website: www.science.oregonstate.edu/ ˜ philliiv/ phillipsen@gmail.com

First tree diagrams

Dear Evoldir members,

I have noticed many evolutionary biologists making an embarrassing mistake of falsely attributing the first use of the tree analogy to Darwin. This has occurred in numerous documentaries and on websites which I will pass on naming here. Ironically, the earliest use of the tree analogy diagram to depict evolution was published in the year of Darwin's birth (1809) by Lamarck in his book Philosophie Zoologique (see pg 463, http://tinyurl.com/knt7vr). Lamarck even uses botanical terms (branches and rameaux) to describe the origin of animals with respect to this figure. The figure that is usually cited from Darwin's notebook is from 1837 (http://tinyurl.com/6hs5uv), a full 8 years after Lamarck's death. Even with our high admiration for Darwin, we should at least give credit where credit is due, and not forget that much of evolution was becoming understood before Darwin. Explaining the mechanism of natural selection was Darwin's great contribution.

Dr. Joel Parker School of Biological Sciences University of Southampton Bassett Crescent East Southampton SO16 7PX

Phone: +44 023 8059 9007 Fax: +44 023 8059 4269 Email: jdparker@soton.ac.uk Website: http://www.sbs.soton.ac.uk/staff/jdp/jdp.php J.D.Parker@soton.ac.uk

First Tree diagrams 2

David Archibald in the introduction to his work on “Edward Hitchcock's Pre-Darwinian (1840) ”Tree of Life“”< http://www.bio.sdsu.edu/faculty/archibald/Archibald08JHBonline.pdf > gives a good overview on the pre Darwinian tree concept, including Augier's 1801 Arbre botanique, and Lamarck's Lamarck's 1809 “tree” diagram. Most striking I found his translation of a text by the Russian naturalist Peter Simon Pallas from 1766: “But the system of organic bodies is best of all represented by an image of a tree which immediately from the root would lead forth out of the most simple plants and animals a double, variously contiguous animal and vegetable trunk; the first of which would proceed from mollusks to fishes, with a large side branch of insects sent out between these, hence to amphibians and at the farthest tip it would sustain the quadrupeds, but below the quadrupeds it would put forth birds as an equally large side branch.” (Pallas, P.S. 1766. Elenchus zoophytorum sistens generum adumbrationes generaliores et specierum cognitarum succintas descriptiones, cum selectis auctorum synonymis. The Hague: Apud Petrum van Cleef.)

jpgogarten@gmail.com

Fishers classification function coefficients

I am the maintainer of a forward-time population genetics simulation environment simuPOP. This program has a Fst estimator based on Weir and Cockerham 1984. However, because simuPOP simulates large populations and the WC84 algorithm is designed to *estimate* Fst of a population from a random sample, I am trying to implement an *observed* Fst statistic using observed and expected heterozygosities of a population. The problem is that although the diallelic case is well documented in population genetics textbooks, I could not find a reliable reference on how to calculate H_obs (step 8 of http://www.uwyo.edu/dbmcd/popecol/Maylects/FST.html) if there are more than two alleles at a locus.

Thank you very much.

Bo Peng, Ph.D. Instructor Department of Epidemiology The University of Texas M. D. Anderson Cancer Center

“Peng,Bo” <bpeng@mdanderson.org>

Geneticist advice

The author of this upcoming book for parents and children contacted the American Genetic Association in search of a geneticist to assist in designing an educational tool. She would prefer a specialist in non-human genetics. Please contact her if you would like to assist.

“Earn My Keep”

Traditionally, there are two ways for children to earn allowance: by doing chores or by doing nothing at all.

I am writing a book called Earn My Keep, where children earn money (or rewards) by taking on real adult careers. Parents will select one career from a list of 50, children will complete one or two or three of the tasks listed that emulate that career and viola! They earn their keep.

An example: This week my daughter is a contractor. We’re using an old grocery box to make a house for one of her favorite dolls. First we made a ’plan’ (a drawing on a piece of notebook paper). We talked about different shapes for the door...where the windows should go...why there could be a chimney...etc. Then we cut out a door...used glue to add curtains. Today she wants to paint on flowers for the ’window boxes.’ :-> Once that’s done, she will have earned her keep (in this case, $2).

The program’s benefits are exponential, but they hinge on its authenticity – which means that I need/want experts to help me create the career profiles. My Geneticist would, first, come up with a laundry list of what he/she does...it does not have to be fancy by any means. I will then group that list into overarching categories. Once those categories/responsibilities are approved by the Geneticist, I would work on translating them into tasks parents can do with their kids, for little or no money. While my experts are more than welcome to help me do the translation into tasks, I am happy to do it on my own.

The Geneticist will have final approval on anything/everything that goes into his/her chapter. It’s important to me that everyone involved in Earn My Keep is excited about the final product, and feels proud to have been a part.

Alisa T. Weinstein CEO, President Earn My Keep, LLC 240-441-3130 alisa@earnmykeep.com

agajoh@oregonstate.edu

Haldane quote

J. B. S. Haldane is credited infamously as responding to the proposed dilemma ’whether he would give his life to save a drowning brother’ with: “No, but I would to save two brothers or eight cousins.”

I would appreciate receiving any information about a literature source for the quotation.

“J. R. Stone” <jstoner@mcmaster.ca>

Important Papers in Evolution

I am going to try something new with my evolution course this year. Rather than have a single required text for the course, students will be given readings (required and recommended) from a diversity of sources for each topic and encouraged to explore material on their own. My goal is to get my students to see evolutionary biology as a field that transcends the texts, something that should permeate their everyday thinking whether it be in the sciences or their personal lives. Ive found that with all my classes that too many students view the text as more than an anchor point for further exploration, but as the end-all of the class. Ever get the student evaluation that complains that the lectures did not follow the text? Though I usually take this kind of complaint as a compliment (it clearly is not meant to be), it also demonstrates that I have failed in at least one small way in my goal as an educator: a passion for learning and a willingness to go beyond the text books. Thus my experiment this semester: do away with the text and explore the field using a diversity of sources, be it primary literature, web sites, chapters from popular books or texts, where ever we can find useful, engaging material. So here is where I reach out to my colleagues and request their help in making this a success. I have listed below some of the major themes/ topics that I feel should be included in an upper level undergraduate evolution course at a liberal arts college. Nothing new here, and it follows what you would find in most of the recent evolution texts. Please feel free to recommend any additional topics or ordering of topics, but more important, I would like to request recommendations for important readings, papers, links to web sites, simulations, laboratory exercises, chapters from texts or books, anything you can think of for any/each category that would assist the student in not only understanding the fundamentals of evolutionary biology, but also the exciting dynamic nature of the field. To make your suggestions readily available and a resource for the community, my goal is to make this a website. Exactly how I do this has yet to be decided, perhaps as a wiki, but probably as a more structured site. I also hope to include both student and professor reviews of each item, but that is long term. If you are willing to make a recommendation, please send it to me (smccaffe@wheatonma.edu), specifying which topic and/or subheading within a topic your suggestion falls, and whether or not you want to have your name associated with it on the web site by designating anonymous or recommender. Again, the student audience is an upper level (junior/ senior) undergraduate course for science majors. Thanks in advance, and I look forward to all your recommendations.

List of topics

What evolution is and the evolutionary perspective Historical perspective Evidence and patterns in evolution Estimating evolutionary trees Diversification of life Genes, mutations, and genetic variation Genetic drift Natural selection: patterns and models Sexual selection Migration and geographic divergence Inbreeding Linkage Evolution of sex Complex characters and the nature of adaptations Evodevo Patterns of molecular evolution and the genome Kin selection and altruism Macroevolutionary trends Evolution today: culture, society, and evolutionary biology

S. Shawn McCafferty Assistant Professor Department of Biology Wheaton College Norton, MA 02766-2322

Email: smccaffe@wheatonma.edu Phone: 508-286-5642

S Shawn McCafferty <smccaffe@wheatonma.edu>

JournalLinneanSociety paper

Hi everybody! Has anybody the paper: “The influence of recent geography, paleogeography and climate on the composition of the fauna of the central Aegean Islands” in the Biological Journal of the Linnean Society, 2005? It can be interesting for our work and we haven’t access to it. Thank you very much.

Reply to: eduard.sola@ub.edu

MARTA ALVAREZ PRESAS <onaalvarez@ub.edu>

Molecular genetic information system

Dear EvolDir readers,

We are currently developing a data information management system for collecting, managing and storing large amounts of molecular genetic data. In this project, we want to make a general data model to meet basic requirements of various labs. We do need feedback or responses from labs to improve our software, which should be available freely at the end of this year.

Hence, we invite you to invest just a few minutes of your time to complete our questionnaire.

http://spreadsheets.google.com/viewform?formkey=-dDk0amd4ZFlwcTl6Vm9GM2RIX2hLYXc6MA ..

Thank you in advance for your effort.

Sincerely, Truong Van Chi Cong and Linn Groeneveld

Dr. Linn Fenna Groeneveld Institute of Farm Animal Genetics Breeding and Genetic Resources Friedrich Loeffler Institut 31535 Neustadt-Mariensee; Germany Tel: +49 (0) 5034 871 197 linn.groeneveld@fli.bund.de http://www.fli.bund.de/1477.html lfgroene@tzv.fal.de lfgroene@tzv.fal.de

---

Ne from Migrate

Dear Evoldir community,

I am using Peter Beerli’s MIGRATE program to estimate Ne for a number of populations for which I have microsatellite data. So far, I am getting reasonable Ne estimates (I assume microsat mutation rates between 10^-4 and 10^-3). I would like to get some feedback on how to properly interpret these coalescent-based estimates. Specifically, I am wondering how the estimates might be biased if:

(1) the assumption of migration-drift equilibrium is violated (2) the assumption of constant population size has been violated (fluctuating pop size or declines) (3)

the organisms have overlapping generations (which is the case with my study organism)

Also, I have used ONeSAMP and LDNe to get estimates of Ne from the linkage-disequilibrium method. In general, the estimates I am getting from MIGRATE are about an order of magnitude larger than the LD-based estimates. Since the estimates from MIGRATE are "long-term" estimates and the LD estimates are "contemporary," does this difference provide evidence in support of population declines? Based on other analyses, I have reason to believe my study populations have undergone decline.

Thanks for any input or suggestions you can provide!

Ivan

Ivan C. Phillipsen Department of Zoology Oregon State University 3029 Cordley Hall Corvallis, OR 97331-2914 Email: philliiv@science.oregonstate.edu

phillipsen@gmail.com

Number of HLA molecules

Dear all

At BioNumbers, the database of useful biological numbers (link below), we would be grateful for a reply to:

What is the number of HLA (Human Leukocyte Antigen)/MHC molecules on the surface of an average human cell?

Reference/s would be much appreciated.

regards,

Uri

Uri Moran Ron Milo's Group Dept of Plant Sciences Weizmann Institute of Science, Rehovot, 76100, Israel +972-8-9344540

BioNumbers, The database of useful Biological numbers www.bionumbers.org (http://bionumbers.hms.harvard.edu/default.aspx)

Uri Moran <uri.moran@weizmann.ac.il>

ONeSAMP Software Problem

Can anyone help? I am using a web-based software package to analyse microsatellite data to work out the effective population sizes of populations of rainbow trout in Chile. The program is called ONeSamp and is written by Prof David Tallmon. The data has been entered in the required 3 digit genepop format, specifying population, alleles, loci and repeat motifs. Organised and ammended data is sent via the internet and results received 2-3 days later. My problem is, is how to represent blank samples (i.e. samples with no data). I have entered these as 000000 but my returned results file is received back as input error and no results. Eveything else (I think) is correct. Considering it takes 2 days to receive results, I don't want to just represent these samples as ?????? as I will be wasting more time if this is wrong! If anyone can help, I would be extremely greatful.

Many thanks, Nia Phillips

ncp08@aber.ac.uk

paper 2

Dear members of Evoldir: Yesterday we sent this original message:

"Hi everybody! Has anybody the paper: "The influence of recent geography, paleogeography and climate on the composition of the fauna of the central Aegean Islands" in the Biological Journal of the Linnean Society, 2005? It can be interesting for our work and we haven't access to it. Thank you very much.

Reply to: eduard.sola@ub.edu "

The email to which answer was a mistake. It's eduardsola@ub.edu instead of eduard.sola@ub.edu. However, some of you have sent your response to onaalvarez@ub.edu direction that it is correct. The fact is that the paper is already in our hands. We wanted to apologize to those that you have answered eduard.sola @ ub.edu and thank you all.

Greetings,

Eduard Solà

MARTA ALVAREZ PRESAS <onaalvarez@ub.edu>

Papers request

Dear Evoldir membersÂ: Â I am looking for the papers mentioned below, toÂwhich unfortunately ÂIÂ do not have access:

Cherry, S. (1996). A comparison of confidence interval methods for habitat use-availability studies. J. Wildl. Manage. 60: 653â 658.

and

Byers, C. R., Steinhorst, R. K. & Krausman, P. R. (1984). Clarification of a technique for analysis of utilizationâavailability data. J. Wildl. Manage. 48: 1050â1053.

I will greatly appreciate if somebody could help me.

Â Many anticipated thanks.

Reply to: bcarmen@uvigo.es

Carmen Burghelea <carmen_burghelea@yahoo.es>

Paraquat use query

Dear EvolDir members,

I am a Ph.D. student, new to the field of Drosophila work. I need to study the evolution of oxidative stress response in *Drosophila melanogaster *using the ROS-generating herbicide Paraquat*.* I have looked into several literatures but couldnt find which Paraquat to use as two types are available in the market, Paraquat dichloride and Paraquat tetrahydroxide. It would be of great help if you can answer my querry as soon as possible.

– Sreoshi Chatterjee Ph.D. scholar, Evolution and Behaviour Ecology Lab, School of Life Sciences, Jawaharlal Nehru University, New Delhi - 110067

sreoshi chatterjee <sreoshichatterjee@gmail.com>

Parsing sequences by distance answers

Dear all,

I have received a number of useful answers to my question regarding the breaking up of alignments based on a sequence distance threshold (see my original question below this message) which I will summarise below.

Two programs were suggested independently by a number of people. These programs are usually employed for analysing communities of soil organisms, and can divide sequences into clusters based on a similarity measure threshold set by the user:

1. Robin Floyd and Simon Creer both kindly pointed me towards the Perl script MOTU_define, which can be found on the website of Mark Blaxters lab at the university of Edingburgh (http://www.nematodes.org/bioinformatics/MOTU/index.shtml). MOTU_define uses blast-based similarity matching, and single linkage clustering.

2. Sujeevan Ratnasingham, Simon Creer and Richard Waterman suggested the program Dotur, by Patrick Schloss from the university of Massachusetts (http://schloss.micro.umass.edu/software/dotur.html). However, this program has recently been incorporated in the new open source, expandible software Mothur (http://schloss.micro.umass.edu/mothur/Main_Page) which can do many cool things, including sequence clustering. It allows you to choose between single linkage (nearest neighbor), complete linkage (furthest neighbor) and average linkage (average neighbor / UPGMA) clustering methods.

In addition, Lee Taylor suggested using the genome assembly program Cap3 (Lee Taylor).

I hope this may help anyone else interested in sequence clustering.

Best,

Robin van Velzen

—–Original Message—– From: evoldir@evol.biology.mcmaster.ca [mailto:evoldir@evol.biology.mcmaster.ca] Sent: woensdag 22 juli 2009 7:25 To: Velzen, Robin van Subject: Other: breaking up alignments based on distances?

Dear EvolDir members,

I have a large (>500 individuals) partial COI DNA sequence alignment which I would like to break up into subsets based on a pairwise sequence distance threshold. For example: break up the alignment into subsets containing individuals with <10% pairwise sequence distance. Ideally, I would want to do this without having to produce a distance tree.

Does anyone know of a program or script that could do this for me?

Any suggestions are most welcome.

Thanks!

Robin van Velzen

Robin van Velzen - PhD student Robin.vanVelzen@wur.nl Biosystematics Group, Wageningen University Generaal Foulkesweg 37, 6703 BL Wageningen, The Netherlands Tel: +31 (0)317 483425 FAX: +31 (0)317 484917 http://www.bis.wur.nl/UK/ www.nationaalherbarium.nl <file://www.nationaalherbarium.nl/>

Robin.vanVelzen@wur.nl Robin.vanVelzen@wur.nl

Phylogenetics software recommendation

Can someone recommend a free basic phylogenetics software to construct a species tree? I tried TREEFINDER that had been announced on this list but could not get it to work either on Windows 2000 Pro or XP Pro. A screen would momentarily flash when I clicked on the executable file, but nothing else came up. I am interested in doing just some simple simulations using imaginary characteristics. If the genealogical relationships in a tree that is built by some of the current free software is dependent on specific molecular sequences, that would be a problem for what I want to do.

Sincerely, Stan Gorodenski

stanlep@commspeed.net

Stan Gorodenski <stanlep@commspeed.net>

Plant Fuzzy-Set-Ordination

Hello,

I have a matrix with 180 plant species (variables, binary) and 270 rows (altitude waterbodies). There is also one categorical variable (4 categories representing similar lakes groups, which resulted from a prior analysis of the transposed matrix). Is there any way to load plant species on those categories in fuzzy-set-ordination analysis? Is there anyone here that has faced this question before or could provide a hint? All my efforts so farhave lead to loading the lakes on the categories (fso in R); but I want to load the plant species.

I would greatly appreciate your help.

Dragos Zaharescu Vigo University

˜ You should be the change you want to see in the world˜ Ghandi

Dragos Zaharescu <zaha_dragos@yahoo.com>

Plant seed samples

We are looking for seeds from European and US populations of several plant species. If you could collect seeds from any of the species listed below or know someone who could or already has these seeds, we would be very grateful for any seeds we can get. For those who send us seeds, we will send Swiss chocolate back. We are looking for the following plant species: Lepidium latifolium Lunaria rediviva Silene dioica Saponaria officinalis Hypericum humifusum Hypericum perforatum Glechoma hederacea Teucrium scorodonia Poa compressa Briza media Linaria vulgaris Veronica chamaedrys Epilobium hirsutum Epilobium obscurum Aegopodium podagraria Peucedanum ostruthium Aster lanceolatus Aster laevis Aster novi-belgii Aster novae-angliae Mimulus guttatus Mimulus moschatus Solidago canadensis Solidago graminifolia

Sampling design: - Please write down some site characteristics (Location (preferably using GPS coordinates, pinpointing the location in Google maps is also a possibility), rough estimation of the population size (50, 100, 200, 500, 1000, 2000, >2000 flowering/fruiting shoots), rough habitat description (forest, meadow etc.), the collection date Seed collection - Take the seeds from 20 plants (preferably >5m apart) in the population. If there are not enough plants, we are happy with any seeds we can get. - Bag seeds/fruits with seeds from different plants separately and write the name of the sampling location on the bag.

Mail the seeds to Lidewij Keser Institute of Plant Sciences University of Bern Altenbergrain 21 CH-3013 Bern Switzerland

Thank you very much.

Lidewij Keser

Keser Lidewij <lidewij.keser@ips.unibe.ch>

Quantify DNA answers

Thanks to all who shared their preferences on quantifying DNA.

My original question was:

Dear colleagues,

Which kind of instrument do you prefer to use to quantify DNA for use

in sequencing? I have used the NanoDrop from Thermo, but was wondering

if anyone has something else that you use.

The most popular answer was the Qubit from Invitrogen. It is a fluorescence-based instrument that uses solutions that you add to your sample and measure, either on a plate reader or on their small footprint fluorometer.

“The fluorometer uses an intercalating dye to bind to the DNA and then fluoresces when excited. This means that unlike the spectro based machines, the reading reflects only the DNA present in the sample and is not influenced by non-DNA which can influence the reading of a spec-based machine. For accuracy, I think the fluorometer is hard to beat.”

Others said they run their samples on an agarose gel, and compare band intensity to a sample of “known” concentration. They needed to make sure they had a PCR product anyway, and with practice is an easy way to “quantify.”

I knew about the pitfalls of UV/Vis measurements, but when the NanoDrop came along, its ease of use outweighed the problems. Now it sounds like the Qubit kits have made fluorescent measurements easier, so it is certainly worth consideration.

Thank you all for your help,

Ann R. Harris

email: annharris@ou.edu<mailto:annharris@ou.edu>

Quantifying DNA

Dear colleagues,

Which kind of instrument do you prefer to use to quantify DNA for use in sequencing? I have used the NanoDrop from Thermo, but was wondering if anyone has something else that you use.

Ann R. Harris email: annharris@ou.edu<mailto:annharris@ou.edu>

“Harris, Ann R.” <annharris@ou.edu>

Rana perezi paper

Dear evoldir members,

I am looking for a paper by Balletto and colaborators on the presence of Rana perezi in Madeira. This paper was published in 1990 but I do not know in which journal. I do not have the exact reference because they are mentioned in a book that I have not access to. Part of this book is available on the web but not the exact reference. I have tried to look for it through the internet but nothing comes out.

Apparently, these authors have used genetic data to claim that R. perezi arrived in the island 400,000 years ago. They are the only ones to make such a claim and wondered whether they misinterpreted the genetic data.

Thank you in advance for any help Hopefully something will come out if this. best wishes Joao Alves

Joao Alves <jmf_alves@yahoo.com>

Scitable and evolution

The Nature Publishing Group has launched a new division called Nature Education, which produces Scitable (http://www.nature.com/scitable), a new FREE resource for undergraduate education in the Life Sciences. Currently, Scitable provides content on genetics. Two of the topic areas within Genetics are "Population and Quantitative Genetics" and "Evolutionary Genetics."

We are very grateful to those members of the community who have contributed the articles that allowed us to launch Scitable. As Scitable continues to develop, we are seeking additional content articles (1,000-2,000 words) that provide concise overviews of topics in evolutionary genetics. Ideally, the article would cite primary literature that can be provided to users as full-text. Through Scitable, full-text articles of Nature titles (Nature, Nature Genetics, etc.) are frequently made available alongside links to open-access journals.

While all ideas are welcome, for the Population and Evolutionary Genetics areas we are especially seeking articles that deal with conservation and ecological genetics, applications of population and quantitative genetics, the coalescent, statistical tests of neutrality and other hypotheses, genome evolution, and evo-devo.

If you have ideas relating to the organization of Scitable and/or wish to contribute, please contact Rich Kliman (rmkliman@cedarcrest.edu). We would be grateful if you would bring this invitation to the attention of colleagues who may not subscribe to EvolDir.

We also seek instructors who will help us with beta-testing. In addition to content that links to full-text journal articles, Scitable allows instructors to set up classroom pages that host course material. These classroom pages can be used to host a combination of the instructor's own course materials and supplemental Scitable articles. In Fall 2009, Scitable will be offering new course readings called "Essentials in Genetics", that include explanations of key genetics concepts supported by animations and interactive media. In addition to a variety of supplemental course content, Scitable provides a social media space for both faculty and students that includes chat tools and discussion forums.

Rich Kliman, Lead Editor, Evolutionary Genetics Topic Room Ilona Miko, Senior Scientific Editor, Scitable

Rmkliman@cedarcrest.edu Rmkliman@cedarcrest.edu

Software Circuitscape3 4

Hi folks,

Weve released Circuitscape 3.4 connectivity analysis software. Circuitscape uses circuit theory to predict connectivity for gene flow, animal movement, and conservation planning. Version 3.4 includes new features and improvements in memory management.

Executable versions for Windows and Mac, and Python source files for Linux, are all freely available. You can download these and read about applications of circuit theory in ecology, landscape genetics, and conservation at www.circuitscape.org . –

Brad McRae The Nature Conservancy 1917 1st Avenue Seattle, WA 98101 Tel: (541) 223-1170 email: bmcrae@tnc.org http://www.nceas.ucsb.edu/~mcrae/ Brad McRae <mcrae@circuitscape.org>

Software FastTree2 0 0

We announce FastTree 2, a tool for inferring approximately maximum-likelihood trees for large alignments. FastTree is more accurate than PhyML 3's default settings and 100-1,000 times faster than PhyML or RAxML. FastTree analyzed an alignment of >200,000 16S ribosomal RNAs in a day on a desktop computer.

Models: Jukes-Cantor or GTR (nucleotide) or JTT (amino acid) Rate variation across sites: the CAT approximation (1 rate per site) Support values: local SH-like supports (or global bootstrap)

FastTree 2 is available at http://www.microbesonline.org/fasttree/ Morgan N. Price & Paramvir S. Dehal Physical Biosciences Division Lawrence Berkeley National Lab fasttree@microbesonline.org

morgannprice@yahoo.com

Software NexusDataEditor

Users of NDE who haven't been able to get it to install on Vista can download a new installer from http://taxonomy.zoology.gla.ac.uk/rod/-NDE/nde.html#Download (just click on the "Download" link). I've tested this on Windows XP and Vista, and it seems to work. NDE itself is about a decade old, and I've turned my attention to other things, but I hope this will help those NDE users who still find the program useful, but have been left out in the could by upgrading to Vista.

Regards

Rod

Roderic Page Professor of Taxonomy DEEB, FBLS Graham Kerr Building University of Glasgow Glasgow G12 8QQ, UK

Email: r.page@bio.gla.ac.uk Tel: +44 141 330 4778 Fax: +44 141 330 2792 AIM: rodpage1962@aim.com Facebook: http://www.facebook.com/profile.php?id=-1112517192 Twitter: http://twitter.com/rdmpage Blog: http://iphylo.blogspot.com Home page: http://taxonomy.zoology.gla.ac.uk/rod/rod.html r.page@bio.gla.ac.uk r.page@bio.gla.ac.uk

---

SouthAfrica Volunteers SmallMammalEvolution

Volunteers needed as field assistants for the project:

Evolution and Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

>From December 2009 onwards

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work relating to evolution, ecology and behavior before starting an MsC or PhD project.

Project: We study the evolutionary and ecological reasons of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o‘ clock), and stops its activity with dusk (19 o‘ clock). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small group.

Work of field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field; maintenance of the research station.

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1000 (around 90 Euro) must be paid for accommodation at the research station. For students with their own undergraduate project, a fee of Rand 1250 (approx. 110 Euro) per month applies. Students must buy their own food etc in Springbok (costs of about R 2000 or 170 Euro/month). Including extras, you should expect costs of about 300 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: At the moment we are looking for volunteers to start in December 2009. Volunteers who want to start later in 2010 can also apply now. Volunteers are expected to stay at least 2 months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to carsten.schradin@zool.uzh.ch.

More information under www.stripedmouse.com Contact via e-mail: carsten.schradin@zool.uzh.ch

Dr. Carsten Schradin

Research Assistant, Zoological Institute, Department of Animal Behavior,

University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland.

Tel: +41 - (0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences,

University of the Witwatersrand, South Africa.

WORKING AS A FIELD ASSISTANT IN GOEGAP NATURE RESERVE

A report by Romy Höppli, student at the University of Zurich, who staid in Goegap June to August 2008

Blue skies without a single cloud for six weeks - rocky mountains with little vegetation - yellow, orange and pink fields of flowers in whatever direction you look - small mammals, lizards and birds in our front yard and Mountain Zebras, Springbok and Ostrich right next door...

This was my time at the Succulent Karoo Research Station in Goegap Nature Reserve in South Africa! During six weeks from the beginning of July until the middle of August I've been living here, studying mice, experiencing nature like never before and being part of a small community where there was always something to laugh and joke about!

After arriving in Goegap, right the next morning my scientific adventure in South Africa began: Setting and checking traps, nest observations and radio-tracking were our daily routine. While I got bitten by the mice quite often in the beginning and my right middle finger was scarred all over, I improved quickly shaking the mice out of the traps, weighing them and checking the number of the ear tag. Other duties like cleaning the cages of the mice in the captive colony, washing the dirt from probably several months out of the traps, painting the new Wendy House and putting in a floor and curtains quickly added to our daily field work activities.

It was never boring in Goegap! There was always something to do:

— / —

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

---

Swift tern egg pictures

Dear all,

I am a Diploma student at Max Planck Institute for Ornithology in Germany and working on the evolution of egg coloration. For my project I am looking for egg pictures of swift terns (Sterna bergii). If you work on swift terns or know anyone doing so it would be great to get in touch, as I am interested in getting an opportunity of taking some pictures of swift tern eggs.

Thank you!

Best, Janine Quaas

MPI for Ornithology Eberhard-Gwinner-Str. 5 82319 Seewiesen Germany +49(0)8157-932423 jquaas@orn.mpg.de

Janine Quaas <jquaas@orn.mpg.de>

PostDocs

Belgium GenomeBioinformatics

Postdoctoral project: Genome analysis of a degenerate asexual tetraploid â the bdelloid rotifer /Adineta vaga./

/ /

Selection of candidates for a postdoctoral grant to submit to the Belgian Fonds de la Recherche Scientifique (FNRS) by Sept. 15^th 2009. This FNRS-sponsored postdoctoral position is requested by Karine Van Doninck (University of Namur â FUNDP, Belgium) together with the postdoctoral candidate to participate in the project on the forthcoming availability by Genoscope of the first assembled whole genome sequence of the bdelloid rotifer /Adineta vaga/.

Rotifers of Class Bdelloidea are remarkable in having evolved for millions of years, apparently without males and meiosis and therefore termed an “evolutionary scandal” by John Maynard Smith. Sequencing the genome of the bdelloid rotifer /Adineta vaga/ will make it the first representative of the Phylum Rotifera and of the early branching triploblasts to which it belongs. The availability of their genome sequence will also facilitate further tests investigating the genomic consequences of long-term evolution without meiosis and confirm their status of degenerate tetraploid.

The genome sequencing project of /A.vaga/ has started and therefore a researcher with a strong background in Bioinformatics and in genomics is requested to start in January 2010. The postdoctoral candidate will work with Karine Van Doninck at the University of Namur (Belgium) and Olivier Jaillon at the Genoscope â CEA (Paris, France) and will participate in the interpretation of the annotated genome, especially with respect to the evolutionary and biological characteristics of bdelloid rotifers.

The FRFC Belgian non-taxable postdoctoral fellowship can be for 2 or 3 years with a maximum salary of 37.000 euro/year.

To be eligible the candidate should have the following characteristics:

- did not reside or work in Belgium during 24 months the last 3 years

- obtained his PhD less then 6 years ago

- has a strong publication record

Recent publications include:

- Van Doninck K, Mandigo ML, Hur JH, Wang P, Guglielmini J, Milinkovitch MC, Lane WS, Meselson M. Phylogenomics of unusual histone H2A Variants in Bdelloid rotifers. PLoS Genet. 2009 Mar;5(3).

- Hur JH, Van Doninck K, Mandigo ML, Meselson M. Degenerate tetraploidy was established before bdelloid rotifer families diverged. Mol Biol Evol. 2009 26:375-83.

- Mark Welch DB, Mark Welch JL, Meselson M. Evidence for degenerate tetraploidy in bdelloid rotifers. 2008 Proc Natl Acad Sci 105:5145-9.

- Jaillon O. /et al./ Translational control of intron splicing in eukaryotes. Nature. 2008 Jan 17;451(7176):359-62.

- Jaillon O. /et al./ - French-Italian Public Consortium for Grapevine Genome Characterization. The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. Nature. 2007 Sep 27;449(7161):463-7.

- Aury JM, Jaillon O, Duret L, Noel B, Jubin C, Porcel BM, SÃ©gurens B, Daubin V, Anthouard V, Aiach N, Arnaiz O, Billaut A, Beisson J, Blanc I, Bouhouche K, CÃmara F, Duharcourt S, Guigo R, Gogendeau D, Katinka M, Keller AM, Kissmehl R, Klotz C, Koll F, Le MouÃ«l A, LepÃre G, Malinsky S, Nowacki M, Nowak JK, Plattner H, Poulain J, Ruiz F, Serrano V, Zagulski M, Dessen P, BÃ©termier M, Weissenbach J, Scarpelli C, Schächter V, Sperling L, Meyer E, Cohen J, Wincker P. Global trends of whole-genome duplications revealed by the ciliate Paramecium tetraurelia. Nature. 2006 Nov 9;444(7116):171-8.

If you have further questions concerning this position, please contact Karine Van Doninck (kvandoni@fundp.ac.be <mailto:kvandoni@fundp.ac.be>).

Interested candidates should email a letter of application, its curriculum vitae including a brief description of recent research, and the names, email addresses and telephones of three references by September 3rd, 2009 to Karine Van Doninck (kvandoni@fundp.ac.be <mailto:kvandoni@fundp.ac.be>) and Olivier Jaillon (ojaillon@genoscope.cns.fr <mailto:ojaillon@genoscope.cns.fr>).

Karine Van Doninck <karine.vandoninck@fundp.ac.be>

Bergen SalmonidStatisticalGenetics

Post-doctoral position in statistical genetics

The Institute of Marine Research has a two-year post-doctoral position available in the Population Genetics and Ecology research group. The position will be located in Bergen.

The position will be linked to the MENTOR research project which will study natural selection in wild and cultivated Atlantic salmon in the wild with the aid of a high-density SNP marker chip. The work of the appointee will focus on statistical analysis of genetic data based on SNP and microsatellite markers, and publishing. The aim is to identify genes under selection and map QTLs in salmon in the wild.

We wish to appoint a person with a doctorate in statistical genetics or a related field. The appointee will need to be able to document experience of modern methods of statistical analysis that can be used to relate large amounts of genetic data to biological traits. Familiarity with linkage analysis, genome mapping and population genetics would be an advantage. Experience of working with fish is not required.

The Institute emphasises personal qualities such as good communication and cooperative skills and the ability to work independently, and on experience of publishing in recognised international journals.

We offer:

* a positive, challenging and creative work environment
* the opportunity to work in a national institute with a high level of international contact * flexible hours, a good pension scheme and a wide range of welfare services.

The Institute offers governmental regulated salaries as Post-doctor (code 1352).

For more information, please contact Research Group Leader Terje Svaasand,

Email: Terje.Svaasand@imr.no, tel: +47 55236891

or Project leader Oystein Skaala, Email: Oystein.Skaala@imr.no, tel: +47 47627878,

or visit our web-site at www.imr.no < http://www.imr.no/ >

The Institute of Marine Research is an “inclusive work-life” employer that encourages diversity, and we encourage all qualified candidates to apply for this position. Women are particularly encouraged to apply.

Please apply in writing, enclosing a CV, copies of relevant recommendations and academic transcripts together with a set of publications, to: Institute of Marine Research, Personnel Division, P.O. Box 1870 Nordnes, NO-5817 Bergen, Norway.

Application number: “29-09”. Closing date for applications: 05.09.2009.

The Institute of Marine Research is one of Europe’s largest centres of marine research. We have a staff of around 700 and a wide range of research facilities and laboratories of high international standard. The Institute owns and operates six research vessels. Our main offices are in Bergen, and we have a department in Tromsø and research stations in Matre, Austevoll and Flødevigen.

"\"Michael Møller Hansen\"" <mmh@biology.au.dk>

ColoradoStateU EvolutionaryGenomics

Postdoc: Genome Evolution

A post-doctoral position in genome evolution is available in the Biology Department at Colorado State University. The successful candidate will use 454 data to study the mutational processes underlying extreme genomic expansion in plethodontid salamanders. Plethodontids have among the largest vertebrate genomes from 15 to 75 Gb. Although such genomes are known to consist largely of repetitive DNA, the repeat elements, their mutational dynamics, and the ways in which these dynamics translate into large and variable genome sizes remain almost completely uncharacterized. The goal of our project is to generate large-scale genomic data from numerous species of plethodontids and analyze the tempo and mode of novel repeat element evolution in a phylogenetic context. Such genomic analyses will be combined with ongoing comparative methods-based analyses of plethodontid genome size evolution.

A Ph.D. in evolutionary or comparative genomics, or in a closely-related field, is required by the position start-date. The successful candidate will be expected to interact with the CSU Center for Bioinformatics as well as graduate and undergraduate students and post-docs in our growing lab group. This project is being conducted in collaboration with the UC Denver-based Consortium for Comparative Genomics, directed by David Pollock; the successful candidate will interact with both the Pollock lab group and the Consortium on data collection and analysis.

The Department of Biology at Colorado State University is an interdisciplinary group with a strong crew of evolutionary biologists. CSU is heavily oriented towards life sciences. In addition to the Department of Biology in the College of Natural Sciences, CSU has four other colleges dedicated to life science research: Applied Human Sciences, Agricultural Sciences, Veterinary Medicine & Biomedical Sciences, and the Warner College of Natural Resources. In addition, the Centers for Disease Control and Prevention, the United States Department of Agriculture, and the United States Geological Survey have active laboratories in Fort Collins.

Fort Collins is a beautiful city of 120,000 people located at the base of the Rocky Mountains. We enjoy easy access to world-class outdoor recreation and 300+ days of sunshine each year.

The position is available as soon as a suitable candidate is identified. Start-date is negotiable.

For full consideration, materials must be received no later than Friday, September 18, 2009. However, applications will be accepted until the position is filled. For questions regarding the position, please contact Rachel Mueller: Rachel.Mueller@colostate.edu. Also, please visit the lab website: http://rydberg.biology.colostate.edu/muellerlab To apply for the position, please submit the following application materials as a single pdf file: (1) CV, (2) one-page statement of research interests, (3) up to three recent publications, and (4) contact information for three referees to: http://www.natsci.colostate.edu/employment/BioPdoc/ Colorado State University does not discriminate on the basis of race, age, color, religion, national origin, gender, disability, sexual orientation, veteran status or disability. The University complies with the Civil Rights Act of 1964, related Executive Orders 11246 and 11375, Title IX of the Education Amendments Act of 1972, Sections 503 and 504 of the Rehabilitation Act of 1973, Section 402 of the Vietnam Era Veteran's readjustment Act of 1974, the Age Discrimination in Employment Act of 1967, as amended, Americans with Disabilities Act of 1990, the Civil Rights Act of 1991, and all civil rights laws of the State of Colorado. Accordingly, equal opportunity of employment and admission shall be extended to all persons and the University shall promote equal opportunity and treatment through a positive and continuing affirmative action program. The Office of Equal Opportunity and Diversity is located in 101 Student Services. In order to assist Colorado State University in meeting its affirmative action responsibilities, ethnic minorities, women and other protected class members are encouraged to apply and to so identify themselves. Colorado State University is committed to providing a safe and productive learning and living community. To achieve that goal, we conduct background investigations for all final candidates being considered for employment. Background checks may include, but are not limited to, criminal history, national sex offender search and motor vehicle history.

_

Rachel Lockridge Mueller Assistant Professor Department of Biology Colorado State University Fort Collins, CO 80523-1878 (970) 491-6717

rlm@colostate.edu rlm@colostate.edu

DukeU PrimateOlfactoryEvolution

Duke University

Department of Evolutionary Anthropology

Associate in Research

Applications are invited for a postdoctoral position to study the evolution of olfactory communication in primates. The post is funded by the National Science Foundation and is immediately available, for one year, with the possibility of extension. The work combines behavioral, chemical, and genetic approaches, and is conducted at Duke University (http://www.baa.duke.edu/) and its Lemur Center (http://lemur.duke.edu/). Previous and current projects have focused on the ring-tailed lemur and the mandrill, with planned extensions to other species.

The successful candidate will have earned a PhD in a relevant discipline at the time of appointment. Applicants should have a strong background in one or more of the following areas: animal behavior, behavioral ecology, chemical ecology, evolutionary biology, population genetics, proteomics.

Please email an application to Christine Drea (cdrea@duke.edu), consisting of a cover letter summarizing your qualifications and interests, a curriculum vitae, representative reprints or preprints, and the names and contact information for two references. Evaluation of applicants will begin immediately and will continue until the position is filled. Duke University is an Affirmative Action/Equal Opportunity Employer.

Christine Drea <cdrea@duke.edu>

EmoryU VisualPigmentEvolution

Postdoctoral Positions at Emory University

The Long-term goal of our research is to elucidate the mechanisms of

1) the spectral tuning of visual pigments

2) the adaptive evolution of dim-light and color vision

3) infrared vision

Selected References:

Yokoyama, S., Tada, T., Zhang, H. and Britt, L. (2008) Elucidation of phenotypic adaptations: molecular analyses of dim-light vision proteins in vertebrates. PNAS 105: 13480-13485. Altun, A., Yokoyama, S. and Morokuma, K. (2008) Spectral tuning in visual pigments: An ONIOM(QM:MM) study on bovine rhodopsin and its mutants. J. Phys. Chem. B 112: 6814-6827.

Yokoyama, S. (2008) Evolution of dim-light and color vision pigments.

Annu. Rev. Genomics Hum. Genet. 9: 259-282.

We are looking for recent graduates who are well versed either 1) in experimental molecular biology/genetics or 2) in sequencing and annotating ESTs.

If you are interested, please send CV to Shozo Yokoyama (Email:syokoya@emory.edu).

Shozo Yokoyama, Ph. D. Asa G. Candler Professor of Biology Department of Biology Emory University 1510 Clifton Road Rollins Research Center Atlanta, GA 30322 Tel:404-727-5379 FAX:404-727-2880 Email:syokoya@emory.edu

Shozo Yokoyama <syokoya@emory.edu>

GoettingenU SymbiosisEvolution

The “Geomicrobiology and Symbiosis” junior research group (http://www.uni-goettingen.de/en/102704.html) in the Courant Research Centre Geobiology at the University of Goettingen invites applications for a postdoctoral position, starting on December 1, 2009.

Topic: Chemoautotrophic symbioses have evolved independently in diverse animal and bacterial phyla and are ubiquitous in marine environments such as deep-sea hydrothermal vents, cold seeps and shallow organic-rich sediments. Recently, the first example of a terrestrial chemoautotrophic symbiosis was discovered in the sulfide- rich limestone caves of Frasassi, Italy (Dattagupta, S. et al. The ISME Journal, 3, 935-943). This symbiosis is likely to have evolved less than one million years ago, making it tens to millions of years younger than its marine counterparts. It could thus provide valuable insight into the initiation and early evolution of chemoautotrophic symbioses. The study will investigate factors contributing to host- recognition and specificity, as well as mechanisms enabling dominance of the symbiotic phylotype in its host environment.

Requirements: Applicants must be fluent in English and have completed a Ph.D. in Geomicrobiology, Microbial Ecology or a closely related field. They must be competent with classical (bacterial isolation) and modern molecular methods for microbial analyses; experience with pyrosequencing, genomics, and bioinformatics is a plus. Fieldwork experience and at minimum, an interest in cave exploration, is desired. International applicants are welcome. The University of Goettingen seeks to increase the participation of women in areas in which they are currently underrepresented and therefore explicitly urges women to apply. Disabled persons with equivalent aptitude will be favoured.

Employment: We offer a two-year Postdoc position with the possibility of extension to three years. Postdoc salary is based on the German TV-L system, level 13.

Environment: Goettingen is a quaint and traditional German university town with an international student-based community. The Courant Research Centre is one of seven interdisciplinary research centres (www.uni-goettingen.de/crc) recently established by Goettingen University. The Centre offers a wide range of state-of-the-art analytical facilities and an excellent environment for interdisciplinary research.

Application (Deadline: October 1, 2009): Candidates should send a curriculum vita and a statement of research interests by email to Dr. Sharmishtha Dattagupta (sdattag@uni-goettingen.de). They should also arrange for two reference letters to be sent *directly* by the referees before the deadline.

sdattag@uni-goettingen.de sdattag@uni-goettingen.de

HarvardU MalariaPopGenet

Postdoctoral in malaria population genomics

A postdoctoral position is available immediately to conduct population genomic analyses of the malaria parasite P. falciparum. Data will be derived from SNP genotyping arrays and Illumina/Solexa sequencing. Research activities will include screens for natural selection, comparison of data collected on different platforms, analysis of linkage disequilibrium, and association studies for drug resistance and other phenotypes.

The successful applicant will be based in the laboratory of Daniel L. Hartl at Harvard University and will also interact with Daniel E. Neafsey at the Broad Institute in Cambridge, MA. Applicants should have a strong background in population genetics and computational analysis, as well as a deep interest in applying evolutionary tools to address public health problems. Demonstrated ability to code in perl/python/R or the equivalent is essential.

Applicants should email their CV and the names and contact information of three references to Daniel L. Hartl <dhartl@oeb.harvard.edu>. Harvard University and the Broad Institute are equal opportunity/affirmative action employers.

dhartl@oeb.harvard.edu dhartl@oeb.harvard.edu

HarvardU ParasitePhylogenetics

Postdoctoral Position: Phylogenetic Comparative Research on Mammalian Parasites

A postdoctoral position is available to conduct comparative research on infectious diseases in primates and other mammals. Research activities will include phylogeny-based tests of parasite richness and prevalence, parasite biogeography, and development of informatics tools for studying infectious disease dynamics in a broad ecological and evolutionary context.

The research will take place in the Department of Human Evolutionary Biology at Harvard University. The initial appointment will be for one year, with additional years of funding available conditional on satisfactory performance. Salary will be based on previous experience and includes benefits.

The position requires an independent, enthusiastic and innovative researcher with an interest in applying comparative approaches to real- world questions involving infectious diseases. Competitive individuals will have experience in one or more of the following areas: phylogenetic comparative methods, analyses of spatial data, reconstruction of phylogeny, bioinformatics, and programming (especially, but not limited to, R).

Please email an application to Charles Nunn (cnunn@oeb.harvard.edu) consisting of a CV, statement of research interests and names of two people who can be contacted to provide letters of reference. Evaluation of applicants will begin on September 3 and will continue until the position is filled.

Harvard University is an Affirmative Action/Equal Opportunity Employer.

Charles L. Nunn

Department of Human Evolutionary Biology Peabody Museum 11 Divinity Avenue Harvard University Cambridge MA 02138

http://www.fas.harvard.edu/~primecol primate phylogeny: http://10ktrees.fas.harvard.edu/ mammal parasites: www.mammalparasites.org phylogeny of sleep: www.bu.edu/phylogeny/index.html 617 495 4710 (office) 510 206 5716 (cell)

nunn@fas.harvard.edu nunn@fas.harvard.edu

HarvardU RotiferGenomeEvolution

Postdoctoral Fellowship - Harvard University

Bdelloid Genetic Transfer and Population Structure

An NSF-sponsored postdoctoral position is available in the laboratory of Matthew Meselson at Harvard University in Cambridge Massachusetts for the investigation of homologous genetic transfer in natural populations of bdelloid rotifers.

Although lacking males and any form of sexual reproduction and therefore termed an "evolutionary scandal" by John Maynard Smith, our recent observations indicate that bdelloids do, after all, engage in homologous genetic transfer, thereby apparently resolving the challenge posed by bdelloids to the view that long-term evolutionary success requires some form of mixis. The population structure within which such transfer occurs, however, appears to be highly unusual and its mechanism remains to be elucidated.

The fellowship project entails collection of bdelloid rotifers from sites in northeast United States; sequencing of mitochondrial genes to identify mitochondrial clades; DNA sequencing at loci on several chromosomes of bdelloids within the same clade; characterization of the parameters of homologous genetic transfer; and the development and testing of models of bdelloid genetic transfer and population structure to explain the observations obtained. Certain aspects of the work will be facilitated by the forthcoming availability of the first annotated whole genome sequence of a bdelloid rotifer.

The position requires an individual with a strong background in DNA sequencing and computational analysis and in population genetics theory who is committed to attacking and solving fundamental problems in biology.

Our recent publications include:

Hur JH, Van Doninck K, Mandigo ML, Meselson M. 2009. Degenerate tetraploidy was established before bdelloid rotifer families diverged. Mol Biol Evol. 26:375-83.

Gladyshev EA, Meselson M, Arkhipova IR. 2008. Massive horizontal gene transfer in bdelloid rotifers. Science 320:1210-3.

Gladyshev E, Meselson M. 2008. Extreme resistance of bdelloid rotifers to ionizing radiation. Proc Natl Acad Sci 105:5139-44.

Mark Welch DB, Mark Welch JL, Meselson M. 2008. Evidence for degenerate tetraploidy in bdelloid rotifers. Proc Natl Acad Sci 105:5145-9.

The appointment is for a period of up to two years with possibility of renewal. Salary is commensurate with experience based on the NIH guidelines.

Interested persons should email a letter of application, a curriculum vitae including a brief description of recent research, and the names, institutions and email addresses of three references.

Harvard is an Affirmative Action/Equal Employment Opportunity/ADA employer

Interested applicants should contact Matthew Meselson at < msm@wjh.harvard.edu>

Matthew Meselson <msmeselson@gmail.com>

Italy EpidemiologicalSystemDynamics

Title: Post-doc in data analysis and modelling of eco-epidemiological system dynamics (038_AMB_PDESD)

Research Centre: The research carried out at the Environment Department of Edmund Mach Foundation encompasses both ecological and molecular studies. It focuses on the functional integrity and biodiversity of aquatic (mainly plankton, diatoms and salmonid fishes) and land taxa (mainly vertebrate fauna and their parasites, higher plants including annual species and forest trees) that are subject to anthropic pressure and global climate changes. The ACE-SAP (Alpine Ecosystems in a Changing Environment: Biodiversity Sensitivity and Adaptive Potential) Major Proposal is a collaborative project funded by the Autonomous Province of Trento involving three regional institutions (Edmund Mach Foundation, Natural History Museum of Trento, Civic Museum of Rovereto) and one external partner (University of Davis, California).

Description: We are seeking a highly motivated and independent individual to carry out a research project on the Data management and analysis; application of statistical methods to the solutions of eco-epidemiological problems; use of advance statistical software packages and development of specific procedure in compatible programming languages; model building, analysis and interpretation, parameter estimation, sensitivity analysis and simulations of different scenarios; drafting scientific papers and reports; attending national and international conferences and workshops.

IT knowledge: Statistical packages (e.g. R, S-Plus, GenStat); Mathematical software (e.g. Mathematical, Matlab, Maple); Programming languages (e.g. C, Fortran).

More information and application: http://www.fondazioneedmundmach.it/-sperimentazione_context2.jsp?ID_LINK=3419&area=6 Re-open announcement - Deadline for application: 31st August 2009

Daniele Barbacovi Fondazione Edmund Mach Research Centre - Human Resources Office Via Mach 1, 38010 S. Michele all'Adige (TN) - Italy Phone +39 0461 615542 - Fax + 39 0461 650956 Skype daniele.barbacovi_crfem http://www.fondazioneedmundmach.eu daniele.barbacovi@iasma.it daniele.barbacovi@iasma.it

Leibniz FishPopulationGenetics

Post Doc - Population Genetics of Fish

The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) (www.igb-berlin.de) within the Forschungsverbund Berlin e.V. is the leading research centre for aquatic ecology and inland fisheries in Germany. It is closely linked to all three Berlin universities and offers cutting-edge research facilities (experimental ponds, lakes, tanks, genetics laboratories).

Within the Department of Biology and Ecology of Fishes of IGB a motivated PostDoc in fish population genetics is sought to complement an emerging young research group (Junior Professor, 2 PostDocs, 4 PhD students) conducting inter- and transdisciplinary research on recreational fisheries. The intended start date is 1 October 2009, and the position is available for up to four years. The position is available pending approval of a grant to study the social-ecology of fish stocking submitted to the German Ministry for Education and Research (http://www.sozial-oekologische-forschung.org/de/1410.php).

Topic: Understanding the evolutionary implications of fish stocking practices in inland water managed by angling clubs in Germany. The successful candidate is expected to develop an independent research program focused on understanding the extent of hybridisation between stocked and wild fish and its implications for individual and population fitness. The research can be laboratory- and field-based, but field studies in freshwaters managed by German angling clubs are required. The candidate is expected to co-supervise selected members of the research group and generate results of both academic and practical interest.

Salary is paid according to the TVoeD (German Civil Service). In keeping with the IGB policy regarding gender equity, female applicants are particularly encouraged. Disabled people with identical qualifications will be favoured.

Requirements: -PhD in population genetics, molecular biology or evolutionary biology, preferably with a focus on fish. -Proven academic record in terms of research output in journals -Ability to work both independently as well as in a team -Interest in working in an interdisciplinary team alongside both natural and social scientists -Above-average communication skills, including writing skills -Very good working knowledge of English -Familiarity with recreational angling and German language is a benefit

Application materials: Please send your application package in one combined PDF electronically no later than September, 18, 2009 to arlinghaus@igb-berlin.de (Prof. Dr. Robert Arlinghaus). The application package should include:

-cover letter -letter of personal research goals -letter of research perspective related to the topic of the application -CV -copies of relevant certificates (eg Abitur for German applicants) -list of publications and presentations -examples of most important papers -names and email-addresses of three reviewers

For further information please contact:

Prof. Dr. Robert Arlinghaus Leibniz-Institute of Freshwater Ecology and Inland Fisheries Department of Biology and Ecology of Fishes Müggelseedamm 310 12587 Berlin, Germany arlinghaus@igb-berlin.de

www.igb-berlin.de/ ˜ arlinghaus www.adaptfish.igb-berlin.de monaghan@igb-berlin.de monaghan@igb-berlin.de

LeicesterU HumanEvolutionaryBioinformatics

Bioinformatician Post-Doctoral Research Associate

Department of Genetics, University of Leicester Salary Grade 7: £30,594 to £35,469 p.a.

Fixed Term Contract available immediately until 31st July 2014

Ref: MBP00043

Sex, genomes, history: molecular, evolutionary and cultural effects on human genetic diversity

A bioinformatician post-doc position is available as part of a Wellcome-Trust-funded project to investigate the long- and short-term evolution of sequences on the sex chromosomes, the effects of sex- specific population processes, and the implications for understanding human population histories. Candidates should possess a PhD (or soon to be completed) in bioinformatics or biological sciences with a strong computer programming component, experience in standard techniques in bioinformatics, and strong programming skills.

For further information and to apply online, see http://www.jobs.ac.uk/jobs/YD189/-Bioinformatician_Research_Associate/r or contact Mark Jobling

Closing Date: 18 August 2009

Prof Mark A. Jobling Wellcome Trust Senior Research Fellow in Basic Biomedical Science Department of Genetics Room G5, Adrian Building University of Leicester University Road Leicester LE1 7RH UK

tel.: +44 (0)116 252 3427 fax: +44 (0)116 252 3378 email: maj4@le.ac.uk web: http://www.le.ac.uk/-genetics/maj4/maj4.html Times Higher Education University of the Year 2008-9

maj4@leicester.ac.uk maj4@leicester.ac.uk

LeicesterU HumanEvolutionaryGenetics

Laboratory Post-Doctoral Research Associates (2 Positions)

Department of Genetics, University of Leicester

Salary Grade 7: £30,594 to £35,469 p.a. Fixed Term Contract available immediately until 31st July 2014

Ref: MBP00044

Sex, genomes, history: molecular, evolutionary and cultural effects on human genetic diversity

Two lab-based post-doc positions are available as part of a Wellcome- Trust-funded 5-year project to investigate the long- and short-term evolution of sequences on the sex chromosomes, the effects of sex- specific population processes, and the implications for understanding human population histories. Candidates should possess a PhD in Molecular Genetics or Population/Evolutionary Genetics, and experience of PCR-based techniques of genome variation analysis.

For further information and to apply online, see http://www.jobs.ac.uk/jobs/YD190/-Research_Associates_2_Positions/r or contact Mark Jobling

Closing Date: 18 August 2009

Prof Mark A. Jobling Wellcome Trust Senior Research Fellow in Basic Biomedical Science Department of Genetics Room G5, Adrian Building University of Leicester University Road Leicester LE1 7RH UK

tel.: +44 (0)116 252 3427 fax: +44 (0)116 252 3378 email: maj4@le.ac.uk web: http://www.le.ac.uk/-genetics/maj4/maj4.html Times Higher Education University of the Year 2008-9

maj4@leicester.ac.uk maj4@leicester.ac.uk

LeidenU 2 EvolutionaryModeling

Two Postdoc positions (2 years each) at Leiden University (Netherlands).

The Postdocs will take part in a large collaborative project (BetNet), funded by the Dutch Science Foundation. Participating institutes: see below, and the Groningen Biomolecular Sciences and Biotechnology Institute (GBB, University of Groningen). The project is aimed at resolving the dynamics of gene regulation networks, by using the quantitative demands on the shape of bacterial bet-hedging strategy distributions that are imposed by fluctuating selection environments. As a model system, we study the adaptation of the distribution of sporulation-initiation timing in B.subtilis to randomly changing environments and cue reliability.

Subproject: Evolutionary Modeling; at the Institute of Environmental Sciences (CML) This subproject focuses on modeling state-dependent bacterial population dynamics and examining which bet-hedging strategies are evolutionarily stable in different selection regimes. Models will include size-, age-, and sporulation state dependence, as well as environmental information such as cue reliability. Requirements: PhD degree in Mathematics, Physics or Mathematical Biology, with a specialization in modeling empirical systems.

Subproject: Bioinformatics; at the Mathematical Institute (MI) and the Leiden institute of Advanced Computer Science (LIACS). This subproject focuses on mathematical modeling, simulation and parameter identification of the relevant gene regulation network. The project aims at developing models that properly capture the stochastic effects of signaling and gene regulatory networks. Simulations will be using stochastic simulation algorithms (SSA). Parameter identification will involve niching genetic algorithms for SSA search landscapes. Requirements: PhD degree in Mathematics, Computer Science or Computational Biology, with a specialization in stochastic modeling and simulation or genetic algorithms.

Applications: send a CV + accompanying letter stating the subproject to Patsy Haccou: haccou@math.leidenuniv.nl (Can also be contacted for further information or a complete project description). Application deadline: 15 september 2009.

haccou@math.leidenuniv.nl

LMU UMunich TheoreticalEvolution

Postdoc: UNIVERSITY of MUNICH (LMU)

Department Biology, Evolutionary Ecology

POST-DOCTORAL POSITION IN THEORETICAL EVOLUTIONARY ECOLOGY: GENERAL GENETIC MODELS ON PHENOTYPIC PLASTICITY

A unifying quantitative genetic model that includes spatial and temporal variations of the environment, irreversibly and reversibly plastic phenotypic traits, reliability of inducing cues and time delays for phenotypic response will be developed to study the role of phenotypic plasticity in the process of adaptation by modifying and directing the evolutionary response of organisms under diverse selection regimes.

The position is available starting October 1, 2009, but will remain open until filled. The post is available for up to 3 years. Initial appointment is for one year.

A solid background in evolutionary biology and previous experience in modeling are desirable. The successful candidate is expected to interact also with other scientists of EES (see www.eeslmu.de).

Applicants should submit (email preferred) a letter of interest, a complete CV, reprints (pdf-files) of not more than three papers, and name and contact information of at least two references to:

wilfried.gabriel@lmu.de <mailto:wilfried.gabriel@lmu.de>

Wilfried Gabriel Professor of Ecology Evolutionary Ecology Department Biologie II University of Munich (LMU) Grosshaderner Str. 2 D-82152 Planegg-Martinsried Germany

Tel: ++49 89 2180 74 202

The University of Munich is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled.

email: wilfried.gabriel@LMU.de

MichiganStateU EvolutionaryGenomics

Postdoctoral Position in Transcriptional Regulation Evolution

A postdoctoral position is available in the laboratory of Shin-Han Shiu in the Department of Plant Biology at Michigan State University (http://shiulab.plantbiology.msu.edu) to study the evolution of transcriptional regulatory networks in multi- and unicellular photosynthetic species. The project will focus on determining the regulatory network component turnover and their effects on fitness using a combination of molecular genetics, experimental evolution, and state-of-the-art high throughput omics technologies. Specifically, regulatory network in abiotic stress responses (e.g. light, CO2, and N-starvation) and chloroplast functions (e.g. amino acid and lipid biosynthesis, chloroplast biogenesis) will be emphasized. The project is inherently interdisciplinary and the successful candidate is expected to be involved in both computational and experimental works. In addition, the postdoctoral fellow will be encouraged to attend workshops in organizational development and in college education to enhance their training experience.

Candidates should have background in at least two of the following areas: (1) computational analysis of gene regulatory data, (2) experimental studies of gene expression, epigenetic regulation, and functions of transcription factors and their binding sites in any model system, (3) experimental evolution studies using microorganisms. Candidates with a strong computational background should have demonstrated experience (publications, thesis, or meeting abstracts) in scientific programming (any language), analysis of transcriptomics data, and whole-genome level study. For candidates with mainly an experimental background, demonstrated experience in basic programming (in any language) and large-scale data analysis (e.g. microarray study) is desired.

Candidates should send a SINGLE PDF or MS Word file containing (1) a cover letter summarizing research interests (1-2 pages), (2) CV with information on academic/work experience, awards, publications, and names/contact information for 3 references by email to Shin-Han Shiu (shius at msu dot edu). Applications will be reviewed as they are received. Informal inquiries are welcome.

–

Shin-Han Shiu Dept. of Plant Biology Michigan State University East Lansing, MI 48824 (O) 517-353-7196 (L) 517-353-7244 http://shiulab.plantbiology.msu.edu shius@msu.edu shius@msu.edu

---

NewZealand PlantEvolutionaryGenetics

Postdoctoral Fellow - Plant Ecological Genetics Lincoln, New Zealand

Manaaki Whenua - Landcare Research is New Zealand's foremost environmental research organisation specialising in sustainable management of land resources optimising primary production, enhancing biodiversity, increasing the resource efficiency of businesses, and conserving and restoring the natural assets of our communities.

The Landcare Research Ecological Genetics group is seeking a postdoctoral research fellow for a fixed term of three years. This role will investigate the weed potential of commercial Brassica lines in the environment. It is expected that the candidate will play a role in experimentally assessing the risk of new species and cultivars to better assess the risk of new importations. The position will be 100% research, with lab and field facilities located at Lincoln with some potential for further work in our Auckland molecular biology lab.

You will have a PhD in plant molecular biology (primarily population genetics) and plant reproductive biology / plant breeding. You will also have well-developed interpersonal skills, be highly organised and enjoy working both independently and within a team environment. You will be self-motivated, willing to work outdoors, and have published peer-reviewed papers in this subject area.

You will be based at our Lincoln office, just 20 minutes away from Christchurch. Christchurch, the garden city of New Zealand, is well-known for its natural and architectural beauty with beautiful 19th century buildings, extensive gardens, and sandy beaches.

Landcare Research - Manaaki Whenua aims to be an "employer of choice". As an employee of Landcare Research, you will enjoy generous employment benefits - including a contribution to superannuation/pension savings and relocation costs if required. Landcare Research is also an Accredited Employer with the New Zealand Immigration Service. If required, assistance with visa requirements will be provided.

For a copy of the position description and to apply please go to www.landcareresearch.co.nz/jobs All applications must be received online by 7 October 2009. For specific queries please contact Gary Houliston, houlistong@landcareresearch.co.nz

Marie Gray <GrayM@landcareresearch.co.nz>

OldDominionU MarineMolEvolution

POST-DOCTORAL Position in Marine Molecular Ecology

The Department of Biological Sciences at Old Dominion University, a "Doctoral Research - Extensive" state university, has an opening for a Post-Doctoral Research Associate position in marine molecular ecology and evolution. The appointment is for one year (renewable up to 3 years maximum) beginning January 2010. This position involves participation in an NSF-funded project to examine the population genetic and phylogeographic patterns of marine species in the Indo-Malay-Philippine archipelago and offers an excellent opportunity to develop a long-term research program in the world's most diverse marine environments. The successful candidate will be expected to live full time in Indonesia and potentially the Philippines and Malaysia planning and carrying out field sampling trips, and supervising the operations of a molecular laboratory. In addition, the successful candidate will be expected to teach a course in molecular ecology, supervise and mentor both American and foreign graduate and undergraduate students in the laboratory and field, maintain the project website, and take a prominent role in administering the project. All analyses, and research authorship, will be in collaboration with host country scientists, so the successful candidate will have a major role in developing collaborative projects with foreign scientists and students as well as obtaining all necessary research permits from foreign governments. While there are significant teaching and administrative responsibilities, the patient and flexible candidate will find good opportunities to develop related independent research activities. Applicants must have a PhD at the time of employment. Please submit a curriculum vitae, statement of interest, and the names, telephone numbers, and addresses (postal and email) of three references to: Kent E. Carpenter, Department of Biological Sciences, Old Dominion University, Norfolk, VA 23529-0266 USA; or to kcarpent@odu.edu (electronic submission of materials is preferred). Review of applications will begin on December 1, 2009 and will continue until a suitable candidate is found. Women and minorities are encouraged to apply. Old Dominion University is an Affirmative Action/Equal Opportunity Employer and requires compliance with the Immigration Reform and Control Act of 1986

"Carpenter, Kent E." <kcarpent@odu.edu>

PlantTreeLife ComputPhylogenetics

Postdoctoral Research Positions-Computational Phylogenetics/Phyloinformatics

Multiple postdoctoral positions are available for research and cyberinfrastructure development associated with reconstructing the green plant tree of life. Positions are sponsored by the iPlant Collaborative (http://iplantcollaborative.org), which is supporting cyberinfrastructure across the plant sciences. Individuals would work with one of a number of identified investigators focusing on specific issues in phylogenetic cyberinfrastructure development. These include high performance computing and scalable tree construction (A. Stamatakis-Technical University, Munich; email: stamatak@cs.tum.edu), data set assembly (Doug Soltis-U Florida; email: dsoltis@botany.ufl.edu, Pam Soltis-U Florida; email: psoltis@flmnh.ufl.edu; Michael Donoghue-Yale; email: michael.donoghue@yale.edu), gene tree reconciliation (Todd Vision-UNC; email: tjv@bio.unc.edu), character evolution (Brian O'Meara-U Tennessee; email: bomeara@utk.edu), and tree visualization (Michael Sanderson, University of Arizona; email: sanderm@email.arizona.edu). Fellows can anticipate working in a highly collaborative, multi-institutional context, with some travel between working groups encouraged. In addition to undertaking basic research in phylogenetic methods, postdocs will be expected to provide advice on and work in collaboration with cyberinfastructure developers in the iPlant team. Qualifications include familiarity with the data, methods, and software of phylogenetic analysis, and programming experience at least at the level of a scripting language such as PERL. Individual PIs may have additional requirements. Inquiries should be directed to any of the team members listed above. Positions are available immediately. A full description of the iPToL (iPlant Tree of Life) project can be found online at http://iptol.iplantcollaborative.org . –

Michael J. Sanderson

Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721

Office: BSW 412 Phone:520-626-6848

lab web site: http://loco.biosci.arizona.edu
UA Biodiversity Informatics Initiative: http:/-

/loco.biosci.arizona.edu/bdii PhyLoTA Browser: http://loco.biosci.arizona.edu/pb r8s software: http://loco.biosci.arizona.edu/r8s sanderm@email.arizona.edu sanderm@email.arizona.edu

PrincetonU CiliateGenomeEvolution

Postdoctoral Research Associate - Evolutionary Biology

Postdoctoral Research Associate position in the Department of Ecology and Evolutionary Biology at Princeton University, with focus of DNA Recombination, Rearrangement, Epigenetics and non-coding RNAs

Professor Laura Landweber seeks postdoctoral research associate to study the mechanism of scrambled gene and genome rearrangements in ciliates, particularly the role of non-coding RNAs or epigenetic factors, using experimental or bioinformatic research tools or both.

Requirements: PhD in molecular biology or relevant field. Strong experimental or computational training, experience, and publications from the Ph.D., ability to work independently and creatively, and strong research and written/oral communication skills are necessary.

For more information about the lab, see http://www.princeton.edu/~lfl < http://www.princeton.edu/~lfl > and recent publications, such as Nature 2008, v451, p153 or Science 2009, v324, p935.

This is a one-year initial appointment with the possibility of renewal. Apply online at http://jobs.princeton.edu/ < http://jobs.princeton.edu/ > . Search for Requisition #0900307 and include a letter, CV, statement of research interest and email addresses of three references. Application review will begin immediately; start date is flexible.

Princeton University is an equal opportunity employer and complies with applicable EEO and affirmative action regulations. For information about applying to Princeton and voluntarily self-identifying, please link to http://www.princeton.edu/dof/about_us/dof_job_openings/ < http://www.princeton.edu/dof/about_us/dof_job_openings/ > .

Diane Carlino Academic Manager Ecology and Evolutionary Biology Princeton University 104A Guyot Hall 609-258-5810 dcarlino@princeton.edu

Diane Carlino <dcarlino@Princeton.EDU>

QueensUBelfast EvolutionaryEpidemiology

Queen's University Belfast

Research Fellow (Epidemiology, Ecology, Statistics, Quantitative Genetics, Mathematics)

School of Biological Sciences Ref: 09/101031

Available for 29 months to investigate the impact of host and pathogen genetic factors on susceptibility to bovine tuberculosis (TB); the post will primarily involve genetic epidemiology investigations with a significant component of data management and statistical analysis.

Candidates without the pre-requisite experience will be considered for appointment to a lower research grade.

Anticipated interview date: Wednesday 16 September 2009.

Salary scale: £29,704 - £38,757 per annum (including contribution points). Closing date: 4.00 pm, Friday 28 August 2009.

Please visit our website for further information and to apply online - www.qub.ac.uk/jobs or alternatively contact the Personnel Department, Queens University Belfast, BT7 1NN. Telephone (028) 90973044 FAX: (028) 90971040 or e-mail on personnel@qub.ac.uk

The University is committed to equality of opportunity and to selection on merit. It therefore welcomes applications from all sections of society and particularly welcomes applications from people with a disability.

Fixed term contract posts are available for the stated period in the first instance but in particular circumstances may be renewed or made permanent subject to availability of funding.

Patricia McCullough <pmccullough@asgireland.com>

RiceU DictyosteliumSocialEvolution

Postdoctoral Fellowship V Rice University

Cooperation and conflict in the social amoeba Dictyostelium discoideum

An NSF-funded postdoctoral position is available immediately in the laboratories of Joan Strassmann and David Queller for research on the social amoeba Dictyostelium discoideum.

Dictyostelium amoebae, when starved, aggregate into a multicellular body in which about a fifth of the cells altruistically die to support and help disperse the remaining cells as living spores. Since the multicellular body can be made up of genetically different clones, there are opportunities for conflict. The social amoeba is fast becoming a model organism of choice for investigations into the evolution of cooperation and conflict, and particularly for studies of these traits and the genetic and genomic level. There are sequenced genomes for two species of Dictyostelium, and quite a few more are underway in our group, including close relatives and resequencing of multiple clones of D. discoideum. Laboratory manipulations, experimental evolution, and genomic work is feasible and likely to answer important questions.

The person who fills this position will investigate social interactions using some of our unique resources such as a large pool of insertional mutants, wild clones, genomic data, and the wonderful ease of social experimentation in a microbial system.

We are looking for a highly motivated and ambitious researcher with experience in molecular, microbial, and/or genomic computational techniques who is interested in empirical research on this exciting system, and in joining a dynamic and fun group of smart, highly motivated, productive, and hard working researchers in one of the great cities of the USA. The ideal candidate will have a Ph.D. in evolutionary biology or a related field and experience with working with microorganisms in an evolutionary framework. Knowledge of computer programming, such as UNIX and a scripting language such as Perl or Ruby are not required but would be a plus.

Publications on the system from our group include the following. Others can be found at the group website (www.ruf.rice.edu/˜evolve).

Ostrowski, E. A., Katoh, M., Shaulsky, G., Queller, D. C., Strassmann, J. E. 2008. Kin discrimination increases with genetic distance in a social amoeba. PLOS Biology 6:2376-2382, e287 Santorelli, L. A., Thompson, C. R. L., Villegas, E., Svetz, J., Dinh, C. Parikh, A., Sucgang, R., Kuspa, A., Strassmann, J. E., Queller, D. C., Shaulsky, G. 2008. Facultative cheater mutants reveal the genetic complexity of cooperation in social amoebae. Nature 451:1107-1110. Gilbert, O. G., Foster, K. R., Mehdiabadi, N. J., Strassmann, J. E., Queller, D. C. 2007. Control of a cheater mutant by kin selection PNAS 104:8913-8917. Strassmann, J. E., Zhu, Y., and Queller, D. C., 2000 Altruism and social cheating in the social amoeba, Dictyostelium discoideum. Nature 408:965-967

The initial appointment will be for up to two years with possibility for renewal. Salary follows NIH guidelines.

Applicants should send us by email a cover letter, CV, statement of research interests and skills, up to 3 reprints, and names, telephone numbers, and email addresses of three references. We will begin reviewing applications on 17 August 2009, and will continue until the position is filled. Send the application to Joan Strassmann, strassm@rice.edu , (Department of Ecology and Evolutionary Biology, MS170, Rice University, 6100 Main St. Houston TX, 77005-1892).

Under-represented minorities and women are particularly encouraged to apply to our diverse group. Rice University is an Affirmative Action/ Equal Opportunity Employer.

Joan E. Strassmann Harry C. and Olga K. Wiess Professor Ecology and Evolutionary Biology, MS 170 Rice University, 6100 Main St., Houston TX 77005-1892 USA

phone: (713) 348-4922 fax: (713) 348-5232 cell: (832) 978-5961 e-mail STRASSM@RICE.EDU http://www.ruf.rice.edu/˜evolve/ Joan Strassmann <strassm@rice.edu>

RiceU GenomeEvolution

A post-doctoral research position is available at Rice University in Houston TX, in the lab of Nicholas Putnam, Department of Ecology and Evolutionary Biology. The lab uses comparative genomics to investigate the relationships between genome evolution at the molecular level and the evolution of novel and diverse phenotypes. A primary focus of the lab is to understand the evolutionary dynamics of genome organization at the level of gene order and chromosomal gene complement across the metazoans.

The postdoc will focus on building and testing models for the evolution of genome organization. We aim to construct tests for the action of selection on recently-discovered features of large-scale genome organization conserved from early metazoan ancestors in the genomes of at least six animal phyla. This will include developing statistics for comparing multiple sequenced genomes to simulation- based models of genome evolution, and algorithms for reconstructing historical scenarios of genome evolution. This work will be performed in collaboration with an interdisciplinary team.

We're looking for a scientist with strong computational skills and research experience in comparative genomics and/or evolutionary biology, with a PhD in Evolutionary Biology, Bioinformatics, Computer Science or a related discipline. Proven written and oral communication skills are essential. This is a full-time, NSF-funded position with full benefits. The initial appointment is for one year, with renewal available for at least two additional years. Salary will be commensurate with experience.

Rice is a top-ranked private research university, located in Houston, Texas. The university offers excellent facilities and a collegial environment. It's campus is contiguous with the Texas Medical Center (TMC), one of the largest concentrations of biomedical research activity in the world. The TMC includes 19 academic institutions, $1 billion dollars spent on research annually, and fifteen thousand physicians, scientists and researchers. Houston, the fourth-largest city in the US, is vibrant and diverse; the Economist magazine recently called it "America's most enthusiastically cosmopolitan city."

To apply, send a letter describing your interest in the position, a copy of your CV, and contact information for three references to Nicholas Putnam (nputnam @ rice . edu).

RuhrU EvolutionBiodiversity

Ruhr-University Bochum / Germany

application deadline: 15. Sept. 2009

We are inviting applications for a Research Associate (wissenschaftliche(r) Mitarbeiter(in)) position (TVL E13) to work in the field of organismic ecology, evolution and/or biodiversity. The successful candidate will be strongly involved in zoological teaching, in the organization of the basic zoological systematics courses, preparation of zoological material for our courses and the management of the zoological collection. An excellent knowledge of arthropods (in particular insects) and other organisms is expected. The Department of Animal Ecology, Evolution and Biodiversity is seeking highly motivated candidates at the postdoc level with documented experience in teaching and research interests in the area of organismic ecology, evolution and or biodiversity, e.g., functional morphology or systematics. The successful candidate will establish independent externally funded projects and supervise students. Knowledge of the German language is required. The position is available starting 1. November 2009 (a later start is possible) for initially 3 years. Following positive evaluation the position can become permanent based on approval by the University. To apply, please send a complete CV, a description of current research interests with an outline of future projects, three major papers and arrange at least two letters of reference to be sent, either by email or mail. Review of applications will begin on 15. September 2009, and will continue until the position is filled. Please send your application by mail or via Email: (tollrian@rub.de)

Ruhr-Universität Bochum is committed to promoting the careers of women and therefore actively welcomes applications from female candidates. As an equal opportunities employer, we also encourage applications from suitably qualified disabled candidates and other groups.

Prof. Dr. Ralph Tollrian Ruhr-Universitat Bochum Evolutionsokologie und Biodiversitat der Tiere Universitatsstr. 150 /Gebaude ND05 D-44780 Bochum phone: +49 (0)234-3224998; 3224563 fax: +49 (0)234-3214114 email: tollrian@rub.de

Ralph Tollrian <tollrian@rub.de>

RutgersU ShellfishEvolution

A postdoctoral associate position is available at the Haskin Shellfish Research Laboratory, Rutgers University, to conduct research on shellfish genetics. The research will focus on the identification of genes related to disease resistance in the eastern oyster and the evolution of these genes in natural populations. Applicants should have a Ph.D. and background in genetics and molecular biology. Prior experience in cloning, sequencing, genotyping and population genetics analysis is preferred. The appointment is for one year with possible renewal. Search will continue until the position is filled. Interested individuals should send a CV, a brief statement of interest, and contact information for three references to: Dr. Ximing Guo, Haskin Shellfish

Research Laboratory, Institute of Marine and Coastal Sciences, Rutgers University, 6959 Miller Avenue, Port Norris, NJ 08349. Phone: (856) 785-0074 x4324; Fax: (856) 785-1544; Email: xguo@hsrl.rutgers.edu. Web: http://www.imcs.rutgers.edu. Rutgers University is a an Affirmative Action/Equal Opportunity Employer

Ximing Guo, Professor Haskin Shellfish Research Laboratory Institute of Marine and Coastal Sciences Rutgers University 6959 Miller Avenue, Port Norris, NJ 08349 Ph: 856-785-0074 x4324 FAX: 856-785-1544 Email: xguo@hsrl.rutgers.edu

xguo@hsrl.rutgers.edu

SanFrancisco AvianMolecularSystematics

POSTDOC: Avian molecular systematics and virus coevolution

California Academy of Sciences San Francisco, California

We invite applications for a postdoctoral research fellowship to collaborate on studies of molecular systematics in birds and their coevolution with viruses. Molecular systematics analyses will focus on Falconiformes among other taxa. Coevolutionary analyses will include microarray and molecular sequence analyses of virus diversity, phylogeography and potential virus roles in declines or extinction of diverse avian host populations. The latter will involve comparison of avian and viral abundances in island and mainland habitats as well as in natural and environmentally-stressed habitats.

We are looking for an enthusiastic and motivated individual to join our research team. The ideal candidate will have experience in molecular techniques including DNA and RNA extraction, sequencing, and gene expression profiling via microarrays, as well background in phylogenetics, molecular evolutionary analyses and avian or virus evolution. The position will be based at the California Academy of Sciences (CAS)in the lab of David Mindell and will collaborate closely with Jack Dumbacher (CAS) and Joe DeRisi (Univ. of California at San Francisco).

CAS and UCSF have vibrant communities of researchers working on evolutionary and systematics topics involving both theory and practice, population dynamics, and infectious disease coevolution with hosts. Our groups have close ties with many other researchers in the bay area. The CAS is situated in Golden Gate Park in San Francisco, within minutes of the ocean, biking and hiking trails, and the rich cultural and culinary offerings of the city.

The position is available as early as September 2009, and can last up to three years. Starting salary will be in the range of $43,000 to $50,000 per year, depending on experience, plus benefits.

To apply please send a CV, letter of interest and contact information for three references to David Mindell at <dmindell@calacademy.org>. Review of applications will begin on 1 September and will continue until the position is filled. The California Academy of Sciences is an Equal Opportunity Employer and welcomes applications from individuals who will contribute to its diversity.

"Mindell, David" <DMindell@calacademy.org>

SaoPauloU PlantEvolution

There is a post-doc position available at Plants Molecular Biology Laboratory at the São Paulo University Agriculture School to work on the herbivory and intracellular protein transport. This position is funded by São Paulo State grant institution (FAPESP). The applicants should have PhD on Biology related area. Must have practical experience on molecular biology techniques, phylogeny inference methodologies (Hypothesis may be inferred using nucleotides or protein data), transcriptome annotation and data mining, EST database assembling and analyses. It is expected advanced skills on GNU/LINUX operational system. PERL and PHP programming not essential but a plus. To apply for this position please send the following documents to mcsf60@yahoo.com.br. 1. Two recommendation letters 2. One presentation letter (1 Page Max) 3. Updated resume, Lattes, the brazilian official resume system also should be used. For further information access http://biomol.esalq.usp.br/-web/english/ Prof. Marcio C. Silva-Filho

junkbox@brandao.eti.br

SouthAfrica StarlingEvolution

*DST V NRF Centre of Excellence for Invasion Biology *

Post-doctoral position

* *

*Host Universities: *University of Pretoria and Stellenbosch University* Project title: *Genetic structure, spatial dynamics and local scale impacts of the invasive common myna /Acridotheres tristis/ in South Africa* Salary: *R150 000 tax free per year for two years.*** *

**The common myna /Acridotheres tristis/ is an Asian starling that has become established in many parts of the world outside of its native range due to accidental or deliberate introductions by humans. The South African population of this species originated from captive birds that escaped in Durban in 1902. A century later, the common myna has become abundant throughout much of South Africa and is considered to pose a serious threat to indigenous biodiversity. This species has significant potential to spread further in southern Africa as populations are expanding north into Limpopo, Botswana and Zimbabwe, and west and south-west into the Free State and Eastern Cape.

Except for the occasional documentation of their overall distribution range, very little is known about the general movement dynamics of mynas. Using molecular techniques and ecological principals, this project will investigate questions related to common mynas focusing on (i) the spatial distribution of genetic variation, (ii) movement patterns in relation to certain landscape variables, (iii) factors affecting the relationship between genetic diversity and gene flow, (iv) source and sink populations, and (v) the distance decay of genetic similarity and gene flow.

Fieldwork will be conducted across the full distribution range of the common myna in South Africa. Work will be conducted in conjunction with the University of Pretoria and Stellenbosch University and time will therefore be spend at both universities. Field experience working with birds and a strong molecular background is an advantage.

*Please send a CV and full academic record, letter of motivation, and two reference letters to Chantal Strumpher (cstrumpher@zoology.up.ac.za <mailto:cstrumpher@zoology.up.ac.za>) by no later than Friday 16 October 2009. *

Start date: January 2010.

More information on the collaborators can be found at:

Bettine van Vuuren (website: http://academic.sun.ac.za/botzoo/vuuren/index.htm),

Cang Hui (website: http://academic.sun.ac.za/cib/team/staff/cang/canghui.htm),

Berndt van Rensburg (website: http://www.up.ac.za/zoology/staff.php?person=164).

Berndt Janse van Rensburg <bjvanrensburg@zoology.up.ac.za>

TexasTechU PlantPopulationGenetics

A Postdoctoral Research Associate position is available in the Department of Plant and Soil Science at Texas Tech University to investigate plant molecular evolution, microbial molecular ecology, or possibly, plant-microbe interactions. The research program focuses on molecular and field evolution of natural populations of orchids and their fungal associates.

REQUIREMENTS

1. A Ph.D. degree in a molecular evolution based discipline in Plant or Biological Sciences, or a closely related field.

2. A strong background in techniques and data analysis methods in molecular biology, i.e., DNA extraction, selecting suitable markers, PCR, molecular data analyses, sequencing, constructing and interpreting phylogenies, etc., for application toward plant population genetics and mycorrhizal diversity studies.

3. The incumbent will be expected to prepare articles for publication in refereed journals and collaborate in preparing grant proposals. The incumbent will primarily work independently, and at times with other lab members.

SALARY and BENEFITS Three-year support @ $40,000/year, plus fringe benefits.

APPLICATION Please submit:

1. Letter of application describing interests and qualifications. The applicant should specifically address how their skills match the position description and requirements;

1. Curriculum Vitae; and

1. Names, complete address, phone, and e-mail information for at least three references to:

Dr. Jyotsna Sharma Department of Plant and Soil Science Texas Tech University PO Box 42122; Lubbock, TX 79409 jyotsna.sharma@ttu.edu<mailto:jyotsna.sharma@ttu.edu>

"Sharma, Jyotsna" <jyotsna.sharma@ttu.edu>

UAlgarve Bioinformatics

GRADUATE AND POSTDOCTORAL PROPOSALS* Selection of candidates for a grant proposal to submit to the Portuguese Foundation for Science and Technology (FCT).

The Centre for Marine Science (CCMAR - http://ccmar.ualg.pt/) at the University of the Algarve, Portugal (http://www.ualg.pt) seeks Ph.D. or Postdoctoral candidates for the implementation of bioinformatic tools to analyse high-throughput transcriptomic data generated by next generation sequencing platforms (Roche/Illumina/Solexa). The experimental data will be derived from Polar eukaryotic phytoplankton communities dominated by diatoms, and the colonial algae Phaeocystis from the Southern and Arctic Oceans. Examples of the questions we seek to answer involve comparisons of community transcriptional profiles from different oceanographic regions, the effects of UVR, and responses of communities to predicted global change scenarios.

Applicants should hold a Ph.D. or M.Sc. in biology or bioinformatics, and have a good publication record in the field. The successful applicant will have a working knowledge of relational databasing, a cross-platfrom scripting language (Python/Perl/Java), and new generation sequencing analysis methods and tools. The successful applicant will also have the opportunity to become involved in molecular biology projects investigating transcriptional responses, molecular phylogenetics, and other areas of phytoplankton research in a new and dynamic group at CCMAR.

A postdoctoral position (open to all nationalities) would be available for a minimum of 3 years with the researcher receiving an untaxed salary of 1495 euros/month. A Ph.D. candidate position (Portuguese nationals only) would be available for 4 years with a standard FCT stipend. The start date for both postdoctoral and Ph.D. positions is January 2010.

Applications should be submitted before 20th August 2009 to Gareth Pearson (gpearson@ualg.pt) or Cymon J. Cox (cymon@ualg.pt). Applicants should send a covering letter detailing their research interests, a current C.V., and the email addresses for 3 professional referees. Informal enquires are welcome to the same address.

CCMAR is located on the Gambelas campus, 4km from Faro, the captial city of the Algarve and close to Faro International Airport (FAO). (http://www.ualg.pt/index.php?option=com_google_maps&Itemid#11&lang=en)

(* all Ph.D. and postdoctoral positions must be proposed to and approved by the Portuguese Foundation for Science and Technology)

Gareth Pearson (Research Associate) MAREE-Marine Ecology and Evolution (http://ccmar.ualg.pt/maree/) CCMAR - Centre of Marine Sciences, and CIMAR -Laboratório Associado Faculdade de Ciências do Mar e Ambiente, Universidade do Algarve

Mailing address: F.C.M.A., Univ. Algarve, Gambelas, 8005-139 Faro, Portugal Fax: +351 289 800 069 Phone: +351 289 800 928 E-mail: gpearson@ualg.pt

gpearson@ualg.pt

UBritishColumbia EvolGenomics

A Postdoctoral Fellow position is available in the lab of Dr. Keith Adams at the University of British Columbia in the area of evolutionary genomics. My lab's research combines evolutionary biology with molecular genetics and bioinformatics approaches to study how gene expression, regulation, alternative splicing patterns, structures, and sequences evolve. We focus on expression of duplicated genes especially in polyploids and hybrids. See my web page at http://www.botany.ubc.ca/people/kadams.html for a description of current research. I am looking for a postdoc to study genomics of alternative intron splicing patterns in plants. Projects may include examining alternative splicing in hybrids using RNA-seq transcriptome profiling and analyzing alternative splicing patterns in duplicated genes using RNA-seq data. The postdoc also can develop a side project that is related to my lab's research topics. The postdoc can interact with postdocs in other labs, including the Rieseberg and Cronk labs, who study evolutionary genomics and use next generation sequencing to answer evolutionary questions. My lab is housed in new research building with excellent computational infrastructure.

Candidates should have a strong background in evolutionary genomics, molecular evolution, bioinformatics, or genome analysis in any organism. Experience with computational analysis of sequence or expression data is required as is the ability to do scripting in Perl or Python. Experience with next generation sequence analysis (Illumina, 454, or SOLiD) is desirable but not required. The position is available immediately and the preferred start date is before the end of January 2010. Funding is available for at least two years.

For more information contact Keith Adams at keitha@interchange.ubc.ca Informal inquiries about the research area and projects are welcome. To apply, send a CV, a description of your research interests and your Ph.D. research, and contact information for three references to the above email address.

Keith Adams Assistant Professor Botany Department and Centre for Plant Research University of British Columbia Vancouver, Canada

keitha@interchange.ubc.ca keitha@interchange.ubc.ca

UCaliforniaLosAngeles ViralEvolution

POSTDOC: Cross-scale theory for viral emergence

Department of Ecology & Evolutionary Biology UCLA

We invite applications for a postdoctoral research fellowship to develop novel evolutionary theory for the emergence of viral pathogens across species boundaries. The post is linked to an NSF-funded project addressing the joint dynamics of viral invasion and adaptation subject to multiple scales of selection (i.e. replication within hosts and transmission between hosts). The project will build a theoretical framework based on population genetics, population dynamics, metapopulation ecology, and epidemiology, and will work with leading empirical groups to link the theory to field and experimental data. The position will be based in the lab of Jamie Lloyd-Smith (UCLA) and will collaborate closely with John Novembre (UCLA) and Sebastian Schreiber (UC Davis).

We are looking for an enthusiastic and motivated individual to join our research team. The ideal candidate will have a PhD in a quantitative field, with previous experience in stochastic modeling of population genetics or population dynamics. Strong quantitative skills are essential, and good written and oral communication skills are highly desirable.

UCLA has vibrant communities of researchers working on evolutionary theory, population dynamics, and infectious diseases, and our groups have close ties with the School of Public Health and School of Medicine. The university is situated in a prime location in Los Angeles, within minutes of mountains, beaches, and the rich cultural and culinary offerings of the city.

The position is available as early as September 2009, and can last up to three years. Starting salary will be in the range of $47,000 to $53,000 per year (depending on experience), plus benefits. UCLA is an equal opportunity employer.

Inquiries and formal applications (CV, 1-2 page statement of research interests, 2 publications, and names of 3 references) can be submitted to James Lloyd-Smith <jlloydsmith@ucla.edu>. Review of applications will begin on August 24 and will continue until the position is filled.

jlloydsmith@gmail.com

UColorado PlantEvolution

Postdoctoral position. Origin and early evolution of flowering plant reproduction. A two-year postdoctoral position in the laboratory of William (Ned) Friedman will be available beginning in the fall of 2009. Individuals interested in this position should contact William Friedman (ned@colorado.edu). To learn more about the research activities in the Friedman lab, please go to the website http://spot.colorado.edu/˜friedmaw/Friedman_Lab/Friedman_Lab_Homepage.html .

William (Ned) Friedman Professor Department of Ecology and Evolutionary Biology University of Colorado Boulder, CO 80309 USA

303-492-3082 (office) 303-492-8699 (fax) ned@colorado.edu (email)

lab homepage: http://spot.colorado.edu/˜friedmaw/Friedman_Lab/Friedman_Lab_Homepage.html MORPH homepage: http://www.colorado.edu/eeb/MORPH/ Pamela.Diggle@Colorado.EDU Pamela.Diggle@Colorado.EDU

UIdaho MeasuringTreeOfLife

Postdoc: Measuring the tree of life

A postdoctoral position is available in the laboratory of Dr. Luke Harmon to develop and implement comparative statistical methods for measuring the tempo and mode of evolution across vertebrates. The postdoctoral scientist will be involved in research using data from the NSF Tree of Life project to test macroevolutionary hypotheses. The postdoctoral scholar will specialize on the computational aspects of the project, including writing and testing computer code, analyzing simulated data sets, and compiling and analyzing large empirical data sets. The ideal candidate will have a strong computational and/or statistical background and experience developing or using statistical comparative methods. Applicants with a strong background in phylogenetics will also be considered. The successful candidate will contribute to existing collaborative projects across multiple institutions and will also be expected to develop new independent research directions.

To apply: https://www.sites.uidaho.edu/AppTrack/Agency/Applicant/ViewAnnouncement.asp?announcement_no=12508030673 Any questions email lukeh@uidaho.edu or call 208-885-0346

Lab web site: http://www.webpages.uidaho.edu/~lukeh/ Luke Harmon Assistant Professor Biological Sciences University of Idaho 208-885-0346 lukeh@uidaho.edu

UIllinois DiseaseEvolution

The National Institute of Allergy & Infectious Diseases (NIAID), Division of Intramural Research (DIR), Laboratory of Clinical Infectious Diseases (LCID) is offering an opportunity for a Postdoctoral Research Fellowship to participate in clinical and translational infectious diseases research.

The LCID conducts clinical and basic studies of human infectious and immunologic diseases, with a focus on the comprehensive understanding of and management of patients and their diseases. The major theme of the LCID continues to be the pathogenesis, pathophysiology, treatment and prevention of infectious diseases.

We are seeking an enthusiastic and highly motivated evolutionary biologist/yeast geneticist to join a large group of clinical and basic science investigators. The project is designed to identify and characterize regions of high genetic plasticity in both the human and pathogen genome that have strong associations with parameters of clinical outcome. Focus will be on infections of the AIDS-related pathogen, Cryptococcus neoformans as well as Candida albicans, the fourth most common blood stream infection in the US. Novel pathways related to virulence identified by a number of genomics methods will be further characterized using yeast and mammalian genetics and immunology in mouse models.

The successful applicant will be responsible for designing and carrying out experiments, analyzing experimental results, preparing manuscripts and helping with the supervision of students. A PhD is required with a strong and published history in molecular genetics. Experience in bioinformatics is preferred. No previous experience in pathogenic fungi is required although experience in yeast genetics would be valuable. Our laboratory provides strong support for the development of independent projects leading to a productive career for post-doctorate candidates.

Interested candidates may contact Dr. John E. Bennett JBENNETT@niaid.nih.gov or Dr. Steven M. Holland at smh@nih.gov for additional information about the position. To apply for the position, candidates must submit a curriculum vitae, bibliography, three letters of reference, a detailed statement of clinical research interests, and up to 3 selected reprints to: Steven M. Holland, LCID/DIR/NIAID, c/o Ericka Thomas, 9000 Rockville Pike, Bldg 10, Room 11N234, MSC 1888, Bethesda, MD 20892-1888 by November 15, 2009.

Peter R. Williamson, MD/PhD Professor of Medicine, Pathology, Microbiology and Immunology University of Illinois at Chicago School of Medicine Section of Infectious Diseases Rm 888, Bld 910, m/c 735 808 S. Wood St. Chicago, IL 60612 tel: (312) 996-6070 fax: (312) 413-1657

Peter Williamson <prw@uic.edu>

ULausanne 3 Bioinformatics

BIOINFORMATICS POSTDOC POSITIONS IN FUNCTIONAL EVOLUTIONARY GENOMICS

Center for Integrative Genomics, University of Lausanne, Switzerland

Three postdoctoral positions (2 years with possible extensions up to 5 years) are available in the evolutionary genomics group of Henrik Kaessmann in the framework of major new projects funded by the European Research Council.

We are seeking highly qualified and motivated applicants with strong skills in computational biology/bioinformatics, preferably also with experience in data mining and comparative or evolutionary genome analysis.

Our group has been interested in a range of topics related to the functional evolution of genomes from primates (e.g., emergence of new genes and their functions) and other mammals (e.g., the origin and evolution of mammalian sex chromosomes). In the framework of a new major line of projects funded by the European Research Council, a large amount of qualitative and quantitative transcriptome data will be produced for a unique collection of tissues from representative mammals by the wet lab unit of the group using next generation sequencing technologies (RNA-Seq). The postdoctoral fellow will perform integrated evolutionary/bioinformatics analyses based on these data and available mammalian genomes. The specific project will be developed together with the candidate.

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

For more information on the group and our institute more generally, please refer to our website: http://www.unil.ch/cig/page7858_en.html Please submit a CV, statement of research interest, and names of three references to: Henrik Kaessmann (Henrik.Kaessmann@unil.ch).

– Henrik Kaessmann, Ph.D. Associate Professor Center for Integrative Genomics University of Lausanne, Switzerland E-mail: Henrik.Kaessmann@unil.ch Phone: +41 (0)21 692 3960

Some recent publications from the lab:

Henrichsen, C., Vinckenbosch, N., Zöllner, S., Chaignat, E., Pradervand, S., Frédéric Schütz, Ruedi, M., *Kaessmann, H. and *Reymond, A. (2009) Segmental copy number variation shapes tissue transcriptomes. Nature Genet. 41: 429-9.

Potrzebowski, L., Vinckenbosch, N., Marques, A. C., Chalmel, F., Jegou, B. & Kaessmann, H. (2008) Chromosomal Gene Movements Reflect the Recent Origin and Biology of Therian Sex Chromosomes. PLoS Biol. 6: e80.

Brawand, D., Wahli, W. & Kaessmann, H. (2008) Loss of egg yolk genes in mammals and the origin of lactation and placentation. PLoS Biol. 6: e63.

Rosso, L., Marques, A. C., Weier, M., Lambert, N., Lambot, M.-A., Vanderhaeghen, P. & Kaessmann, H. (2008) Birth and Rapid Subcellular Adaptation of a Hominoid-Specific CDC14 Protein. PLoS Biol. 6: e140.

Vinckenbosch, N., Dupanloup, I. & Kaessmann, H. (2006) Evolutionary fate of retroposed gene copies in the human genome. Proc. Natl. Acad. Sci. U. S. A. 103: 3220-3225.

Marques, A., Dupanloup, I., Vinckenbosch, N., Reymond, A. & Kaessmann, H. (2005) Emergence of young human genes after a burst of retroposition in primates. PLoS Biol. 3: e357.

Burki, F. & Kaessmann, H. (2004) Birth and adaptive evolution of a hominoid gene supporting high neurotransmitter flux. Nature Genet. 10: 1061-1063.

Henrik.Kaessmann@unil.ch Henrik.Kaessmann@unil.ch

ULibreBruxelles AfricanPlantEvolution

Postdoc on evolutionary genetics / evolutionary ecology of African plants

The group of Dr Olivier Hardy at the Université Libre de Bruxelles (Belgium) is seeking a candidate for a 2 years postdoctoral position to work on evolutionary genetics / evolutionary ecology of central African plant species. The candidate should have experience in population genetics, phylogeography, phylogenetics and/or community ecology modeling. Experience with tropical plants is a plus. The candidate will contribute to new projects funded by the Belgian National Fund for Scientific Research (FNRS). One project is entitled "Population dynamics of trees and herbaceous species characteristic of central African rain forests in relation to past human and climate perturbations", and the other "Organization of plant biodiversity across African rain forests at different levels of integration using genetic markers: phylogeography, DNA barcoding, and phylogenetic structure of communities". The research project of the candidate will be flexible and adapted to his previous experience. The candidate will be based in Brussels, will have access to a molecular lab and is also expected to do field missions in Africa. Interested candidates should send their CV to Olivier Hardy (ohardy@ulb.ac.be) as soon as possible (deadline 15 September). More details about the projects will be provided. Olivier Hardy will eventually propose one candidate for a postdoctoral grant from the FNRS (only non-Belgian candidates are eligible). Decision is expected in early December (expected success rate is about 75%) and the grant can start in January 2010. Salary is ca. 2000 euros/month. The team lead by Olivier Hardy (cf. http://www.ulb.ac.be/sciences/-ecoevol/index_EN.html) is currently composed of 4 postdocs and 4 PhD students. Research topics focus on African rainforests and include phylogeographic studies of several forest dwelling tree, herbaceous and epiphyte (orchids) species; population and quantitative genetics of some timber tree species; molecular sytematics (orchids, Psychotria); development of DNA barcoding approaches for tree species; (phylo)diversity patterns of tree communities and plant-environment relationships. Most field work occurs in Cameroon, Gabon or Benin in collaboration with local researchers. Olivier Hardy is also doing modeling research in population genetics and community ecology, and develops software for data analyses.

Some recent publications: Born C., Hardy O. J., Ossari S., Attéké C., Wickings E. J., Chevallier M.-H., Hossaert-McKey M. (2008) Small-scale spatial genetic structure in the Central African rainforest tree species, Aucoumea klaineana: a hierarchical approach to infer the impact of limited gene dispersal, population history and habitat fragmentation. Molecular Ecology 17: 2041-2050. Dick C. W., Hardy O. J., Jones F. A., Petit R. (2008) Spatial scales of pollen and seed-mediated gene flow in tropical rain forest trees. Tropical Plant Biology 1: 20-33. Hardy O. J., L. Jost. (2008) Interpreting and estimating measures of community phylogenetic structuring. Journal of Ecology 96: 849-852 Hardy O. J. (2008) Testing the spatial phylogenetic structure of local communities : statistical performances of different null models and test statistics on a locally neutral community. Journal of Ecology 96: 914-926. Duminil J., Hardy O. J., Petit R.J. (2009) Plant traits correlated with generation time directly affect inbreeding depression and mating system and indirectly genetic structure. BMC Evolutionary Biology 2009, 9:177. Parmentier I., Hardy O. J. (2009) The impact of ecological differentiation and dispersal limitation on species turnover and phylogenetic structure of inselberg's plant communities. Ecography (in press) Navascués M., Hardy O. J., Burgarella C. (2009) Characterization of demographic expansions from pairwise comparisons of linked microsatellite haplotypes. Genetics (in press). Bizoux J-P., Daïnou K., Bourland N., Hardy O.J., Heuertz M., Mahy G., Doucet JL. (2009) Spatial genetic structure in Milicia excelsa (Moraceae) indicates extensive gene dispersal in a low density wind pollinated tropical tree. Molecular Ecology (in press).

ohardy@ulb.ac.be ohardy@ulb.ac.be

UManchester PhylogeneticModeling

Project: The Evolutionary Fate of Gene Duplicates PI: Simon Whelan, University of Manchester, UK

How organisms acquire new genes with novel functions remains an open question. One major mechanism is through differential fates of gene duplicates, whereby duplicate copies acquire new functions (neofunctionalisation) or segregate existing function (subfunctionalisation). Our ability to identify gene fate is hindered by the limited computational tools available. This project will develop new tools and use them study well characterized gene duplication events.

This computational project is based in the Bioinformatics and Evolutionary research groupings at the Faculty of Life Sciences. During the project you will design novel phylogenetic substitution models that allow for heterogeneous evolution and may discriminate between neo- and sub-functionalisation. You will implement the models in a computer program and apply them to the yeast whole genome duplication. Prior experience in phylogenetic methods, computer programming (e.g. C/C++; Java), yeast genomics, or some combination thereof is desirable.

For further details of the post please see: http:/-/www.manchester.ac.uk/aboutus/jobs/research/-vacancy/index.htm?ref=163263 Or contact Simon Whelan (simon.whelan@manchester.ac.uk)

Simon Whelan T: +44-(0)161 3068901 F: +44 (0)161 2755586 Faculty of Life Sciences, University of Manchester, Michael Smith Building, Oxford Road, Manchester, M13 9PT, UK URL: http://www.ls.manchester.ac.uk/people/profile/-index.asp?id=3678 simon.whelan@manchester.ac.uk simon.whelan@manchester.ac.uk

UMichigan UGeorgia 2 AvianFluEvolution

****POSTDOCTORAL RESEARCH ASSOCIATES**** Department of Ecology & Evolutionary Biology and the Center for the Study of Complex Systems, University of Michigan, USA

and

Odum School of Ecology, University of Georgia

Applications are invited for two postdoctoral research fellowships in epidemiological and ecological modeling and phylogenetics of Avian Influenza Viruses. These posts are part of a long-term collaborative project between Dr Pej Rohani (University of Michigan) and Drs Drake and Stallknecht (University of Georgia). One postdoctoral position is NSF-funded and will focus on the development of mathematical and computational models relating to the persistence, transmission dynamics and evolution of Avian Influenza Viruses within North American wild bird populations. This position will be primarily supervised by Dr Pej Rohani and the candidate will be based at the University of Michigan. The second position, funded by the James S. McDonnell Foundation will focus on the phylodynamics of Avian Influenza Viruses. This position will be primarily supervised by Dr John Drake at the University of Georgia.

The ideal candidates would have a PhD in a highly quantitative field, with previous experience in the analysis of ecological or epidemiological systems.

The positions are potentially for 3 years, with a salary in the range of $37,000-45,000 per year (depending on experience), plus fringe benefits.

For further information about the University of Michigan project, contact Pej Rohani (rohani@umich.edu). For further information about the University of Georgia project, contact John Drake (jdrake@uga.edu). Applicants should send a detailed CV, together with a brief statement of research interests and three references.

Review of applications will start on October 1 and will continue until the posts have been filled.

Pejman Rohani <rohani@uga.edu>

UMissouri MolecularEvolution

Post-doctoral Fellow' Department of Fisheries and Wildlife and Division of Biological Sciences, University of Missouri (Columbia, MO)

As part of an NSF-supported study examining the importance of genetic variability for predicting the likelihood of wildlife infection by diverse parasites, we seek a post-doctoral researcher to provide the conceptual advances needed to better understand how neutral genetic variability and MHC loci variability predict the likelihood of infection of wildlife by diverse micro and macroparasites. Parasites are typically aggregated among hosts, with some individuals more likely to be infected than others or bearing greater parasite burdens. This likelihood of an individual being parasitized can be predicted from characteristics of the host (e.g. age, sex) as well as the place the host inhabits and the timing of the sampling of the host. The genetic variability of the host may also contribute to the likelihood and severity of infection, but the importance of this relative to other predictors of parasitism is unclear.

We have accrued a large dataset on raccoons (ca 700 individuals) and their parasites (ectoparasites, nematodes, and microparasites) and are working to better understand the disease ecology of this system. The postdoctoral fellow will oversee laboratory genetic analyses of the raccoons, with particular emphasis on analyzing MHC variability and understanding whether this variability, as well as the presence of specific MHC alleles, helps predict the likelihood and extent of parasitism as well as the parasite community of a host individual. Opportunities may exist for further field work as well as involvement in other projects of mutual interest.

The position is currently open and can be filled immediately. Funding for the position is available for two years.

The successful candidate will demonstrate a strong work ethic, an interest in both theoretical and applied ecology, strong laboratory and quantitative skills, and a demonstrated commitment to publication of results in peer-reviewed outlets.

Preference will be given to candidates with research experience in molecular ecology, wildlife disease ecology, or ecological parasitology.

REQUIREMENTS: PhD in biology, ecology, parasitology, or a related field.

SALARY: This position is full time and is eligible for a full benefits package. The salary is ca $34,000/yr.

Submit via email a cover letter that includes a description of work experience and career goals, resume, and the names and contact information (phone and e-mail address) of 3 references to:

Dr. Matt Gompper Department of Fisheries and Wildlife Sciences, University of Missouri E-mail: gompperm@missouri.edu

Or

Dr. Lori Eggert, Division of Biological Sciences, University of Missouri Email: eggertl@missouri.edu

eggertl@missouri.edu eggertl@missouri.edu

UMuenster MolEvolution

Postdoctoral Positions in Molecular Evolution at the IEB:

Highly motivated individuals are sought for the following projects:

Project/Position 1 (Computational): MODULAR EVOLUTION OF PROTEINS BY DOMAIN ARRANGEMENTS (Ref EBB-09PD02-DOM):

Proteins evolve, to a large extent, by modular rearrangements of conserved functional units. We aim at using and, where necessary developing, algorithms to reconstruct the evolutionary scenarios of modular arrangements, to rapidly identify homologous proteins and analysing genome evolution in terms of modular rearrangements. Post-holders will build on earlier research by investigating the rearrangements in vertebrates, arthropods and by participation in several genome projects. In particular we aim to understand how newly arising domain arrangements after a gene duplication become selectively advantagous, e.g. by specific loss of domains or optimising suboptimal functions.

See: AD Moore et al. Arrangements in the modular evolution of proteins, Trends in Biochem Sci, 33:09, 2008 (and references therein)

Required qualifications:

* PhD in natural sciences such as biochemistry, biology or biophysics and research experience in a biological area OR * PhD in computer science, statistics or bioinformatics with experience and/or desire to excel in a biological area * Basic skills in statistics and/or programming * Motivation and proven ability to carry out research independently * Good communication skills, fluency in English

Project/Position2 (Experimental): EXPERIMENTAL MOLECULAR EVOLUTION OF ENZYME FUNCTION (Ref EBB-09PD04-EXP):

For this project we seek an excellent molecular biologist with a strong interest in evolution and a wide range of experimental skills in order to investigate the influence of functional promiscouity (enzymes with dual function) on the evolvability of new, previously latent functions und various selection pressures which mimic natural conditions. The post-holder will lead a small team of students and technical support is provided. The project is in collaboration with structural biologists and experimentalists in Cambridge, UK.

Required qualifications:

* PhD in natural sciences such as biochemistry, biology or biophysics and research experience in a biological area OR * PhD in molecular biology, biotechnolgy or similar with further background in evolution * Motivation and proven ability to carry out research independently * Good communication skills, fluency in English * Bioinformatics or programming knowledge is not essential but an advantage.

Candidates are encouraged to develop their own research agenda by supervising students and applying for their own funds but this is not a must. Best qualified candidates will be endorsed for fellowship applications to which we currently have a 100% (4 out of 4) success rate.

Interested candidates should send applications to Prof. Bornberg-Bauer ebb[at]uni-muenster.de as pdf attachment (max. 2 pages) detailing: education and degrees with dates, posts held, list of peer reviewed publications, 2-3 names of potential referees and a short statement of research interest or as letter to:

Prof. Dr. Erich Bornberg-Bauer Institut for Evolution and Biodiversity, Westfälische Wilhelms Universität Münster Hüfferstrasse 1, D-48149 Münster, Germany www.uni-muenster.de/Evolution.ebb CLOSING DATE is September 30th 2009. Commencing date is flexible, with Jan. 1st 2009 being preferred.

Postdoctoral and PhD positions are usually paid according to the TVL scheme. Teaching and administrative duties are generally low, with amount and balance depending on the particular project as well as background, qualifications and experience of candidates.

For further details see: http://ieb.uni-muenster.de/-bioinf/positions Prof. Erich Bornberg-Bauer PhD, Institute for Evolution and Biodiversity School of Biol.Sciences, University of Muenster, Huefferstr.1 D48149 Germany Tel/Fax: +49(0)251-83-21630/24668 web: www.uni-muenster.de/evolution/ebb/ "E. Bornberg" <ebb@uni-muenster.de>

UNebraska Omaha ComputationalBiol

A Postdoctoral Associate position in Computational Biology is available in the laboratory of Dr. Guoqing Lu, in the Department of Biology at the University of Nebraska at Omaha.

The successful candidate will be responsible for developing novel and applying existing computational algorithms to analyze lineages and genotypes of influenza viruses and participate in implementing and evaluating a Web-based system for the influenza viral genotype prediction. Candidates with a Ph.D. degree in Computational Biology or a relevant field and with some research experience are desirable, but individuals in substantial progress toward their Ph.D. can be considered. Candidates with a strong background in molecular evolution but willing to learn Bioinformatics are encouraged to apply. Salary and benefits will be commensurate with experience and in accordance with NIH guidelines. Visit the website http://bioinfo-srv1.awh.unomaha.edu/glu for more information about this project. To learn more about us, please visit the website http://bioinfo-srv1.awh.unomaha.edu/glu.

Review of applications will begin immediately and continue until the position is filled. Please send curriculum vitae, a statement of research interests, and contact information of three references to e-mail:glu3@mail.unomaha.edu, and include Postdoctoral Application in the Subject line.

Many thanks,

Guoqing Lu

Assistant Professor in Bioinformatics Department of Biology University of Nebraska at Omaha Omaha, NE 68182-0040 Tel: 1-402-5543195 Fax: 1-402-5543532

Guoqing Lu <glu3@mail.unomaha.edu>

UNorthernBritishColumbia EntomologicalPopGenomics

UNBC POSTDOCTORAL POSITIONS IN ENTOMOLOGY AND POPULATION GENOMICS

Natural Resources and Environmental Studies Institute, University of Northern British Columbia, Canada

Three postdoctoral research positions (Genome Canada/ Genome BC funded) are available for new research on mountain pine beetle biochemistry and population genomics. These positions are part of a large-scale research program on the mountain pine beetle (MPB) epidemic in Western Canada. See www.thetriaproject.ca for more details.

Entomology (Dr. Dezene Huber) V 2 positions: P Functional characterization of MPB gene products related to detoxification of host secondary metabolites: example genes include cytochromes P450, carboxylexterases, and glutathione S-transferases. Successful candidates should be familiar with insect, yeast and bacterial expression systems and able to perform functional characterization enzyme assays. P Molecular genetic mechanisms of cold tolerance in MPB: successful candidates should have field and lab research skills, including preparation of samples for RT-qPCR, microarray and proteomic analyses. The ability to design, plan, and carry out replicated, ecologically-based experiments is a necessary qualification. Population Genomics (Dr. Brent Murray) V 1 position: P Investigating the integrated landscape genomics of the MPB system, this position focuses on the study of neutral (microsatellite) variation among collections of MPB populations. Previous experience with field collection and population genetic/genomic analysis is an asset. All qualified persons should apply; however, Canadians/permanent residents of Canada are given priority. Only qualified applicants will receive a reply. Noting position for application, apply with CV and names of three references to: Project Director Kyeema Burns (kyeema@interchange.ubc.ca).

Thanks

Brent

Brent W Murray Associate Professor, Biology Ecosystem Science and Management Program University of Northern British Columbia 3333 University Way Prince George, BC, Canada, V2N 4Z9 (250) 960-5638 murrayb <murrayb@unbc.ca>

USheffield GrassPortal

Postdoc: quantitative plant ecology / evolutionary biology

Applications are invited for a full-time postdoctoral position for 18 months in the Department of Animal and Plant Sciences at the University of Sheffield, UK. It is funded by the Joint Information Systems Committee (JISC), with a start date of 1 Sept 2009, or as soon as possible thereafter. The grant is held by Colin Osborne, with Rob Freckleton and Victoria Uren (Department of Computer Sciences) as co-investigators, and the Royal Botanic Gardens Kew, and the software development company Knowledge-Now as project partners. The project has a strong international component, with further project partners at the University of Lausanne, Brown University, and University of Washington.

The project has been funded to develop GrassPortal, a world-class evolutionary data facility that will provide users with the analytical and visualization tools to explore the environment and evolution of every one of the 11,000 grass species on Earth. The development of this facility will integrate millions of species occurrence data from digitised herbarium collections with an accurate multi- dimensional spatial representation of the global environment. The applicant will be expected to have strong quantitative skills and will be responsible for acquiring, processing and modelling the large datasets necessary to develop GrassPortal. There is significant scope within the project for developing research applications for this new resource in evolutionary biology, climate change science, and conservation biology.

The position will be advertised formally at www.jobs.ac.uk and http://www.sheffield.ac.uk/jobs/-research.html in the coming weeks. In the meantime, informal enquiries are welcomed, and should be addressed to Colin Osborne at c.p.osborne@sheffield.ac.uk

Colin Osborne Dept. Animal and Plant Sciences University of Sheffield

tel: +44-114-222-0146 http://www.shef.ac.uk/-aps/staff/acadstaff/osborne.html http://-web.me.com/colin.osborne/lab/home.html c.p.osborne@SHEFFIELD.AC.UK

UTexasAustin EvolutionBiol

Please distribute the following job advertisement:

Postdoctoral Fellow in Integrative Biology.

The Section of Integrative Biology at the University of Texas at Austin invites applications for a Postdoctoral Fellow in Integrative Biology. This subject area is broadly defined to include evolution, ecology, and behavior. The Fellow will be expected to conduct an independent high-quality research program that intersects with the interests of two or more faculty in the Section. For information about the Section of Integrative Biology, visit http://www.biosci.utexas.edu/ib/ . In addition, one semester per year the Fellow will coteach an undergraduate course on Research Methods, as part of the UTeach program for training K-12 science teachers. For information about the UTeach program, visit http://www.uteach.utexas.edu/ Qualified applicants should have a history of original research in evolution, ecology, and/or behavior and must have completed their Ph.D. prior to starting work at the University of Texas. The Fellow is expected to begin working at the University of Texas as early as January 2010, and no later than August 2010.

The position is for two years, subject to annual review. There is an annual salary of $36,000 with an additional $6,000 per year in research support for travel, equipment, or supplies.

We particularly encourage applications from candidates that have recently completed, or will soon complete, their Ph.D. Candidates are encouraged to contact potential faculty sponsors prior to applying.

Applicants should electronically submit a single pdf file containing the following, in order:

1) Coverletter, including proposed faculty sponsors (max 1 page)

2) A CV.

3) Copies of two publications (including papers in press)

4) Statement of research accomplishments (max 2 pages).

5) Statement describing the candidate's proposed research for the duration of this postdoctoral position (max 2 pages).

6) Statement describing the candidate's teaching expe-

rience and philosophy (max 2 pages)

7) List of three references, with contact information (email, telephone, and mailing address). We will request letters directly from these references, after identifying top candidates.

The application pdf file should be emailed to danbolnick@mail.utexas.edu. Applications must be received by September 15, 2009. For questions about this position, contact Dr. Dan Bolnick (danbolnick@mail.utexas.edu).

The University of Texas is an Equal Opportunity Employer.

Dr. Daniel I. Bolnick Assistant Professor Section of Integrative Biology One University Station C0930 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878 danbolnick@mail.utexas.edu

UVienna EvolutionOfApomixis

A postdoctoral position is available at the Department of Systematic and Evolutionary Botany, University of Vienna, Austria, within project âEffects of hybridization on expression of apomixis in the /Ranunculus auricomus/ complexâ (http://www.fwf.ac.at/en/projects/-projekt_datenbank.asp), funded by the Austrian Research Foundation FWF and the Deutsche Forschungsgemeinschaft DFG. The aim of the project is to study the evolution of apomixis via hybridization in a natural model system of flowering plants. A comparative analysis of sexual species, natural allopolyploid apomicts and experimentally produced hybrids in the /Ranunculus auricomus/ complex will be conducted to assess alterations, timing and genetic background of developmental pathways.

The postdoctoral fellow will study embryo sac development and modes of seed formation for a detailed assessment of developmental staging and phenotypic variation of modes of reproduction, on plant material available in the experimental fields of the Institute in Vienna. He/she will elaborate micro-dissection techniques for tissue-specific gene expression profiling. This task will be done in collaboration with the IPK Gatersleben, Germany by a whole transcriptome analysis via 454 sequencing, and tissue-specific microarrays.

The candidate should have a PhD in plant biology and experience in embryology and cytology of apomictic plants. Excellent skills in histological techniques (e.g. clearing techniques) and DIC microscopy are essential. Experience in micro-dissection techniques is desirable. We seek a highly motivated candidate who is able to conduct a self-standing research within an international team. The candidate will have the opportunity to broaden methodical skills, and may also learn apomixis phenotyping via flow cytometric seed screening. The close collaboration with molecular biologists at the IPK Gatersleben will further offer the opportunities for research visits of this Institute to broadening the expertise in the evolution of apomixis, to improve further methodical skills and to establish scientific contacts.

The position is full time available for two years, with an option for an extension to three years. Salaries according to FWF rates (http://www.fwf.ac.at/de/projects/-personalkostensaetze.html)

Please send your letter of application, CV and publication list, plus two reference letters as a pdf file to: Dr. Elvira Hörandl, elvira.hoerandl@univie.ac.at <mailto:elvira.hoerandl@univie.ac.at>, Department of Systematic and Evolutionary Botany, University of Vienna, Austria, by 30th September 2009.

Elvira Hoerandl <elvira.hoerandl@univie.ac.at>

UYork PlantBreedingGenetics

A Post-Doctoral Research Associate is available within the high profile Artemisia Research Project at York University. The job would suit someone with a background in quantitative genetics, population genetics or plant breeding.

Details on the position and application procedure can be found there: https://www22.i-grasp.com/fe/-tpl_YorkUni01.asp?newms=jj&id=27717 The closing date is Friday, 21st Aug 2009.

Thanks,

– Dr. Vincent Segura Genetics and Plant Breeding Team CNAP Artemisia Research Project Centre for Novel Agricultural Products Department of Biology (Area 7) PO Box 373 The University of York York YO10 5YW UK email: vs523@york.ac.uk http://www.york.ac.uk/org/cnap/-artemisiaproject/index.htm Tel: +44 (0)1904 32 8836 Fax: +44 (0)1904 32 8830 vs523@york.ac.uk vs523@york.ac.uk

VanderbiltU 2 Bioinformatics

Two Postdoc Fellows in Bioinformatics in FGSR

Functional Genomics Shared Resource (FGSR), Vanderbilt University Medical Center

Two postdoctoral positions are available immediately to join the Vanderbilt Microarray Shared Resource (VMSR, http://array.mc.vanderbilt.edu/). The VMSR is currently under expansion and in the transition to Functional Genomics Shared Resource (FGSR). The successful candidates are expected to join the Informatics Group which includes bioinformatics engineers and post-doctoral fellows and is under the leadership of Dr. Zhongming Zhao, Chief Bioinformatics Officer in Vanderbilt-Ingram Cancer Center. The candidates will perform advanced analysis of the data generated from the collaborative projects in FGSR. Currently, data generated and analyzed by VMSR has been published in many high profiling journals including Nature series and Science. The positions are supported by the Vanderbilt-Ingram Cancer Center and NIH grants.

The qualified candidates should be highly motivated and have a Ph.D. in bioinformatics, computational biology, molecular biology, or related when the job starts. The successful candidates should have experience in analyzing high-throughput genomic data derived from microarray and some other high throughput technologies (e.g., GWAS, CNVs) and proved skills in at least one programming language (Perl, Java, or C/C++). Good understanding of molecular biology and familiarity with biostatistics are desirable. Applicants should send a CV, brief statement of research interests, and reference to: Zhongming Zhao (zhongming.zhao@vanderbilt.edu), Chief Bioinformatics Officer, Vanderbilt-Ingram Cancer Center. Please specify the position "Bioinformatics Postdoc in FGSR" in the application.

– Zhongming Zhao, Ph.D. Associate Professor, Departments of Biomedical Informatics, Psychiatry, and Cancer Biology Vanderbilt University Medical Center Phone: 615-343-9158 Fax: 615-936-8545

zhongming.zhao@Vanderbilt.Edu zhongming.zhao@Vanderbilt.Edu

VirginiaPolytechnicInst ComputationalBiol

A post-doctorate position in Computational Biology is immediately available at Virginia Polytechnic Institute (Virginia Tech), Department of Computer Science.

The projects can be any or a combination of work on evolutionary/comparative genomics, phylogenetics, data mining of disease association studies, network biology, and algorithm and software development for large-scale sequence analysis.

Excellent opportunities for collaborative research exist within the department's Bioinformatics group and other academic departments and the Virginia Bioinformatics Institute (VBI) at Virginia Tech.

The start date is flexible. Applicants should submit a curriculum vitae and a brief summary of current research and future research interests. Applicants should also arrange for three letters of recommendation to be sent to Dr. Liqing Zhang (lqzhang@vt.edu). The candidates should have a PhD in either (1) molecular evolution, (2) population genetics, (3) algorithms or data mining with bioinformatics experience, or a related field, and a strong computational background.

liqingzhangvt@gmail.com

WageningenU 2 MuseumDNAanalysis

Postdoc position in molecular biology / DNA isolation from museum specimens

Two postdoc positions are available at Wageningen University, Netherlands (28 months) and the Museum of Natural History Berlin, Germany (30 months) conditional to approval by the funding agency. The project is part of a 4 year Joint Research Activity within the SYNTHESYS2 programme funded by the European Union FP7 and aims at developing efficient DNA isolation methods for the analysis of museum specimens and will be integrated within a larger programme involving ancient bone studies.

Museum collections constitute a DNA archive allowing us to explore genetic diversity in specimens over the last 250 years. They are increasingly exploited as ancient DNA repositories for DNA based systematic and ecological studies, and represent years of collecting efforts, often in difficult, complex and remote regions, such as tropical rain forests, or ones that have since been disturbed/ distroyed by human action. The potential for high-throughput automated DNA extraction coupled with recent innovations in DNA sequencing technology (e.g., miniaturisation, pyrosequencing) has highlighted the need for efficient methods for recovering high quality DNA from historical specimens for both evolutionary and diagnostic studies.

We are looking for two postdoctoral researchers with experience with techniques in molecular biology, especially the extraction of DNA from animal and plant/fungal tissues. The successful candidates should have a good background or keen interest in the (bio)chemistry of ancient museum specimen DNA preservation, a good understanding of current systematic research practice, as well as of data basing. Good communication skills, the ability to work independently and to interact with different taxonomist/museum communities are prerequisites.

The two projects involve the following:

Plants/fungi (Wageningen)

P Identify the main obstacles to successful DNA extraction/ amplification from herbarium specimens.

P Optimise protocols for DNA extraction from old (>70 yr), alcohol- preserved, or secondary metabolite-rich herbarium specimens of a wide range of plants and fungal clades, with a view to enabling subsequent large-scale and high-throughput automation of DNA extraction from herbarium material.

P Assessment of post-mortem damage in old herbarium specimens using next-generation sequencing

Invertebrates with muco-polysaccharide rich tissue (Berlin)

P Develop and test safer and more effective DNA isolation procedure from muco-polysaccharide-rich tissue, mainly molluscs, focussing on museum specimens of varying age (5-150 years).

Both projects involve the setup of a web database as an efficient tool to disseminate protocols and user experiences.

We offer an intellectually stimulating research environment in some of Europes largest natural history museums with well-equipped state-of- the-art lab facilities, and with partnerships in leading molecular systematic labs in the Netherlands, the UK and Denmark.

The position at offer at the Museum of Natural History Berlin will be full time at salary level IIa BAT-O (Anwendungstarifvertrag HU Berlin). The Museum of Natural History Berlin is an equal opportunities employer, applications by qualified women are particularly encouraged. Severely disabled applicants with equal qualification will be given preference. The position at Wageningen is full time at scale 10, and more information can be obtained as indicated below.

To apply, please send an e-mail application including CV, PhD certificate, diploma, names and addresses of two referees and a brief letter of motivation by 22 August 2009 to Freek Bakker (freek.bakker@wur.nl - plant/fungi position) or Thomas von Rintelen (thomas.rintelen@mfn-berlin.de V invertebrate position; please cite job reference number 28/2009), who will also be happy to provide additional information.

Thomas von Rintelen <thomas.rintelen@mfn-berlin.de>

WorkshopsCourses

Berlin EvolutionFish Nov23-25

We would like to announce a Workshop that will be held during the upcoming International Conference on the Evolutionary Ecology of Fishes, Nov. 23-25, 2009 in Berlin, Germany (http://www.fishevolution.igb-berlin.de/index.html).

The Workshop, Communication in troubled waters: The evolutionary implications of changing environments on communication systems in fishes will bring together experts in the field of fish communication and evolution, including several sensory modalities, to discuss the influence of changing environments on communication and the maintenance of biodiversity (http://www.fishevolution.igb-berlin.de/workshop1.html).

There will be one plenary lecture by Dr. Andrew Hendry (McGill University, Canada) on the evolutionary implications of environmental change in general, followed by invited talks on the evolutionary effects of environmental change on specific sensory systems. Confirmed speakers so far include:

-Dr. Andrew Hendry (McGill University, Canada), Humans, evolution, and the future of biodiversity**

- Prof. Hans-Joachim Wagner (Anatom. Inst. Universitaet Tuebingen, Germany), Retinae with grouped photoreceptors: adaptations for life in murky waters

- Dr. Martine Maan (EAWAG Centre for Ecology, Evolution and Biogeochemistry, Switzerland), Intraspecific sexual selection and interspecific mate choice across a turbidity gradient

- Dr. Clara Amorim (Unidade de Investigacao em Eco-Etologia, ISPA, Portugal), Fish sounds and mate choice

- Dr. Anne Christine Utne-Palm (University of Bergen, Norway), Visual detection in fish: the effect of turbidity and spectral composition

- Dr. Ulrika Candolin (University of Helsinki, Finland), TBA

- Dr. Iain Barber (University of Leicester, UK), TBA

- Dr. Ralph Tiedeman (University of Potsdam, Germany), TBA

If you would like to attend the workshop, please register for the conference by September 1st, 2009 using the conference website above.

If you have any questions regarding the Workshop, please feel free to contact us.

Regards,

Suzanne Gray and Inke van der Sluijs gray.suzanne@gmail.com inke.vandersluijs@mail.mcgill.ca Postdoctoral Fellows, Chapman Lab Department of Biology, McGill University Montreal, Canada H3A 1B1 Phone: 514-398-4122

Suzanne Gray <gray.suzanne@gmail.com>

Birkbeck London Biodiversity Oct16-Nov20

Free Taxonomy and Biodiversity lectures

'What's in a Name? Taxonomy and Biodiversity': Saving our Experts from Extinction

< http://www.linnean.org/ > The Linnean Society of London / < http://www.bbk.ac.uk/environment/prospective/ecss > Ecology and Conservation Studies Society Joint Lecture Series in conjunction with < http://www.bbk.ac.uk/environment > Birkbeck Institute of Environment, University of London

This series of lectures focuses on the importance of being able to define and identify the natural world with examples of the need and uses of giving species a name, and organising them into systems of classification.

The introductory overview will review uncertainty in the numbers of species on Earth and their extinction rates, and survey how resulting problems can be addressed for effective conservation action. Following lectures will highlight the importance of taxonomy to fungi, forensics, invertebrates, and control of illegal use of endangered species. In the final session a panel of experts will review how the next generation of naturalists can be inspired and discuss how to encourage more people to enter the field of taxonomy, where there is a critical shortage.

Join the debate. All welcome. Free admission but booking is essential.

The venue on 16 October is the John Snow Lecture Theatre, London School of Hygiene and Tropical Medicine, Keppell Street, WC1E 7HT. For all other dates the venue is Room B04, Birkbeck University of London, 43 Gordon Square, WC1H 0PD.

Email: <mailto:environmentevents@FLL.bbk.ac.uk?bcc=environment@bbk.ac.uk,environment@fce.bbk.ac.uk,environment@fll.bbk.ac.uk,secretary@geography.bbk.ac.uk&subject=Taxonomy%20and%20Biodiversity%20Lectures> environmentevents@FLL.bbk.ac.uk for booking details, (or telephone 020 631 6473)

All lectures are from 6.30pm to 8.30 pm on the following Fridays. Doors open at 6.00pm.

. 16 October 'Taxonomy, Systematics and Conservation Biology' Professor Lord Robert May of Oxford, past President of the Royal Society

. 23 October 'Out of Sight, Out of Mind: our lives depend on the hidden kingdom - Fungi' Professor Lynne Boddy, President of the British Mycological Society

. 30 October 'Control of Illegal Use of Endangered Species and Incorrectly Identified Species' Professor Monique Simmonds, Jodrell Laboratory, Royal Botanic Gardens, Kew

. 6 November 'Botany, palynology, and mycology: powerful weapons in the forensic armoury' Patricia Wiltshire, Forensic Ecologist

. 13 November 'Taxonomy, Natural History and the Digital World' Dr Malcolm J. Scoble, Keeper of Entomology, Natural History Museum

. 20 November Panel Presentation and Discussion: 'Inspiring New Naturalists and Taxonomists' Working with Children: Gail Bromley, Education Development Manager, RBG, Kew Higher Education: David Streeter, Reader in Ecology, University of Sussex Professional Taxonomy: Dr Mike Fay, Head of Genetics, Jodrell Laboratory, RBG, Kew

Full details of speakers and their lectures can be accessed at < http://www.bbk.ac.uk/environment/news/lectures > http://www.bbk.ac.uk/environment/news/lectures

Jeremy Wright, Lecture Series Promotion, Ecology and Conservation Studies Society, and Birkbeck - London University, 17 Croftdown Road, London, NW5 1EL, UK Tel: 020-7485-7903. Mobile: 07845 900 499

Jeremy Wright <Jeremy.Wright@walkern.org.uk>

China biogeography

Please distribute to any undergraduates who might be interested:

Unique (and Low-Cost) Opportunity for Ten Undergraduates 2010 Ecological Genetics Field Study Abroad in China

Learn Chinese and Ecological Genetics at the Unversity of Georgia

With funding from NSF's Partnerships for International Research and Education (PIRE) program, we are offering 10 undergraduates (U.S. citizens or permanent residents only) the opportunity to participate in a unique study abroad opportunity in China during the spring and summer of 2010. This is the 3rd year of the program and students have found it to be enormously rewarding.

The research focus of our PIRE grant is a forensic biogeographic study of species that are native to China and invasive in the southeastern U.S. as well as a growing number of species native to the southeastern U.S. and invasive in China.

Each summer, we run an 8 week field course where we visit biological communities throughout China. After the field course, students can elect to continue in short-term (3-week) research internships in our partner labs in China.

Students will need to be prepared to take full advantage of this experience. Therefore, during the spring semester, students must enroll at the University of Georgia (UGA) and take 3 courses; two in intensive elementary Mandarin Chinese and a laboratory course in genetics. No prior experience with Chinese language is required, although students should have had at least a course in introductory biology and preferably courses in ecology and evolutionary biology.

The cost to the student of the summer program is minimal: the grant covers travel to and within China, lodging and most meals. The student is responsible for health insurance, visa costs and personal expenses. Students are also responsible for the costs of enrolling at the University of Georgia for all required courses (12 credit hours) (all students are charged at the in-state tuition rate of ~$250 per credit hour plus fees).

The deadline for applications is October 16, 2009.

Applications for the 2010 program are available on our website: http://www.genetics.uga.edu/pire/-undergrad.html. We encourage any interested students to contact Dr. Mauricio for more information (mauricio@uga.edu).

Rodney Mauricio Program Director, UGA-China PIRE

–

Rodney Mauricio, Ph.D. Department of Genetics Phone: (706) 542-1417 University of Georgia FAX: (706) 542-3910 Athens, GA 30602-7223 e-mail: mauricio@uga.edu

Lab Web Page: http://www.genetics.uga.edu/-mauriciolab PIRE Grant Web Page: http:/-/www.genetics.uga.edu/pire mauricio@uga.edu mauricio@uga.edu

---

CzechRepublic ComparativeGenomics Jan24-Feb5

Workshop on Comparative Genomics, Europe 2010

Cesky Krumlov, Czech Republic

24 January - 5 February 2010

Application Deadline: 1 October 2009

http://workshop.molecularevolution.org/ Michael P. Cummings and Scott A. Handley, Co-Directors Naiara Rodriquez-Ezpeleta, Associate Director

The Workshop on Comparative Genomics consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of comparative genomics. Faculty are chosen exclusively for their effectiveness in teaching theory and practice in comparative genomics. Included among the faculty are developers and other experts in the use of computer programs and packages such as Ensembl, Galaxy, and Species Assignment Package who provide demonstrations and consultations. The course is designed for established investigators, postdoctoral scholars, and advanced graduate students. Scientists with strong interests in the uses of short-read sequence data, analytical methods, comparative structure of genomes, SNP detection and analysis, CNV, genome visualization tools and related areas are encouraged to apply for admission. Lectures and computer laboratories total ~90 hours of scheduled instruction. Admission is limited and highly competitive, with admissions decisions determined by an international committee.

Topics to be covered include:

- Sequencing technologies: short-read sequencing technologies of various types - Assembly and alignment: basic analyses in de novo and resequencing studies - Gene finding and annotation: functional description of genomic data - Genome characterization: gene content; genome structure; synteny; SNPs; copy number variation (CNV) - Assigning sequences to taxonomic groups in metagenomic studies: moving from sequences of unknown taxa to known taxa

2010 Fee: 2250 USD. Fee include opening reception and mid-course dinner, but does not include other meals or housing. Special discounted pricing has been arranged for hotels, pensions and hostels.

For more information and online application see the Workshop web site -

http://workshop.molecularevolution.org/ The Workshop on Molecular Evolution is also being offered immediately before the Workshop on Comparative Genomics.

mike@umiacs.umd.edu mike@umiacs.umd.edu

CzechRepublic MolEvol Jan10-22

Workshop on Molecular Evolution, Europe 2010

Cesky Krumlov, Czech Republic

10 - 22 January 2010, individual research session 22 - 29 January 2010

Application Deadline: 1 October 2009

http://workshop.molecularevolution.org/ Michael P. Cummings and Scott A. Handley, Co-Directors Naiara Rodriquez-Ezpeleta, Associate Director

The Workshop on Molecular Evolution has been the finest course on the subject since first offered in 1988 in Woods Hole, USA. The Workshop will again be offerred in Europe, in January 2010. The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. Faculty are chosen exclusively for their effectiveness in teaching theory and practice in molecular evolution. Included among the faculty are developers and other experts in the use of computer programs and packages such as BLAST, BEAST, Clustal W and Clustal X, FASTA, FigTree, Genealogical Sorting Index, GARLI, LAMARC, MAFFT, Migrate-N, MrBayes, PAML, PAUP*, and SeaView who provide demonstrations and consultations.

The course is designed for established investigators, postdoctoral scholars, and advanced graduate students with prior experience in molecular evolution and related fields. Scientists with strong interests in molecular evolution, phylogenetics, population genetics, and related fields are encouraged to apply for admission. Scheduled lectures and computer laboratories total ~90 hours of instruction. An optional all-computer laboratory of 54+ hours of independent work with guidance and consultation of some faculty and teaching assistants is offered during the third week. Admission is limited and highly competitive, with admissions decisions determined by an international committee.

Topics to be covered include:

- Databases and sequence matching: database searching: protein sequence versus protein structure; homology; mathematical, statistical, and theoretical aspects of sequence database searches - Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis; hypothesis testing - Maximum likelihood theory and practice in phylogenetics and population genetics: coalescent theory; maximum likelihood estimation of population genetic parameters - Molecular evolution integrated at organism and higher levels: population biology; biogeography; ecology; systematics and conservation; population genetics - Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution - Comparative genomics: genome content; genome structure; genome evolution - Molecular evolution of recently diverged species

2010 Fee: 1800 USD, plus an additional 750 USD for the highly recommended, but optional, third week of all-computer laboratory for work on your own data with guidance and consultation of some faculty and teaching assistants. Fees include opening reception and mid-course dinner, but do not include other meals or housing. Special discounted pricing has been arranged for hotels, pensions and hostels.

For more information and online application see the Workshop web site -

http://workshop.molecularevolution.org/ The Workshop on Comparative Genomics is also being offered immediately following the Workshop on Molecular Evolution.

mike@umiacs.umd.edu mike@umiacs.umd.edu

Florida Conservation Genetics Feb7-20 2

Space is filling up for CONGEN 2010.

The American Genetic Association (http://www.theaga.org) in conjunction with the National Cancer, Institute, The Laboratory of Genomic Diversity, Frederick, Maryland (http://home.ncifcrf.gov/ccr/lgd), NOAHS, Smithsonian Institute and the White Oak Conservation Center (http://www.wocenter.org/) is presenting a 13 day intensive course February 7th thru February 20th, 2010, at the White Oak Conservation Center in Florida, USA.

The course will be directed by Dr. Stephen J. OBrien, and taught by renowned scientists in methods, interpretation, and applications of molecular genetic analyses for conservation of endangered species, who will also share a variety of their personal experiences in this important field.

Applicants should be conservation-minded scientists (advanced graduate students, post-docs, teachers, and researchers with advanced degrees) from academia, government, non-government organizations, or industry who are studying the genetics of endangered species and who will apply the knowledge gained from this course to the conservation of such species. Interested individuals can contact us at congen@ncifcrf.gov or visit the website at http://home.ncifcrf.gov/ccr/lgd/congen2010/index.asp for course details.

Deadline: Application package, with required attachments must be received by September 18, 2009. Tuition includes housing, all meals, and transfers from / to White Oak. Limited financial support is available.

Dr. Warren Johnson Laboratory of Genomic Diversity National Cancer Institute Frederick, Maryland USA 21702-1201

TEL: 301-846-7483 FAX: 301-846-6327 johnsonw@ncifcrf.gov

Warren Johnson <warjohns@mail.nih.gov>

UppsalaU EvolClimateChange Oct26-30

Postgraduate course: Impact of climate change on species, populations and communities (The genetics and ecology of environmental change)

Course period: 2009/10/26 - 2009/10/30

Venue: Evolutionary Biology Center (EBC) Uppsala University, Sweden

Teachers: Elizabeth Hadly Stanford University, Stanford, CA, Keith Bennett University, Belfast, UK, Mats Björklund Uppsala University, Sweden, Cecilia Johansson Uppsala University, Sweden

The course considers the response of organisms to climate change on Quaternary timescales (the last two million years), in terms of movement, genetic change and extinction, using both fossil and genetic evidence. It aims to examining climate change from the perspective of genetics and ecology Leading scientists in evolutionary genetics and palaeoecology will present how these fields integrate with ecological and geological perspectives on climate change.

The course is intended for PhD students and researchers in biology, geology and related fields with basic knowledge in genetics and ecology. Topics: 1) Causes and scales of climate change â overview of meteorological climate changes Scales of current climate changes â Scales of past climate change â Quaternary environmental change - Causes, physical evidence and rates â Reconstructing past climate and vegetation change from the fossil record â Computer assignment - Using global databases to access data on vegetation change since the last ice age and visualise responses to climate change â 2) Ecological and genetic response to climate change - Insights from modern taxa. How climatic change affects phenotypes and genotypes â Tolerance, phenotypic plasticity and evolvability â Population size, genetic variation and viability â Interactions and competition among species 3) Ecological and genetic response to climate change - Insights from the fossil record. Phylochronology, molecular evolution, ancient DNA and phylogenetics â Bringing together modern and ancient data â Bayesian estimation of the timing and severity of a population bottleneck from ancient DNA â Computer assignment - Bayesian Serial SimCoal (BayeSSC): a coalescent program for simulation of molecular data in ancient populations â 4) Evolutionary significance of climate change. Does environmental change control evolutionary patterns? - Predicting evolutionary responses to climate change â Discussion section focused on assigned primary literature.

Registrations: Contact Laura Parducci laura.parducci@ebc.uu.se before 2009 10 09

Laura Parducci Evolutionary Biology Centre

Dept of Evolutionary Functional Genomics Uppsala University Norbyvägen 18D SE-752 36 Uppsala

Phone: +46-18-4716414 Fax: +46-18-4716424 Email: laura.parducci@ebc.uu.se Web: www.genetik.uu.se

UUppsala BayesianStatsForEvolution

Bayesian statistics: An introduction to multilevel models and the R package MCMCglmm (7-9 October 2009)

Bayesian statistics become increasingly important in the field of evolutionary biology and particularly for analyses involving multilevel and/or hierarchical models such as those used in comparative studies and in animal models. The aim of this workshop is to give an introduction to the use of Bayesian statistics as an alternative to other statistical approaches for hierarchical modeling (e.g. maximum likelihood). The statistical package MCMCglmm for R was created by Dr Jarrod Hadfield and Dr Loeske Kruuk and published at the beginning of 2009. This package is a useful and powerful tool based on Bayesian statistics for all scientists interested in multi-level/hierarchical models applied in many different fields of evolutionary biology. During this 3-day workshop, Dr Hadfield will introduce the participants to (1) the basics of glmm and MCMC, (2) multivariate and random regressions and (3) the use of MCMCglmm with pedigrees and phylogenies. Participants need to have a basic knowledge of statistics and Bayesian methods and of the programming language R. The course is free and is be open to a maximum of 25 participants selected by order of registration.

Teacher: Dr Jarrod Hadfield

Venue: Evolutionary Biology Centre, University of Uppsala, Sweden

Form: 3-day workshop

Registration: Contact Simone Immler (simone.immler@ebc.uu.se) to register for this course.

– Dr Simone Immler Animal Ecology Department of Ecology and Evolution Evolutionary Biology Centre University of Uppsala Norbyvägen 18d SE - 752 36 Uppsala Sweden

Email: simone.immler@ebc.uu.se Phone: +46 (0)18 471 2634 Fax: +46 (0)18 471 6484

Simone Immler <simone.immler@ebc.uu.se>

UWashington Statgen online

The University of Washington is developing a suite of online versions of its graduate courses in statistical genetics. A general biostatistics course, BIOST 511, is offered by Dr. Jim Hughes in the Fall quarter (October - December). Statistical Genetics I: Population Genetics is offered by Dr. Elizabeth Thompson in the Spring quarter (April-June). Dr. Bruce Weir will offer Statistical Genetics II: Quantitative Genetics in the Fall of 2009 (October - December). Details on this course and how to register for three hours of graduate-level credit can be obtained from him at bsweir@u.washington.edu

Statistical Genetics II covers the distribution of allele frequencies across populations (e.g. Holsinger and Weir "Genetics in geographically structured populations: defining, estimating and interpreting FST" Nature Reviews Genetics 10:639-650, 2009); Continuous variation and the partitioning of variance and covariance among relatives, estimation of heritabilty (e.g. Visscher "Whole genome approaches to quantitative genetics" Genetica 136:351-358, 2009); QTL and association mapping for quantitative traits (e.g. Weir "Linkage diseequilibrium and association mapping" Annual Review of Genomics and Human Genetics 9:129-142, 2008). Current topics such as that described by Hill, Goddard and Visscher ("Data and theory point to mainly additive genetic variance for complex traits" PLoS Genetics 4:e1000008, 2008) will be discussed.

– Bruce S Weir Professor and Chair Department of Biostatistics University of Washington Seattle, WA 98195-7232

Phone: (206) 221-7947 Email: bsweir@u.washington.edu

Bruce Weir <bsweir@u.washington.edu>

Instructions

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

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

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains 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.

Afterword

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.