
E v o l D i r

August 1, 2009

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

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.



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Conferences

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Italy Evolution and Systems Oct18-23

I contact you once again from the European Science Foundation regarding a conference we are organising, on 'Systems Chemistry II: Evolution and Systems'. The title can be misleading, the main theme of the conference is actually hidden in the subtitle: evolution and systems.

The meeting will focus on how the essential principles of systems and models, as used in systems chemistry, can inform wider areas of study. It is an opportunity for natural, life and social scientists to discuss theories of evolution, development and the origin of life. Speakers will come from many different backgrounds from both academia and industry.

COST-ESF conference on Systems Chemistry II: Evolutions and Systems, 18-23 Oct 2009, Acquafredda di Maratea, Italy The meeting will focus on how the essential principles of systems and models, as used in systems chemistry, can inform wider areas of study. It is an opportunity for natural, life and social scientists to discuss theories of evolution, development and the origin of life. Speakers will come from many different backgrounds from both academia and industry.

Grants available to support the participation of

young researchers Deadline for applications and abstracts: 27 July 2009 For more information and to apply, visit www.esf.org/conferences/09332 < <http://www.esf.org/conferences/09332> >

Ivanka ANGELOVA <iangelova@esf.org>

KansasCity GenomicsSymposium,Nov13-15

SAVE THE DATES.

and plan to attend the 7th Annual "Genes in Ecology, Ecology in Genes" Symposium on November 13, 14, & 15, 2009, in Kansas City.

We will convene in the Muehlbach/Marriott Hotel in downtown Kansas City at 6:00 p.m. and conclude on Sunday at noon.

Registration will be opening soon!

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! Confirmed speakers include the following:

PLENARY SPEAKER:

-Jonathan F. Wendel, Plenary Speaker, Department of Ecology, Evolution, and Organismal Biology, Iowa State University

FEATURED SPEAKERS:

-Andres Aguilar, School of Natural Sciences, University of California, Merced

-May R. Berenbaum, Entomology, University of Illinois at Urbana-Champaign

-Jeffrey L. Feder, Biological Sciences, University of Notre Dame

-David Queller, Ecology and Evolution, Rice University

-Matthew Rockman, Center for Genomics and Systems Biology, Biology, New York University

-Erica Bree Rosenblum, Biological Sciences, University of Idaho

-Jay F. Storz, Biological Sciences, University of Nebraska-Lincoln

-Christopher Toomajian, Plant Pathology, Kansas State University

-Michael J. Wade, Graduate Student Invited Speaker, Biology, Indiana University

POSTER SESSIONS: 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, ecogen.ksu.edu, as details are finalized. Please share this announcement with colleagues and students who are interested in learning more about the field of Ecological Genomics. 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.

Ecological Genomics Institute Directors:

Dr. Loretta Johnson

Dr. Michael Herman

Kansas State University, Division of Biology

by

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

Program Coordinator

Ecological Genomics Institute, www.ecogen.ksu.edu

Kansas State University, Division of Biology, 318 Ackert

Manhattan, KS 66506-4901

Phone: (785) 532-3482, Fax: (785) 532-6653

Doris Merrill <dmerrill@ksu.edu>

Laxenburg Austria Evolution of Cooperation Sep15-18

Dear all,

>From the 15th to the 18th of September 2009 we are organizing an international conference on the

EVOLUTION OF COOPERATION- MODELS AND THEORIES (website: <http://www.tect.iiasa.ac.at>)

Empirical insights and theoretical methods underlying the evolutionary theory of cooperation are currently undergoing a phase of rapid expansion and partial reorientation. The goal of this conference is to showcase complementary approaches to evolutionary problems dealing with the social dilemmas surrounding human cooperation. The main emphasis will be on theory, or rather theories, but these will not only be compared from a mathematical viewpoint: throughout the conference, model-based lectures will be complemented by lectures on salient empirical findings. In this way, the conference will provide a platform for comparing and orchestrating different research approaches.

The conference will be held in the conference center of the former summer palace of the Habsburg family in Laxenburg, near Vienna, Austria, home of the International Institute for Applied Systems Analysis (IIASA). The conference is organized as part of the EUROCORES Programme on The Evolution of Cooperation and Trading (TECT), coordinated by the European Science Foundation (ESF) and funded by a range of national research agencies. Laxenburg is a beautiful village 15 km south of Vienna sporting a magnificent 2.8 km² of royal gardens including the 200 years old knight's castle Franzensburg.

Confirmed invited speakers

Ken Binmore, UK

Rob Boyd, USA

Ross Cressman, USA

Aart de Zeeuw, Netherlands

Michael Doebeli, Canada
 Armin Falk, Germany
 Jeffrey Fletcher, USA
 Drew Fudenberg, USA
 Simon Gaechter, UK
 Herbert Gintis, Hungary
 Peter Hammerstein, Germany
 Christoph Hauert, Canada
 Michael Hochberg, France
 Yoh Iwasa, Japan
 Vincent Jansen, UK
 Michihiro Kandori, USA
 Hanna Kokko, Finland
 Olof Leimar, Sweden
 Simon A. Levin, USA
 Eric Maskin, USA
 John McNamara, UK
 Ronald Noë, France
 Martin Nowak, USA
 Hisashi Ohtsuki, Japan
 J.M. Pacheco, Portugal
 David Queller, UK
 Anxo Sanchez, Spain
 Istvan Scheuring, Hungary
 Thomas N. Sherratt, Canada
 Brian Skyrms, USA
 György Szabo, Hungary
 Eörs Szathmary, Hungary
 Yamagishi Toshio, Japan
 Arne Traulsen, Germany
 Fernando Vega Redondo, Spain
 Conference organizers
 Ulf Dieckmann, IIASA, Austria
 Karl Sigmund, IIASA and University of Vienna, Austria

Participation is open to everyone. Thanks to support by ESF and IIASA, we only charge a small registration fee to cover lunches, coffee breaks etc. In addition to the invited presentations, the conference will feature two poster sessions to which all participants are invited

to contribute. If you are interested in participating, please register here. The reduced early-registration fee is available until July 15th. Please register as early as possible, as the total number of participants is limited.

With best wishes,

Karl Sigmund & Ulf Dieckmann

Ulf Dieckmann Program Leader Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

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Ulf Dieckmann <dieckmann@iiasa.ac.at>

Leiden Systematics Aug10-14 ExtendedDeadline

Extended deadlines for Systematics 2009 10-14 August, in Leiden (www.biosyst.eu < <http://www.biosyst.eu/> >).

To accommodate insistent requests we have extended the period during which you can still register at the regular fee for the upcoming Systematics 2009 conference and submit a presentation. The deadline for submission is now July 8, 9:00 AM GMT.

Please note that these late submissions will be assigned to the open sessions, and that the availability of a time slot for an oral presentation is not guaranteed. Please allow us a few days after the deadline to construct a schedule on basis of which you will be notified about your presentation. For late inclusion in a specific symposium, please inquire with the organizers.

Also note that an extra fee of 50 EURO will definitely be charged for later registrations, irrespective of any reductions that may be applicable!

You can register and submit an abstract through the webpage www.biosyst.eu < <http://www.biosyst.eu/> > . If you have problems in accessing this website, please contact me directly (hovenkamp@nhn.leidenuniv.nl).

Peter Hovenkamp Nationaal Herbarium Nederland, Leiden branch www.nationaalherbarium.nl

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hovenkamp@nhn.leidenuniv.nl

[hov-](mailto:hovenkamp@nhn.leidenuniv.nl)

London Darwin200 Nov12-13

Meeting announcement.

Darwin 200 Discussion Meeting Royal Society/Genetics Society:

Genetics and the causes of evolution: 150 years of progress since Darwin November 12/13, 2009 at the Royal Society, London.

Organised by Michael Bonsall (University of Oxford) and Brian Charlesworth (University of Edinburgh)

Speakers are Spencer C.H Barrett, Nick Barton, Dan Bradley, Anthony Brown, Tracey Chapman, Jerry Coyne, Laurent Duret, Steven Frank, Hopi Hoekstra, Ben Kerr, Josephine Pemberton, Anna Di Rienzo, Dolph Schluter, Paul Sharp, Naoyuki Takahata, Holly Wichman and John Willis. Wen-Hsiung Li will present the Mendel Lecture of the Genetics Society.

This meeting is free to attend, but pre-registration (online) is essential. The online registration form and programme information can be found at royalsocietypublishing.org/events.

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

Medellin Columbia InsectEvolution Oct20-23

Dear all,

I am writing to invite you to participate on a entomology meeting that will be held at Medellín, Colombia at Universidad Nacional de Colombia on 20 to 23 October 2009.

In this meeting we invited speakers on subjects related to evolution, population genetics, ecology and integrated pest management of insects.

The prices of the registration are 60 US dollars for the mini-courses, and for the talks that will be held from 21-23 October, between 10-40 US dollars for students (national and international students) and 60 US dollars for professionals.

If you are interested in the meeting, please contact

Clara Saldamando for further details to encuentroentomologia2009@gmail.com or to cisaldam@unal.edu.co

The congress includes mini-courses during 20, 21 and 22 October given by

- 1) Pablo Benavides PhD. "Establecimiento de un programa de manejo integrado de la broca del café en Colombia"
- 2) Claudia Medina PhD. "Taxonomía de escarabajos coprófagos"
- 3) Raúl Medina PhD. "Análisis molecular y genética de poblaciones de insectos plaga"
- 4) Fernando Montealegre PhD. "Taxonomía de Tettigonidae"
- 5) Nilkla Wahlberg PhD. "Using molecular data to get a timeframe for evolution"

The invited speakers are: 21 October

- a) Oscar Ortega MSc. Unalmed "Avances de la ecología de insectos en la Universidad Nacional de Colombia, sede Medellín"
- b) Solange Sánchez MSc. (CES) "El uso de productos naturales para el control de garrapatas"
- c) Alejandro Madrigal MSc. "Biocontroladores de plagas" (UNALMED)
- d) Nicolás Jaramillo PhD. "Morfometría: el estudio cuantitativo de la variabilidad morfológica" (UNIVERSIDAD DE ANTIOQUIA)

22 October

- a) Fernando Montealegre (UNIVERSIDAD DE BRISTOL;INGLATERRA) "Comunicación acústica en Ensiífera (Orthoptera): biomecánica de generadores y receptores de sonido"
- b) Mauricio Linares PhD. (UNIANDES) "Especiación de *Heliconius* sp. por hibridación"

- c) Victor Rico PhD (INSTITUTIO DE BIOLOGIA, MEXICO) "Redes Complejas en Interacciones Hormiga-Planta"

- d) Inge Ambrecht PhD (UNIVALLE) "Insectos en cafeales"

23 October

- a) Kris A. G. Wyckhuys PhD (UNIVERSIDAD JORGE TADEO LOZANO) "Agroecología de insectos y frutales"
- b) Patricia Chacón PhD (UNIVALLE) "Ecología de hormigas"
- c) Nilklas Wahlberg PhD (UNIVERSIDAD DE

TORKU, FINLANDIA) “An awkward age for butterflies: Molecular phylogenetics and the timeframe of macroevolution”

d) Claudia Medina PhD (INSTITUTO VON HUMBOLDT) “Avances en sistemática de Insectos en Colombia”

e) Raúl Medina PhD (COLLEGE STATION; TEXAS) “Descubriendo los Factores que Promueven la Diferenciación Genética entre Poblaciones de Insectos”

f) Pablo Benavides PhD (CENICAFE) “Aspectos biológicos y genéticos de la broca del café”

g) Gustavo López MSc (CES) “Control de garrapatas en rumiantes”

h) Rodrigo Vergara MSc (UNALMED) “El MIP en Colombia: Realizaciones y Posibilidades Futuras”

cisaldam@unal.edu.co

MexicoCity DNA Barcode Nov7-13 Call for Abstracts

Dear Colleagues,

The Third International Barcode of Life Conference will take place in Mexico City from 7-13 November 2009. The conference website (www.dnabarcodes2009.org) has been updated to include the following:

- * Registration Form (online or PDF)
- * Online abstract submission
- * Online application form for travel bursaries (developing country participants only)
- * Hotel Reservations (online or PDF)
- * Travel Information

Because of delays in releasing these webpages, the deadline for submission of abstracts and applications for travel bursaries has been extended to 3 August 2009.

Discounts for early registration are available until 11 September 2009:

- * Delegates: US\$200
- * Delegates from developing countries: US\$125
- * Students: US\$75

If you have any questions about the conference, please write to inquiries.dnabarcodes2009@si.edu.

If you have problems with the conference website or online forms, please write to bol@servimed.com.mx <<mailto:ameifac-dia@servimed.com.mx>> .

We hope to see you in Mexico City in November!

Best regards,

David

David E. Schindel, Executive Secretary

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

MexicoCity DNA Barcode Nov7-13 DeadlineExtended

Due to popular demand and some early technical website problems, the deadlines for submissions of abstracts and applications for travel bursaries for the Third International Barcode of Life Conference in Mexico City have been extended.

The new deadlines are 3 August 2009. Decisions on abstracts and travel bursary applications will be sent out on 15 August.

The Conference website is at www.dnabarcodes2009.org.

If you have questions or problems with the online submission forms, please write to inquiries.dnabarcodes2009@si.edu.

We look forward to seeing you in Mexico City!

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

<blocked::mailto:Schindeld@si.edu> CBOL WEB-SITE: <http://www.barcoding.si.edu> <blocked::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>

Oxford GMOD Community Meeting Aug6-7

There will be a GMOD Community Meeting, 6-7 August, 2009 at the University of Oxford, in Oxford, UK.

GMOD (<http://gmod.org>) is a collection of interoperable, open-source software components for managing, visualizing, annotating, and sharing biological data. GMOD is also a community of users and developers addressing common challenges with their biological data. The popularity of next generation sequencing and other high-throughput methods has made this GMOD meeting particularly timely.

GMOD meetings are an excellent opportunity to learn best practices from other researchers, to meet GMOD users and developers, and to learn and affect what is coming in the project. As with previous meetings, there will be a mixture of project talks, component-focused talks, and user talks.

Registration for the meeting is now open and space is available on a first come, first served basis. Attendance is limited to the first 55 people to register. The meeting cost is £50.

See http://gmod.org/wiki/August_2009_GMOD_Meeting for more information.

Please join us in Oxford this August.

Thanks,

Dave Clements GMOD Help Desk

– Register now for the August GMOD Meeting: http://gmod.org/wiki/August_2009_GMOD_Meeting
clementsnescent@gmail.com

PuntadelEste VertebrateMorphology Jul26-31

Dear Evolutionary Biologists:

This is a new invitation to enjoy the endless pleasures of our discipline, once the gathering in Punta del Este from 26th to 31st July 2010 is confirmed. We proudly claim that the 9th International Congress of Vertebrate Morphology will have a really low registration fee. As a matter of fact, one of the lowest if compared with similarly sized and reputable events, past and present: only USD 300 for regular members and USD 150 for students.

A bargain, isn't it? However, if you decided to register prior to October 1st, then it'll amount next to nothing. Well, almost: USD 220 for regular attendees and USD 100 for students.

And cheap won't mean low quality, as we are committed to turn this event into something unforgettable. However, for that, we'll need you to be here. Please register as soon as possible, using our web page or directly in that of Jetmar, our dependable travel agency: (<http://www.jetmar.com.uy/icvm2010/>), and let them help you about housing and other details. If you have any difficulties, please right to us at once and we'll do our best.

The final deadline for registration and abstract submission is February 10th, 2010. After this date, only posters will be accepted.

Once you have registered (and paid...), you'll be able to submit your abstract.

We can give you some hints on the scientific program, but there'll be more to follow in the near future: we'll have about 15 symposia and workshops, published in the website, and 5 first class plenary lectures:

Arkhat Abzhanov (Harvard, USA)

Melina Hale (Chicago, USA)

Peter Wainwright (Davis, USA)

Gabriel Marroig (USP, Brazil) and

Eugenia del Pino (PUC, Ecuador).

Please feel free to spread this second circular as much as you can.

Richard A. Fariña and Enrique P. Lessa

<http://icvm-9.edu.uy/> passer@fcien.edu.uy

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>

Toulouse Evolution and Medicine Oct19

Meeting announcement

Evolution & Medicine Symposium

October 19, 2009 at the Natural History Museum, Toulouse

Organised by Philipp Heeb (CNRS), Etienne Danchin (CNRS), and Christophe Thebaud (University of Toulouse)

The focus for the symposium is a celebration of the bicentenary of Darwin's birth and the fundamental role that evolutionary science plays in modern biology and its applications to human health and medicine. The symposium will reflect on the various areas of societal concerns and needs related to human health and medicine where evolutionary research has led to new understandings of long-standing problems. All presentations will be given by specially invited speakers, who are all renowned for their work at the interface between evolutionary biology and medicine, and there will be ample time for discussion.

Speakers are Randolph Nesse (U Michigan), Steven Austad (U Texas), Carlo Maley (The Wistar Inst), Lluís Quintana-Murci (Pasteur Inst), Sylvain Gandon (CNRS Montpellier), John Taylor (UC Berkeley)

This symposium is free to attend, but registration will be limited to 150 participants. So pre-registration (online) is essential. The online registration form and programme information can be found at:

<http://www.evolmed.fr/> Philipp Heeb (heeb@cict.fr)
UMR 5174 CNRS - Univ Paul Sabatier F-31062
Toulouse Cedex 4 France

Philipp Heeb <heeb@cict.fr>

UCollegeLondon NatSelection Jul7 2

LONDON EVOLUTIONARY RESEARCH NETWORK DEBATE

“Is natural selection at the group level an important evolutionary force?”

Tuesday 7 July, 3.30pm

JZ Young Lecture Theatre, Anatomy Building, University College London

Map: http://www.ucl.ac.uk/maps/ucl-maps/-map2_hi_res < http://www.ucl.ac.uk/maps/ucl-maps/map2_hi_res >

(Square C3 of the map - entrances in Gower Street or via Malet Place)

Professor Stuart West, Professor of Evolutionary Biology, University of Oxford

Professor Herbert Gintis, Professor of Economics, Santa Fe Institute,

Professor Mark Pagel, Professor of Evolutionary Biology, Reading University

Professor Samir Okasha, Professor of Philosophy of Science, University of Bristol

Main presentations

3:30pm Speaker 1

3:50pm Speaker 2

4:10pm Speaker 3

4:30pm Speaker 4

4:50pm Refreshments

Speaker rebuttals

5:20pm Speaker 1

5:30pm Speaker 2

5:40pm Speaker 3

5:50pm Speaker 4

6:00pm 30 minute Q & A with audience

6:30pm Finish

The order of speakers will be decided by drawing lots at the start of the event.

Entry and refreshments free of charge.

Gillian Pepper MSc Student - Evolutionary Psychology
Brunel University

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/-profile/GillianPepper> >

Gillian Pepper <ht08ggp1@brunel.ac.uk>

UNebraskaLincoln BIOT-2009 Oct9-11

****Reminder for BIOT-2009 Symposium deadlines****

Submission deadline for full papers and 2-page abstracts (for oral presentations) is Wednesday, July 22, 2009 for the Annual Biotechnology & Bioinformatics Symposium. However, based on the response we have received, if you need more time to submit a full paper, we will try to accommodate it. Please email Barbara Gnirk, bgnirk1@unl.edu as early as possible, but BEFORE July 22, 2009 to let us know. We look forward to hearing from you.

For more information on BIOT-2009 visit our website at: <http://www.biotconf.org/> BIOT-2009, the 6th Annual Biotechnology & Bioinformatics Symposium October 9-11, 2009 at the University of Nebraska, Lincoln, NE. <http://www.biotconf.org/> The 6th Annual Biotechnology & Bioinformatics Symposium, BIOT-2009, will showcase research and development activities in bioinformatics & computational biology, and biotechnology, promoting future interdisciplinary activity and research in these areas. Speakers will be invited from both accepted papers and abstracts. Accepted papers and abstracts will be printed in the proceedings. Abstracts for poster presentations will also be accepted.

We invite contributions in any area of Biotechnology and Bioinformatics, theoretical as well as practical. This year the following topics are particularly empha-

sized: Machine learning application in bioinformatics Distributed database, semantic Web, and ontologies Intelligent user interface and decision support Omics approaches and systems biology High-throughput sequencing technologies and related data analysis RNA interference, microRNA, epigenetics Bioinformatics application in plant science and plan biotechnology Molecular evolution, phylogeny, and phylogenomics Education in computational biology and bioinformatics

Please see the BIOT-2009 website (<http://www.biotconf.org/>) for more information on paper/abstract submissions and registration.

Please note that the submission deadline for full papers and 2-page abstracts (for oral presentation) has been extended to July 22, 2009.

Symposium Co-Chairs: Etsuko Moriyama School of Biological Sciences and Center for Plant Science Innovation emoriyama2@unl.edu

Leen-Kiat Soh Computer Science & Engineering lsoh2@unl.edu

Stephen Scott Computer Science & Engineering sscott2@unl.edu

emoriyama2@unlnotes.unl.edu
emoriyama2@unlnotes.unl.edu

UNebraskaLincoln BIOT2009 Oct9-11 3

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emoriyama2@unlnotes.unl.edu
emoriyama2@unlnotes.unl.edu

UOtago MolEcolXII2009 Nov27-29

12TH NEW ZEALAND MOLECULAR ECOLOGY MEETING , November 27-29 2009

It is a pleasure to announce that the 12th New Zealand Molecular Ecology Meeting will be hosted by the University of Otago, Friday Nov 27 to Sunday Nov 29 2009.

We have been fortunate to procure the Tautuku Outdoor Education Centre in the Catlins as a venue. For those of you who attended the Pounaweia meeting in 2003, this year's venue is a little farther south, set on the edge of podocarp forest, behind idyllic Tautuku beach.

Please circulate this email to anyone that might be interested. If you did NOT receive this email directly, please send your email address to me (g.wallis@otago.ac.nz) to be included in a second mailing next month. In this and any other correspondence, please use "MolEcol09" in the subject heading.

We look forward to seeing you here in November!

Graham Wallis Jon Waters –

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Assoc Prof, Genetics <http://www.otago.ac.nz/-Zoology/staff/academic/wallis.html> Graham Wallis <graham.wallis@stonebow.otago.ac.nz>

Uruguay Darwin200 Sep2-6 NewDeadlines

Dear colleagues,

After considering several requests and detecting some troubles with our diffusion strategy the organizing committee of the event "150 years of Darwin's Evolutionary Theory: A South American Celebration" to be held between 2-6 September at the Barradas Hotel (<http://www.hotelbarradas.com.uy/>), Punta del Este, Uruguay, has decided to extend the deadline for submitting abstracts and applying for fellow-

ships until SUNDAY 19th JULY, more information at www.darwin200.edu.uy. The event will include plenary lectures, symposia and poster sessions.

Plenary speakers:

* Giorgio Bernardi * Leonardo Boff (to be confirmed) * Daniel Dennett * Douglas Futuyma * Gaston Gonnet * Eviatar Nevo * Alain Pavé * Francisco Salzano * Emile Zuckerkandl

Symposia (chairs *)

- Evolutionary Genomics and Molecular Evolution Fernando Álvarez*, Hugo Naya*, Giorgio Bernardi, Gastón Gonnet, Olivier Gascuel, Pablo Goloboff, Wojciech Makalowski, Michel Tibayrenc To be confirmed: Cecilia Saccone, Norihiro Okada

- Evolutionary Physiology: Francisco Bozinovic*, Ernesto Gianoli, Carlos Navas, Pablo Sabat, Ariovaldo P. Cruz-Neto, Enrique Caviedes- Vidal

- Viral Evolution: Juan Cristina*, Raul Andino, Eckard Wimmer

- Paleontology and Evolution: Richard Fariña*, Sergio Martínez*, Sergio Vizcaíno, Laura del Río

- Human Evolution: Monica Sans*, Francisco Salzano, Héctor Puccarelli

- Darwinism and Society: Alción Cheroni*, N Villarreal*, Daniel Dennett. To be confirmed: Leonardo Boff

It will be a pleasure to be you hosts in September,

For registering, fellowships and further information

<http://www.darwin200.edu.uy> darwin200@fcien.edu.uy

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BiKF Germany Biodiversity

The Biodiversity and Climate Research Centre (BiK-F) has recently been founded by the Senckenbergische Naturforschende Gesellschaft, the Goethe-Universität Frankfurt am Main, and additional partners. It is funded by the Hessian State Initiative for the Development of Scientific and Economic Excellence (LOEWE). The mission of the Centre is to carry out internationally outstanding research on the interactions of biodiversity and climate change at the organism level. The Project Area C “Adaptation and Climate” invites applications for the position of a

Ph.D. position “Planktonbank” PG C 5.5 [Ref. #C 30]
BAT II a/2

One of the main focus of the research programme “Adaptation and Climate” is to study adaptation of aquatic organisms to climate changes. Resting stages of freshwater plankton represent a valuable source for monitoring evolutionary change over time. In order to unravel the evolutionary potential and response to recent climatic changes, we will explore lake sediment cores to identify ecologically relevant traits underlying climatic stress tolerance.

The main objectives of the project are (1) to expose *Daphnia* clones to different temperature regimes using life history experiments (2) to determine genetic responses underlying phenotypic evolution in response to global change. Resting eggs of plankton species from lake sediment cores will be studied to assess the evolutionary potential of current and extinct populations.

The applicant should hold an earned master’s degree or diploma in biology and is expected to have expertise in the following areas: application of molecular markers for population genetics and ecology; life history experiments; aquatic ecology. The successful candidate will cooperate with various groups of biologists working on the long term impact of climate change on natural pop-

ulations. Very good written and oral English language skills and interest in joining a multidisciplinary research team are required.

The Research Centre BiK-F advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference. The contract will start September 1st, 2009, and will be restricted until December 31st, 2010. An extension for another two years is possible, but depending on funding. The duty station will be at the Biologie-Campus, Siesmayerstraße 70-72, Frankfurt am Main, Germany. Official employer is Senckenbergische Naturforschende Gesellschaft.

Please send your application by mail or preferably e-mail, including a detailed CV and 2 references as soon as possible to Prof. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany, E-mail to Personal & Service: anette.ohl@senckenberg.de. For enquiries about the scientific framework and practical work please write to Prof. B. Streit, E-mail: mailto:streit@bio.uni-frankfurt.de or streit@bio.uni-frankfurt.de or K. Schwenk E-mail: schwenk@uni-landau.de.

[kschwenk <k.schwenk@bio.uni-frankfurt.de>](mailto:kschwenk@bio.uni-frankfurt.de)

ETH Zurich EvolutionaryBiol

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

The Department Aquatic Ecology (group of Piet Spaak) seeks a

PhD student in Evolutionary Biology

The PhD student will participate in a collaborative research project with Juliane Hollender (Environmental

Chemistry, Eawag) and Flavio Anselmetti (Sedimentology, Eawag) to study the invasion of *Daphnia* during the past 100 years in lakes north and south of the Swiss Alps, using genetic information from diapausing eggs buried in lake sediments. Furthermore, by hatching *Daphnia* from past layers we want to study experimentally the role of contaminants on the success of *Daphnia* taxa (resurrection ecology). This study aims to blend the excellent research facilities both in environmental chemistry and evolutionary biology at Eawag. Another PhD student in the project studies the fate of pollutants over time in sediment cores of the same lakes. The focus of this project will be on evolutionary aspects.

For this project, financed by the Swiss Science foundation, we are looking for a highly motivated candidate with interests in evolutionary biology, population genetics and environmental disturbance. Although field work is also involved, most of the work will be done in the lab (conducting experiments and screening diapausing eggs using molecular tools). Some of the work on lakes south of the Alps might be done in Italy.

We offer a stimulating research environment in a lively and social institute in Dübendorf (near Zürich) in a department with several other evolutionary and ecological research groups. The position will be for a period of three years, and should start as soon as possible (September 2009 or soon thereafter). The ideal candidate has both experimental as well as molecular skills (PCR, genotyping). A Diploma or Masters degree (or equivalent) in biology or related subject is necessary for admission. The working language in the group is English.

Applications should include a letter of interest with a description of pertinent experience, curriculum vitae, a list of publications (if any), the names (with e-mail addresses) of two potential referees, and copies of certificates of academic qualifications.

Please submit your application by 7 August 2009 as one single PDF file to Sandra Isenring, Eawag, Human Resources Department: recruiting@eawag.ch, indicating reference number 094402. For further information, consult www.eawag.ch or contact Piet Spaak (Tel. +41 44 823 5617) spaak@eawag.ch.

Piet Spaak Eawag Aquatic Ecology Überlandstrasse 133 P.O. Box 611 8600 Dübendorf Switzerland Phone: +41 (0)44 823 56 17 Fax: +41 (0)44 823 58 17 spaak@eawag.ch <http://www.eawag.ch/~spaak>

Piet.Spaak@eawag.ch Piet.Spaak@eawag.ch

Germany HostParasiteCoevolution

Several PhD Positions will be available from October 2009 within the recently started DFG Priority Program 1399 -Host-Parasite Coevolution - Rapid Reciprocal Adaptation and its Genetic Basis'

Research areas include Evolutionary Biology, Parasitology, Genomics, Immunology, Bioinformatics, and more.

The priority program offers cutting edge, cross-disciplinary research. Host-parasite coevolution is used as a powerful and versatile model for analysing the causes and processes of evolutionary adaptation across scales (from genomes to ecosystems). The program is funded by the German Science Foundation (Deutsche Forschungsgemeinschaft, DFG) across various locations in Germany: Berlin, Bonn, Gießen, Halle, Hamburg, Heidelberg, Kiel, Köln, Leipzig, München, Münster, Osnabrück, Plön, Regensburg.

We invite applications from highly qualified candidates of any nationality. Women are especially encouraged to apply. Preference will be given to disabled applicants in case of equivalent qualification.

The application deadline is August 15, 2009.

Information on the various projects and application procedure can be found at:

<http://ieb.uni-muenster.de/spp/jobs> Prof. Dr. Joachim Kurtz

University of Muenster Institute for Evolution and Biodiversity, Animal Evolutionary Ecology Group Huefferstr. 1, D-48149 Muenster, Germany Phone: + 49 251 83 24661 Fax: + 49 251 83 24668 joachim.kurtz@uni-muenster.de <http://www.uni-muenster.de/Evolution/-joachim.kurtz@uni-muenster.de> joachim.kurtz@uni-muenster.de

InstZoology London ChytridFungusEvolution

IoZ supervisor, Dr. Andrew Cunningham, Institute of Zoology

University supervisor, Dr. Matthew Fisher, Imperial

College, London.

The chytrid fungus, *Batrachochytrium dendrobatidis* (Bd) has emerged as a major threat to amphibian survival across the world. Recently, the fungus has been found to be infecting amphibians in the UK. A PhD studentship is offered to investigate the epidemiology of Bd in the UK, including the extent of Bd infection and the role of anthropogenic factors in its emergence. The results of these studies will be synthesised to inform possible Bd control policies in the UK.

The successful applicant will join a team of researchers investigating Bd emergence in the UK and its impact on native species. The studentship will involve the development of spatial models to explain Bd infection dynamics, informing these with results from field sampling (swabbing amphibians, environmental sampling) and laboratory analyses (real-time PCR). Possible additional components of this research include Bd culture and genotyping and experimental infection work to determine the susceptibility of different amphibian species to different strains of Bd.

This challenging studentship is funded by Defra with an annual stipend of Â£18,000 for three years and will be based at the Institute of Zoology, London, UK.

Start date: 1st October 2009.

Jo Keogh PA to Director of the Institute of Zoology
Institute of Zoology Zoological Society of London
Regent's Park London NW1 4RY

tel: 020 7449 6610 fax: 0207 586 2870

<http://www.zsl.org/>

Jo Keogh <jo.Keogh@ioz.ac.uk>

Jena Germany Orchid EvoDevo

*Ph.D. position in Evolutionary Developmental Genetics Department of Genetics (<http://www.uni-jena.de/-Genetics.html>) Friedrich-Schiller University, Jena Germany

Pending approval by funding agencies, we are looking for candidates for a Ph.D. position on Evolutionary and developmental genetics of the orchid flower.

We offer:

- Clearly structured project for which the required prerequisites have been established.

- Close supervision in the laboratory and training in soft skills during the preparation of written and oral work reports.

- New, fully-equipped laboratories.

- Pleasant work environment.

- Jena is a green and attractive university town in central Germany.

We are looking for:

- Motivated, well-organized students who have experience in molecular biology and are interested in developmental or evolutionary biology, and are able to work and think methodically and independently. Such students would have excellent communication skills in English and have fun working in a team.

For informal enquiries and additional information on these positions, please write or send your curriculum vitae with at least two recent references and a statement of research interests to gunter.theissen@uni-jena.de. These positions will remain open until an appropriate candidate is identified.

*

Mariana Mondragon-Palomino, Ph.D. Postdoctoral Researcher Dept. of Genetics Friedrich-Schiller-Universität Philosophenweg 12 D-07743 Jena
mariana.mondragon@uni-jena.de Fax +49 3641-949 302

Mariana Mondragon <m.mondragonpalomino@googlemail.com>

Lyon FishComparativeGenomics

Dear all,

A three years graduate position is available in our team to work on Comparative genomics of sex determination in fish.

Doctoral school Biologie Moléculaire, Intégrative et Cellulaire (BMIC), Ecole Doctorale 340

Research team Team « Génomique Evolutive des Vertébrés », Institut de Génomique Fonctionnelle de Lyon; UMR5242 CNRS/ INRA/ Université Claude Bernard Lyon I/ ENS Ecole Normale Supérieure de Lyon, 46 allée d'Italie, 69364 Lyon Cedex 07, France

PhD supervisor Prof. Jean-Nicolas Volff Jean-Nicolas.Volff@ens-lyon.fr

Title Comparative genomics of sex determination in fish

Project description Scientific background In mammals and birds, sexual development is controlled by rather stable sex determination systems having emerged at least 100 million years ago (XY male and ZW female heterogamety, respectively). In strong contrast, frequent evolutionary changes place sexual development under the control of new sex determination systems in fish (for review, Volff et al. 2007, Sexual Development 1: 85-99). Hence, even two populations belonging to a same species can have different mechanisms of sex determination. Such frequent changes might be involved in pre-/post-zygotic isolation and therefore in speciation. A better understanding of the control of sexual development in fish is essential for aquaculture, which generally uses monosex population to avoid stress linked to reproduction and exploit some sex-linked traits of zootechnical interest. Hence, fish aquaculture is interested in methods allowing molecular sexing of individuals at early stages of their development as well as phenotypical sex inversion through environment-friendly processes. In order to better understand the molecular and evolutionary basis of the variability of sex determination in fish and its impact on biodiversity and speciation, it appears necessary to identify the genes controlling sexual dimorphism in different species and to compare the regulatory cascades under their control. Therefore, we have initiated two projects aiming the positional cloning of sex determination genes in two fish species, le platyfish *Xiphophorus maculatus* and the rainbow trout *Oncorhynchus mykiss*. These species, which diverged at least 200 million years ago, have both a genetic sex determination system (XYW in the platyfish and XY in the trout). In the platyfish, we have already assembled megabase-sized "contigs" of bacterial artificial chromosome (BAC) clones including the region differentiating the X from the Y chromosome. These contigs are currently being sequenced and analyzed in collaboration with the sequencing center Genoscope. This project is funded by the French Research Agency (ANR Blanche seXYphorus, 2008-2010, coordinator JN Volff). In rainbow trout, we aim in collaboration with INRA institutes from Rennes and Jouy-en-Josas to identify a secondary sex-determining gene responsible for the occurrence of males in XX populations. This second project is based on the analysis of candidate genes and BAC contigs containing molecular markers linked to the locus of interest (ANR Génomique Sexytrout, 2008-2011, coordinator INRA Rennes). Whole genome sequencing projects will contribute important sequence data for both species.

Scientific questions This project of comparative func-

tional genomics aims, using sexual development in fish as an example, to better understand the evolutionary dynamics of the regulation of biological processes. Based on data generated by the seXYphorus and Sexytrout projects, the candidate will have to answer the following scientific questions: - What are the genes controlling sexual dimorphism in different fish species? - What is the genomic location of these genes with respect to sex chromosomes and other regions controlling sexual development in different fish species? - What are the functional similarities and differences between these genes in different species, particularly in the hierarchy of the sex determination cascade?

Research program and methods used The candidate will be involved in the genetic, evolutionary and functional analysis of gene candidates for sex determination identified in the projects seXYphorus (sequencing of the sex-determining region in platyfish) and Sexytrout (sequencing of a genomic region containing a secondary sex-determining locus in trout). Genes will be identified through bioinformatics and mapped (collaboration with INRA Jouy-en-Josas for mapping in trout). Gene expression will be analyzed during embryogenesis as well as in adult through qRT-PCR and in situ RNA hybridization in platyfish and trout (collaboration with INRA Rennes) as well as in medaka and zebrafish, two model species for which numerous mutants are available. Male and female gonad sections will be performed to determine the cell types

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

LyonU RiverineGeneticDiversity

Dear Evoldir members,

A PhD position is available in the Laboratory of Fluvial Hydrosystem Ecology, Lyon University, France, to study the effect of surface water / groundwater interactions and habitat turnover on genetic diversity patterns of invertebrate assemblages in braided rivers. Genetic diversity will be studied in 3 aquatic invertebrate species with different dispersal patterns (flying, swimming, crawling) using new microsatellite markers.

Applicants should have a graduate degree in ecology or evolution. Skills in molecular ecology, population

genetics and a strong interest in understanding factors controlling the biodiversity of aquatic ecosystems would be appreciated. The 3-year position starts October 2009 - January 2010 and includes an annual net salary of 17 000 Euros including health insurance.

Interested applicants should contact Prof. Christophe Douady (douady@univ-lyon1.fr) and Dr. Florian Malard (malard@univ-lyon1.fr) until the 30th of July and Dr. Thibault Datry (thibault.datry@cemagref.fr) from the 30th of July to 20th of August and send a letter of interest (CV, research experience and interests, contact information for three references), before August 20. Interviews will be conducted before the end of August.

Sincerely, Christophe Douady

-

Pr Christophe J. Douady < <http://umr5023.univ-lyon1.fr/index.php?pid=284&lang=en> >, PhD

Membre de l'Institut Universitaire de France < <http://cpu.fr/Iuf/> >

Laboratoire d'Ecologie des Hydrosystèmes Fluviaux < <http://umr5023.univ-lyon1.fr/> >

Université Claude Bernard Lyon 1 < <http://www.univ-lyon1.fr/> > - UMR CNRS 5023 < <http://umr5023.univ-lyon1.fr/> >

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christophe DOUADY <douady@univ-lyon1.fr>

MichiganStateU YaleU AscomyceteSexualEvolution

Two NSF-funded Graduate Student positions available to study evolution of sexual development in perithecium-producing ascomycetes. One position is at Michigan State University with Dr. Frances Trail, the other is at Yale University with Dr. Jeffrey

Townsend. The positions will involve comparative transcriptomics and functional genomics, and candidates will gain experience in computational biology. Candidates should have a solid background through coursework and (preferably) lab experience in molecular biology. Experience with fungi will be considered a plus.

Funding available for up to three years. Interested candidates should send an email expressing interest and describing research experience to Dr. Frances Trail at trail@msu.edu or Dr. Jeffrey Townsend at Jeffrey.Townsend@Yale.edu.

<http://www.plantbiology.msu.edu/faculty/faculty-research/frances-trail/>

<http://www.yale.edu/townsend/>

townsend.yale@comcast.net

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>

PennStateU HumanPopulationGenomics

- A graduate student (Ph.D.) position in evolutionary genomics/human population genomics/statistical genomics at Penn State -

A graduate student position is available immediately in the laboratory of Kateryna Makova (http://www.bx.psu.edu/makova_lab/) at Penn State. The current focus of the lab is on deciphering molecular mechanisms of different mutations via whole-genome comparisons and on sex chromosome evolution.

As a successful candidate, you will come to our lab with relevant bioinformatics expertise, including some combination of programming experience, previous use of the R statistical package, and working knowledge of molecular evolution or population genetics. Individuals with either computational or biological background are encouraged to apply. Once hired, you will analyze next-generation sequencing data sets and vertebrate genome alignments, and perform statistical and evolutionary modeling. You will work in close collaboration with statisticians to develop computational models, with wet-lab biologists to validate model predictions, and with the GALAXY team (<http://g2.bx.psu.edu>) to implement our computational tools. You will be joining a dynamic group with an established record (http://www.bx.psu.edu/makova_lab/Publications.php). We are part of the Center for Comparative Genomics and Bioinformatics (<http://www.bx.psu.edu/>) and of the newly established Center for Medical Genomics at Penn State. Penn State is a vibrant scientific community with particular strengths in computational genomics and molecular evolution.

The starting date is flexible, with an earlier date preferred. Interested applicants should send pdfs with CV, a statement of research interests, and contact information of three references to kmakova@bx.psu.edu, indicating graduate student position in the subject line.

Kateryna Makova Associate Professor Center for Comparative Genomics and Bioinformatics Department of Biology 305 Wartik Lab Penn State University University Park, PA 16802 Tel: 814-863-1619 Fax: 814-865-9131 E-mail: kmakova@bx.psu.edu Web: http://www.bx.psu.edu/makova_lab/ Kateryna Makova <kmakova@bx.psu.edu>

RegensburgU Germany
PlantEvolSyst

Open Ph.D. position in plant systematics and evolution at the Institute of Botany of the University of Regensburg (Germany)

Position description: A 3-years Ph.D. position funded by the German Science Foundation (DFG) is presently available in the area of plant systematics and evolution at the Institute of Botany of the University of Regensburg, under the supervision of Prof. Dr. Christoph Oberprieler (<http://www.biologie.uni-regensburg.de/Botanik/Oberprieler/index.html>) and in co-operation with Dr. Robert Vogt (Botanic Garden & Botanical Museum Berlin-Dahlem). The salary will be according the TV-L E13/2. The Ph.D. project will focus on the evolution of polyploidy in the genus *Leucanthemum* (Compositae, Anthemideae) and will use this genus of around 40 species distributed in southern and central Europe as a model to investigate the genetic, genomic, biogeographical and ecological consequences of polyploidy. Work packages envisaged will comprise (a) the reconstruction of the phylogeny of the genus based on nrDNA and cpDNA marker sequences, (b) the modelling of eco-climatological niches of species using GIS techniques, (c) the phylogeography of species groups of this genus, and (d) expression studies of genes of salt tolerance in diploid and polyploid members. The project will include extensive travelling throughout S Europe to collect plant material in natural populations.

Deadline for application: August 15, 2009. If needed, the position will remain open until a suitable candidate is found.

Starting date: between September 1, 2009 and January 1, 2010.

Requirements: Applicants are expected to have their Masters/Diploma degree by the start of the Ph.D. project. Good knowledge of English and German are highly desirable. The ideal candidate will have documented experience in one or more of the following areas: molecular biology, expression techniques, phylogeny reconstruction, population genetics, GIS techniques, botanical field work (including the possession of a driver's licence). The selected candidate will be a member of the Regensburg International Graduate School of Biological Sciences (RIGeL; <http://www.biologie.uni-regensburg.de/RIGeL/index.html>).

How to apply: Please send you application including (a) an application letter addressing your motives for application and your career goals, (b) a detailed CV including a detailed list of molecular, analytical, linguistic, and field work skills, presentations at scientific meetings, and publications (if applicable), and (c) addresses of two academic advisors who could comment on your skills, your dedication to science, and your ability

to work cooperatively in a team. Please, send applications by email to:

Prof. Dr. Christoph Oberprieler Institut für Botanik Universität Regensburg Universitätsstr. 31 D-93053 Regensburg Germany phone +49-(0)941-9433129 fax +49-(0)941-9433106 christoph.oberprieler@biologie.uni-regensburg.de

748-1011 ext 7055 Fax. 705-748-1132

http://forensics.nrdpfc.ca/staff/chris_kyle.html http://web.nrdpfc.ca/bios/dr_chriskyle.html

chris.kyle@nrdpfc.ca

TrentU Population Genetics

Ph.D. Opportunity:

We are seeking a Ph.D. candidate with research experience in the areas of landscape genetics, population genetics, and evolutionary ecology. The student will be charged with genetically discriminating Canada geese from populations that nest, migrate through, or are harvested in Ontario. These geese belong to several management units that differ greatly in origins and demographic trends. These genetic data will be used to refine harvest estimates, including harvest rates, and to assess harvest distribution of the management units and will support management plans and regulation development. The successful candidate will also be encouraged to explore independent research questions within the framework of this project.

Research will be conducted within the Natural Resources DNA Profiling and Forensic Centre (www.nrdpfc.ca) with a collaborative team that includes Dr. Ken Abraham and Rod Brook (Ontario Ministry of Natural Resources), Dr. Christopher Kyle (Trent University), and Jack Hughes (Canadian Wildlife Service).

Applicants should hold a M.Sc. in Landscape/Population Genetics, or a related area. All candidates should submit a letter of application, curriculum vita, and names and contact information for three referees to Dr. Kyle. The position will close on August 15, 2009 or as soon as a suitable candidate is found before that date to begin Sept 2009 or Jan 2010.

Dr. C. J. Kyle, Assistant Professor Research Chair in Wildlife Genetics and Forensics Natural Resources DNA Profiling and Forensics Centre Forensic Science Department, DNA Building, Trent University 2140 East Bank Drive, Peterborough, ON, K9J 7B8 Tel. 705-

UBasel Bacterial Evolution

TWO PHD POSITIONS IN BACTERIAL EVOLUTIONARY GENOMICS at the Biozentrum, University of Basel, Switzerland

Two PhD positions in bacterial evolutionary genomics are available in the group of Prof. E. van Nimwegen at the Biozentrum of the University of Basel, also a member of the Swiss Institute of Bioinformatics. The overarching research interests of our lab concern the evolution of entire genomes and the structure, functioning, and evolution of genome-wide molecular interaction networks that regulate cellular behavior, including transcription regulatory networks and signaling networks.

Our group is highly interdisciplinary with members whose backgrounds range from molecular biology, chemistry, biophysics, to theoretical physics. Although the main focus of the group is on theoretical analysis and modeling, we are currently adding a wet-lab component to study bacterial evolutionary genomics, and have two open positions in experimental evolutionary genomics. Both positions will be co-supervised by Prof. E. van Nimwegen and Dr. O. Silander, who will be heading the wet lab.

The main aim of the first research project is to uncover the selection forces that shape changes in gene-content and phenotypic abilities of bacteria on relatively short evolutionary time scales, and to characterize these selection forces quantitatively. We will use high-throughput phenotypic characterization of related bacterial strains, in combination with sequencing of the entire genomes of selected strains using next generation deep sequencing technology. An integral part of the project will be the theoretical analysis of the obtained data, and relating the results to recent theories that have been developed in our group based on the analysis large-scale analysis of genomics data (e.g. van Nimwegen, Trends in Genet 19:9:479-484 (2003), Molina and van Nimwegen, Biol Direct 3:51 (2008)). In particular, we are interested in characterizing the environmental and evolutionary forces that drive changes in genome

complexity.

The main aim of the second project is to understand de novo evolution of transcriptional regulation and promoter architecture. We will use experimental evolution of bacteria to evolve novel promoter sequences. This will be followed by detailed sequence analysis of the evolved promoters using next generation sequencing technologies. A central part of this project will involve characterization of transcription factor binding motifs (e.g. van Nimwegen, E. BMC Bioinf 8(Suppl 6):S4 (2007)) and computational modeling to predict how transcription factor binding affects expression.

Requirements for the position are a master diploma in biology or biochemistry and a strong background in molecular biology. Knowledge and/or experience in microbiology, bioinformatics, applied mathematics, and programming would all be highly advantageous. The candidates should have good knowledge of English, German is helpful but not necessary. The salary is according to the guidelines of the Swiss National Science Foundation and the entrance date will be by mutual arrangement.

To apply, please send your application letter, CV and the names of two or three references (preferably by email) to

Prof. Erik van Nimwegen erik.vannimwegen@unibas.ch
Department of Bioinformatics Biozentrum, University of Basel Klingelbergstrasse 50/70 CH-4056 Basel / Switzerland

Phone: +41 61 267 1576 email: erik.vannimwegen@unibas.ch

For further information about the group, see: <http://www.biozentrum.unibas.ch/~nimwegen>
olin.silander@env.ethz.ch

UEastAnglia Evolution

NERC-funded PhD studentship opportunity in evolution, ecology or conservation in the School of Biological Sciences at the University of East Anglia, Norwich, UK.

We are seeking applications from highly motivated applicants for a NERC funded PhD position in the area of evolution, ecology or conservation. The exact area of research is not specified at this stage and we encourage applicants to develop a project together with a potential supervisor within the School.

<http://www.uea.ac.uk/bio/bioresearch> Once a project outline has been agreed you should then apply via the link below, by completing an application form and also sending in a covering letter and copy of your CV.

<http://www.uea.ac.uk/bio/courses/bioresdegrees> 1. Why study at the School of Biological Sciences at UEA?

You will find yourself in a dynamic, open and friendly School that delivers excellence in science and which has an international impact. Research in the School covers important issues such as how organisms evolve and interact with their environment, and how to ensure the preservation of ecosystems and their biotas so that future generations can benefit from the scientific insights and ecosystem services that stem from the natural world. We have a particular emphasis on understanding adaptation at both the gene and whole-organism level, and on applying sound basic scientific principles to pressing questions in conservation and applied biology.

You will also enter into a flexible, personal training scheme that delivers the wide range of skills you will need to undertake your PhD as well as those recognised as important for gaining future employment. You will therefore have the opportunity to conduct scientific research at the highest level and be trained to a level to enable you to maximise your options for career progression.

The School of Biological Sciences is an exciting academic community. In the latest Research Assessment Exercise, 90% of research activity in the School was classified as internationally leading, excellent or recognised, and the panel recognised world-leading research across all the school's research themes. We are consistently ranked in the top five for overall student satisfaction amongst mainstream English universities.

2. Eligibility

The full stipend is available only to students satisfying UK residency requirements:

<http://www.nerc.ac.uk/funding/available/postgrad/-eligibility.asp> Students from the EU may be eligible for fees awards only.

For queries please contact: Tracey Chapman, tracey.chapman@uea.ac.uk

“Chapman Tracey Dr (BIO)”
<Tracey.Chapman@uea.ac.uk>

UEdinburgh H1N1evolution

Please note: this studentship is open to UK residents only.

PhD Studentship: The molecular evolution and epidemiology of 2009 swine-origin human influenza A/H1N1.

Background The current pandemic of H1N1 influenza of swine origin demonstrates the difficulty in predicting the risk of the human population to emerging infectious diseases. It's sustained human-to-human transmission has caused the WHO to declare this virus as the first world-wide pandemic of the 21st Century. Although the virus appears to cause mild to moderate symptoms in most cases at the moment, there are concerns about the emergence of drug resistance and a second wave as the UK goes into the Autumn flu season. The current situation offers an excellent opportunity for a talented student with a quantitative background to help understand the spread and evolution of the H1N1 Swine-Origin Influenza Virus (S-OIV), since the scientific community is collecting large amounts of simultaneous epidemiological and genetic data.

This project will apply state-of-the-art methods of molecular epidemiology to synthesize viral genetic and epidemiological information to characterize the emerging influenza epidemic as it happens. The project will have the UK as its focus but influenza is a global disease so the evolutionary dynamics will be put into a global context using the wealth of available virus genetic data. The project will be informed by the now extensive data available on S-OIV 'swine' flu from Spring 2009 and also by new data as it emerges from the future UK influenza seasons. In particular, the interaction between the new A/H1N1 S-OIV strain and our two existing seasonal flu strains (human A/H1N1 & A/H3N2) will be examined. Previous pandemics (in 1957 and 1968) have resulted in the extinction of the originally circulating strain although the re-emergence of A/H1N1 in 1977 has resulted in 2 co-circulating lineages. The emergence of S-OIV gives us a unique opportunity to examine the pandemic phenomenon using genetic and epidemiological approaches.

Person Specification We are looking for an exceptional and enthusiastic PhD candidate to work in Infectious Disease Evolution and Epidemiology. You may have a degree/MSc in mathematics with an interest in genet-

ics/evolution and epidemiology; in biology / medicine with strong training in quantitative methods; or in physics / informatics (or similar) with an interest in biology and the aptitude to apply your skills to an important problem. As the time-scale is short, prior experience in Phylogenetic packages would be an advantage but strong programming and/ or statistical/numerical skills will be essential. The studentship will be held jointly between two highly regarded research groups (Viral Molecular Evolution and Infectious Disease Epidemiology) and may have opportunities to spend time working with Government partners and with other collaborating institutions.

Information about the work being done in the two groups may be found on these websites: <http://tree.bio.ed.ac.uk/> <https://www.wiki.ed.ac.uk/-display/Epigroup/> <http://influenza.bio.ed.ac.uk/> Only UK students may apply for funding.

Please send your CV, 2 references and a 1-page statement of your research interests to Dr. Andrew Rambaut (a.rambaut@ed.ac.uk) or Dr. Nick Savill (nick.savill@ed.ac.uk).

The project will be co-supervised by Dr. Andrew Rambaut, Dr. Nick Savill and Prof. Mark Woolhouse.

Andrew Rambaut Institute of Evolutionary Biology University of Edinburgh Ashworth Laboratories Edinburgh EH9 3JT EMAIL - a.rambaut@ed.ac.uk TEL - +44 131 6508624

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UIdaho ConservationGenetics

Graduate Student Opportunity in Conservation Genetics/Predator Prey Dynamics Dr. Lisette Waits, University of Idaho Laboratory of Conservation and Ecological Genetics Center for Research on Invasive Species and Small Populations

I am currently recruiting one to two graduate students to conduct conservation genetics research as part of a large collaborative project evaluating predator/prey dynamics between caribou and black bear, lynx, and coyote in Newfoundland. As part of an effort to understand and reverse caribou population decline, our research group will be conducting a predator control study. The students working under my supervision will

contribute to the project by using non-invasive genetic sampling of hair and feces to estimate population size, evaluate genetic diversity and population structure, determine relatedness of predators and the diet of each species before and after predator control. The project involves collaboration with the Canadian government, multiple universities and international organizations. Student research projects could be conducted at the MS or PhD level and are expected to start between late August 2009 and January 2010. Graduate stipend is \$17K - \$19K/year and will also include payment of tuition and fees.

Interested applicants should send CV/resume, cover letter/statement of purpose, transcripts, GRE scores plus names and contact info for three references. Please note that I do not need official transcripts and GRE scores at this stage. If you are selected to join my research group, then I will ask you to send all official documents to the University of Idaho graduate school applications office. Electronic (email) submission of applications is encouraged but mail is also fine. Recommended Application Deadline: July 20, but earlier submission is encouraged and late applications will be accepted until suitable candidates are identified.

Lisette Waits, PhD University of Idaho Department of Fish and Wildlife PO Box 441136 Moscow, ID 83844-1136 Phone: (208) 885 7823, Fax: (208) 885 9080 lwaits@uidaho.edu <http://www.cnrhome.uidaho.edu/-default.aspx?pid=72862>

Lisette Waits <lwaits@uidaho.edu>

ULaval EvolutionaryGenomics

ULaval.EvolutionaryGenomics

PhD position available in evolutionary genomics and systems biology

Chosen candidates will study the evolution of genes and genomes using genomics, proteomics and bioinformatic tools. Possible subjects of research include the evolution of gene duplication and gene loss, the evolution and organization of protein-protein interaction networks, the evolution of gene expression and the evolution of phenotypic robustness.

Research will be conducted at the Laval University Institut de Biologie Integrative et des Systemes (IBIS), in Quebec City, Canada. IBIS hosts more than 30 researchers working in genetics, genomics and proteomics

as well as organismic biology. Laval University is one of the oldest universities in North America and is a major research institution in Canada. Quebec city is a magnificent and vibrant city.

Competitive stipend + bonus for students who can obtain external fellowships.

Starting date: September 2009 or January 2010

Interested candidates should contact me directly for informal enquires at:

Christian.landry@bio.ulaval.ca

Christian Landry, PhD

Associate Professor

CIHR New Investigator

Department of Biology

Institute for Integrative and Systems Biology

Pavillon Charles-Eugene-Marchand

1030, Avenue de la Medecine

Laval University

Quebec (Quebec) G1V 0A6

Canada

<http://tiny.cc/ChristianRLandry> Christian Landry
<christian.landry@bio.ulaval.ca>

ULeuven InsectSpermCompetition

PhD student position: University of Leuven, Laboratory of Entomology (Belgium) Sperm competition and the economy of sperm use in insect societies

We are looking for a highly motivated PhD student to join the Laboratory of Entomology at the University of Leuven, Belgium (<http://www.kuleuven.be/bio/ento>) to work on a project on sperm competition and the economy of sperm use in insect societies. Insect societies such as ants, bees and wasps are remarkable in that queens store the sperm of the males they mate with in a sperm storage organ (the spermatheca), in which they keep the sperm alive for their entire lives, sometimes for up to 20 years. This puts an exceptionally strong selection pressure on queens to make economic use of this sperm. The main aims of the project are to determine whether multiple mating in some species might lead to increased sperm competition and a reduced economy of sperm use, and whether there is an

tagonistic coevolution between the queen and the stored sperm over the fertilisation rate of eggs.

The project will be carried out under the joint supervision of Dr. Tom Wenseleers and Prof. Johan Billen.

Candidates should have an interest in evolutionary biology and functional morphology. Prior research experience in working with social insects would be a bonus, but is not strictly required. Funding for both salary and consumables for 3 years is available through a grant from the Fund for Scientific Research Flanders. The starting date of the project can be negotiated (between 1 October 2009 and 1 January 2010). All nationalities are eligible. For details on the formal application procedure please contact Prof. Johan Billen at johan.billen@bio.kuleuven.be.

Prof. Johan Billen Dept. of Biology Laboratory of Entomology Zoological Institute K.U.Leuven Naamsestraat 59 B-3000 Leuven Belgium tel. +32 (0)16 32 39 75 e-mail johan.billen@bio.kuleuven.be web

<http://bio.kuleuven.be/ento> cheers, Tom Wenseleers

Tom Wenseleers <tom.wenseleers@bio.kuleuven.be>

ULisbon Biodiversity Genetics Evolution

Announcement: acceptance of applications for the Doctoral Programme in 'Biodiversity, Genetics & Evolution', year 2009/ 2010

The University of Lisbon (UL) and the University of Porto (UP) have a joint Doctoral Programme in 'Biodiversity, Genetics & Evolution' (BIODIV), in the area of Biological Sciences. The programme is organized by the Faculty of Sciences of the University of Lisbon (FCUL) and the Faculty of Sciences of the University of Porto (FCUP), with the collaboration of the Centre for Environmental Biology (CBA/ FCUL), Research Center in Biodiversity and Genetic Resources (CIBIO/ UL), Institute for Molecular and Cell Biology (IBMC) and Institute of Molecular Pathology and Immunology of the University of Porto (IPATIMUP). These Units develop research of international excellence in Biodiversity, Functional Ecology, Phylogenetics, Evolution, Behaviour, Theoretical Biology, Developmental Biology and Bioinformatics, among other fields, and are equipped with high tech laboratories, as well as a Field Station.

BIODIV is a graduate programme that leads to the acquisition of a PhD degree in several specialties as indicated in the corresponding plans (for further informations see <http://cba.fc.ul.pt> and <http://www.fc.up.pt/fcup/pe/bolonha/curso.php?tc=PD&ano=2009&cod=bge>). The programme includes a first year with several courses, seminars and laboratory rotations, followed by three years of research corresponding to the development of the PhD project and dissertation. The students can take advantage of the resources available in both Universities during the entire period of the programme, though they are registered, and mainly affected to one of the two Universities.

Conditions to apply to BIODIV are the following: i) Having a graduate degree ('Licenciatura' or equivalent) in Biology or related areas, obtained previous to the Bologna Process; ii) Having a Master degree in Biology or related areas; iii) Having equivalent habilitations; and iv) Having a curriculum that certifies capacity to apply for a PhD programme.

The applications, accepted continuously, will be selected for the year 2009/ 2010 in two phases:

1st Phase of selection September 14-18, 2009 - Evaluation and ordering of applications received till September 11, 2009; inscriptions September 21- 30; start of the Doctoral Programme at the beginning of the 1st semester of the scholar year 2009/ 2010

2nd Phase of selection

January 18-22, 2009 - Evaluation and ordering of applications received till January 16, 2010; inscriptions January 25- 29, 2010; start of the Doctoral Programme at the beginning of the 2nd semester of the scholar year 2009/ 2010

Number of vacancies: 15 for each Faculty

Scholar fees: 2750 ? /year

Applications should be sent to 'Gabinete de Estudos Pós-Graduados da Faculdade de Ciências da Universidade de Lisboa' or 'Gabinete de Estudos Pós-Graduados da Faculdade de Ciências da Universidade do Porto'. More details of conditions of access and doctoral plans can be obtained consulting:

FCUL: <http://acesso.fc.ul.pt/?page=doutoramentos>
FCUP: <http://www.fc.up.pt/fcup/pe/bolonha/curso.php?tc=PD&ano=2009&cod=bge>

The candidates are strongly encouraged to search for financial support, by applying to PhD grants or other sources, in Institutions that give these types of support (Fundação para a Ciência e a Tecnologia or other).

>From the Coordinate Commission of the Programme
Margarida Matos Centro de Biologia Ambiental Faculdade de Ciências da Universidade de Lisboa Campo Grande 1749-016 Lisboa Portugal

Margarida Matos <mmatos@fc.ul.pt>

UNeuchatel SocialEvolutionTheory

Dear colleagues,

Two PhD positions are open under the supervision of Dr. Laurent Lehmann to study social evolution theory at the Laboratory of eco-ethology of the University of Neuchatel Switzerland (<http://www2.unine.ch/ethol/>). The positions are funded by the Swiss National Science Foundation and are available for three years. Starting date: end of 2009, beginning of 2010. Salary per annum: 36900 to 45600 CHF.

The focus of the SNF-funded project is to develop gene-culture co-evolutionary models for social interactions, with focus on human evolution. The project will have two different but complementary directions. First, we will seek to develop models, which can explain the evolution of the transition of small-scale egalitarian societies to larger-scale stratified societies. Second, we will seek to develop models aiming at understanding the role of individual and social learning in the expression and dynamics of social behaviours, for example in the context of the usage of adaptive and maladaptive cultural traits. Some related papers on this can be found at <http://www.stanford.edu/~lehmann/>. Depending upon the applicants, the work could be taken in a number of directions.

The Institute of Biology at Neuchatel consists of a dozen groups working in diverse fields of ecology, evolution, physiology and molecular and cell biology. Neuchatel is a University town in the French-speaking part of Switzerland situated between the Jura Mountains and a 40km long lake. The town is well connected with larger centers such as Lausanne, Geneva, Berne, or Zurich by public transportation. For more information, contact Laurent Lehmann (lehmann@stanford.edu).

Applicants must have a university degree that allows entrance to a PhD program. Applicants are required to have good knowledge in mathematics or computer programming. Ideal applicants have a good knowledge of evolutionary biology, behavioural ecology and/or population genetics. A strong interest in understanding

the genetic and cultural factors driving social evolution in humans is an asset. Motivated applicants should submit (1) a one-page letter that summarizes interests and relevant experience, (2) a CV, (3) copies of undergraduate and masters/diploma transcripts, and (4) contact information for 2 references (all as PDFs) to lehmann@stanford.edu.

Best wishes, Laurent Lehmann

Laurent Lehmann <lehmann@stanford.edu>

UOtago EvolutionaryBiol

A PhD studentship in evolutionary ecology and conservation at University of Otago, New Zealand. This project uniquely integrates different disciplines - evolutionary biology, conservation biology, behavioural ecology, genetics and endocrinology - to tackle a multitude of questions. The main aim of this project is to test the assumptions of "Trojan sex chromosome theory" using life bearing Poeciliid fish. Trojan sex chromosome theory utilizes hormonal reversal of sex and skewing sex-ratio to control animal population size. In this project, we will investigate the fitness of sex-reversed individuals and their offspring (trans-generational effects). We will also conduct behavioural experiments for mate choice and intra- and inter-specific aggression in these individuals. Furthermore, we will use computer simulations (individual-based modeling) to integrate all observed parameters to predict outcomes of the application of this theory in the real world. The student will be encouraged to explore their own ideas. The scholarship consists of: a stipend NZD 25,000 every year for 3 years and tuition fee waivers over 3 years. This PhD position (3 years) is open to students, who have completed or are completing their BSc(Hons) or/and MSc (or equivalent), of any citizenships (need to fulfill University English Requirements). The preferred date of start for this PhD is September 1st (or slightly later). The successful applicant will be supervised by Dr Mark Lokman, Dr Gerry Closs, and myself (Shinichi Nakagawa). Please check our departmental webpage (<http://www.otago.ac.nz/zoology>). Our department offers an excellent working environment for PhD students. Also s/he will live in the wonderful city of Dunedin, which is surrounded by beautiful sceneries. We are seeking a highly motivated student with a proven academic record for this very challenging PhD. If you are interested or want to know more about this PhD, please

contact me by email (shinichi.nakagawa@otago.ac.nz ; email subject should say "Trojan fish PhD"). If you would like to apply for this studentship, send me your CV including academic records and names and contacts of 3 referees. The position will be filled as soon as a suitable applicant is found.

Shinichi Nakagawa, PhD (Lecturer of Behavioural Ecology) Department of Zoology University of Otago 340 Great King Street P. O. Box 56 Dunedin, New Zealand Tel: +64-3-479-5046 Fax: +64-3-479-7584 <http://www.otago.ac.nz/zoology/staff/academic/-nakagawa.html> shinichi.nakagawa@otago.ac.nz

UWindsor EvolutionConservation

Graduate student positions available

There are immediate opportunities for qualified graduate students (MSc & PhD) to work in Dan Heath's Evolutionary & Conservation Genetics lab at the Great Lakes Institute for Environmental Research (GLIER) at the University of Windsor (Ontario, Canada).

Projects include; investigating the role of gene transcription evolution in local adaptation in BC salmon, evolutionary ecology and conservation of the Eastern Sand Darter, a threatened species in Ontario, and a population and quantitative genetic analysis of migratory behaviour in salmon and trout.

Students will have opportunities for field and lab work, and will be expected to attend and present at national and international conferences.

Contact Dr. Heath at (519) 253-3000 (ext 3762) dheath@uwindsor.ca www.uwindsor.ca/heathresearchgroup Daniel Heath Great Lakes Institute for Environmental Research University of Windsor 401 Sunset Ave Windsor, Ont, Canada N9B 3P4

E-mail: dheath@uwindsor.ca Phone: (519) 253-3000, Ext 3762 Fax: 971-3616 www.uwindsor.ca/heathresearchgroup/ dheath@uwindsor.ca

UWisconsinMadison ConservationGenetics

PhD Position Available in Conservation Genetics

I am seeking an outstanding student to pursue a PhD in conservation genetics in the Department of Forest and Wildlife Ecology at the University of Wisconsin, Madison. Current research in my lab focuses on characterizing demographic history and understanding the effects of habitat fragmentation on microevolution and population viability, particularly in threatened species.

The doctoral student's dissertation thesis will involve studying the population genetics of Blanding's Turtles in Wisconsin. The objective of the project is to characterize the spatial distribution of genetic variation, identify the timing and magnitude population bottlenecks, determine the extent to which local population are connected by dispersal, and characterize the role of geographic isolation and landscape features on genetic population structure. Funding is in place for two and a half years of graduate student support (\$19,000/year + tuition waiver), including a half-year of funding via teaching assistantships, and for sample collection and labwork. Additional field or lab-based research components can be added depending on shared interests and funding opportunities.

Applicants should possess at minimum a B.Sc., and preferably a M.Sc., specializing in conservation genetics, molecular ecology, or closely related field. Applicants with a strong background in molecular laboratory methods (e.g., DNA extraction, PCR, fragment sizing, and DNA sequencing), genetic data analysis, population modeling, conservation biology, and demonstrated ability to publish in peer-reviewed journals will be given preference. To be considered for this position, please send a cover letter outlining your interests and research background, a curriculum vitae (including GPA and GRE scores), and contact information for three professional references (name, email, phone, address) as either a PDF or MS Word file to mpeery@wisc.edu with 'Conservation Genetics PhD Application' in the subject line.

The selected student is expected to enroll in the Department of Forest and Wildlife Ecology in the Spring (January) 2010 semester (<http://forestandwildlifeecology.wisc.edu/grad.htm>) and apply to the UW Graduate School (< <http://info.gradsch.wisc.edu/education/admissions/> > <http://info.gradsch.wisc.edu/education/admissions/>). Application materials will be accepted until October 1, 2009 or until a suitable candidate is found.

For more info, contact: Zach Peery

Assistant Professor

Department of Forest and Wildlife Ecology

University of Wisconsin, Madison
Madison, WI 53706

Phone: 608-890-2766 mpeery@wisc.edu <http://forestandwildlifeecology.wisc.edu/facstaff/peery.html>

Zach Peery <mpeery@wisc.edu>

UZurich EvolutionaryTheory

A PhD position to work on evolutionary theory is available at the University of Zürich. The focus of the project is on the evolution of conflict and cooperation, with an emphasis on genetic conflicts in microbes. The project will touch on cooperation and conflict, co-evolution, ecological-evolutionary feedbacks and the levels-of-selection problem. While the main part of the project will focus on social evolution, the research may address other questions in evolutionary and ecology, depending on the background of the student. There will be close collaboration with empiricists and students who wish to test their models with empirical approaches will be encouraged to do so.

Zürich is located less than one hour from the Alps, and is a small but vibrant city that is regarded to have one of the best standards of living in the world. There is a large international community and is well connected to all major European cities.

The successful applicant will be supervised by Dr Daniel Rankin, a theoretical evolutionary biologist interested in a wide range of topics, from social evolution to the link between evolution and ecology (see <http://www.rankin.sk/> for details). The department is very international and consists of a very diverse range of individuals who work on a wide range of interesting evolutionary topics. We also work closely with other ecology/evolutionary groups in Zürich and abroad.

Candidates should have a good background in evolutionary biology, ecology or behavioural ecology, and some experience with modeling. The candidate should have a diploma/MSc degree. The working language of the group is English, and knowledge German is very helpful but not necessary. The position, funded by the Swiss NSF, is available to start immediately and will be for three years. The salary will be in line with University of Zurich policy, which is rather generous.

To apply, please send an e-mail with a cover let-

ter, CV and short (<1 page) statement of research interests and experience in a single pdf file to d.rankin@access.uzh.ch. Please mention PhD position“ in the subject of e-mail. Please additionally give the names and contact details of two or three people willing to write letters of recommendation. For full consideration please send your application by Friday 14th August 2009. Due to the large number of applications, if you are not contacted please consider your application unsuccessful.

Further information: Dr Daniel Rankin

e-mail: d.rankin@access.uzh.ch

Daniel Rankin <d.rankin@bioc.uzh.ch>

UZurich PlantEvolution

Two PhD positions funded by the SNF are available from October 2009 at the Institute of Systematic Botany, University of Zürich, to study pollinator mediated selection in orchids with different pollination systems. The project deals with patterns of selection in natural plant populations on a population-specific basis. Additionally, selection dynamics in different pollination systems will be investigated in an experimental approach. You should have a master degree (or equivalent) in any field of biology/ecology and a thorough interest in evolutionary and pollination biology. Further, enthusiasm for field work with plants and insects is required. The two projects are embedded in a larger framework of evolutionary and systematics research at our institute. We are currently a group of 3 professors and 6 academic staff, as well as several PostDocs, PhDs, and Master students investigating mechanisms and patterns of evolution in plants. The institute is located in the pretty botanical gardens and houses modern molecular and chemical ecology labs, including greenhouses and climate chambers for plant cultivation.

Zürich has a large and very active research community at the University of Zürich (www.unizh.ch <<http://www.unizh.ch/>>) and ETH (www.ethz.ch <<http://www.ethz.ch/>>), dealing with various aspects of organismal and molecular biology (www.lifescience-zurich.ch <<http://www.lifescience-zurich.ch/>>). The city also offers excellent quality of life through active cultural programs and infrastructure, as well as an attractive surrounding including the alps in close proximity.

If you are interested in one of the jobs, please send (preferentially by e-mail) a letter describing your motivation, C.V., copy of degrees, publications (manuscripts) if any, and e-mail addresses of two academic referees. If you have further question, don't hesitate to contact me.

Prof. Florian Schiestl

Institute of Systematic Botany Zollikerstrasse 107 CH-8008 Zürich

florian.schiestl@systbot.uzh.ch

YorkU Bee EvolGenetics

Two graduate positions (at the PhD or MSc level) are available in my laboratory at York University's Department of Biology (Toronto, Canada; <http://www.biol.yorku.ca/grad/>) to study several aspects of the honey bee's sociogenomics and evolutionary genetics, starting September 2009. My lab will embark on a research program to connect functional genomics (to identify the genes, and gene networks affecting honey bee behaviour) with population genetics (to examine the evolutionary processes affecting such networks) in order to understand the HOWs and WHYs of the evolution of social behaviour. Please visit <http://zayedlab.apps01.yorku.ca/wordpress/> for more detailed information on my research interests.

My molecular biology laboratory and research apiary will provide students with a rich and diverse training experience. The successful candidates will be exposed

to an integrative and exciting environment at the intersection of population genetics (quantifying genetic diversity across the honey bee genome, querying the genome for evidence of selection), quantitative genetics (quantitative trait loci [QTL] mapping, estimating the genetic architecture of behavioural traits), genomics (measuring global gene expression and protein levels), and bioinformatics, in addition to learning about bee behaviour and natural history. Further, York University is the third largest university in Canada, and the Department of Biology is home to a large and diverse group of researchers, and Toronto is a great city to live and work.

If you are interested in joining my laboratory, please email me (zayed@yorku.ca) a copy of your CV/resume along with a statement of your research interests. Interested candidates must meet the Department of Biology's admission requirements (<http://www.biol.yorku.ca/grad/admit.htm>), and have previous undergraduate or graduate training in at least one of the following fields: molecular biology / genetics, animal behaviour, evolutionary biology, mathematics / statistics, and computer science. Students with non-biology backgrounds (e.g. computer science, mathematics, physics, etc.) are welcome. Canadian or international candidates with a graduate scholarship will receive a top-up to their funds.

Sincerely, Amro

Dr. Amro Zayed Assistant Professor Department of Biology York University 4700 Keele Street Toronto, ON M3J 1P3, Canada Tel.: 416-736-2100 Ext. 20213 Email: zayed@yorku.ca Web: <http://zayedlab.apps01.yorku.ca/wordpress/>

azayed@life.uiuc.edu azayed@life.uiuc.edu

Jobs

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CaliforniaStateU EvolutionaryBiologist

Assistant Professorships CSUN

California State University, Northridge invites applications for three tenure-track positions in the Department of Biology, starting August 2010. Applicants must have a Ph.D. and post-doctoral experience. Each successful candidate shall develop a vigorous research program involving undergraduate and M.S. students, seek extramural research funding, and demonstrate teaching excellence.

Microbiologist: Focusing on prokaryotic biology relating to any aspect of the health sciences. Teaching options include Medical Microbiology, Principles of Microbiology, a specialty course, and Introductory Biology.

Evolutionary Biologist: Explaining patterns or processes of diversification among species or populations. Teaching options include a course on the diversity of a group of terrestrial organisms, Molecular Systematic, Evolution, and Introductory Biology.

Molecular Geneticist: Emphasizing genomic or proteomic approaches to problems in eukaryotic genetics. Teaching options include Molecular Genetics, Genetics, Introductory Biology, and a specialized graduate course.

Applicants should submit a cover letter to the respective search committee, including a curriculum vitae, a summary of teaching experiences, statements of research interests and teaching philosophy, and three publications. Applicants should arrange to have three letters of recommendation sent: biology.dept@csun.edu or Department of Biology, California State University, 18111 Nordhoff Street, Northridge, CA 91330-8303. Screening shall begin on October 1, 2009.

Linda Gharakhanian <lgar@csun.edu>

DukeU ResTech PlantEvolution

Research Technician in ecological and evolutionary genetics Professor Mark Rausher Duke University

I am seeking a full time technician to assist in laboratory, greenhouse, and field research on projects related to flower color adaptation, and speciation in the Texas wildflower *Phlox drummondii*. This position is available for up to two and a half years, with half the time each year spent at Duke University in Durham, NC performing lab and greenhouse research, and half the time assisting with field work in the area around Austin, TX. A minimum commitment of one year is expected.

This project involves identifying the genetic basis of flower color adaptations and measuring selection on flower color variation in a natural field setting. A successful candidate will also have an opportunity to pursue an independent project in this system.

Ideally, applicants should have a BA in biology or related field, prior independent research experience, an understanding of the fields of genetics and evolution, independence, motivation, and the ability to work well in a research team. In addition, experience working with molecular techniques in the lab, working with plants, and a willingness to spend long, hot days in the Texas sun are desirable.

To Apply: Please email a CV, a cover letter describing your qualifications and interests, and the names and contact information for three references to mrausher@duke.edu. If you have any questions or would like clarification please feel free to contact before applying.

Review of applications will begin August 14th and continue until a successful candidate is found.

Mark D. Rausher Phone: 919-684-2295 Department of Biology Fax: 919-660-7293 Box 90338 Lab Website: <http://www.duke.edu/~mrausher/labpage.htm> Duke University Durham, NC 27708

mrausher@duke.edu mrausher@duke.edu

ETH Zurich Bioinformatics

EPHE Paris MolPopGenetics

Job : Assistant-professor in molecular population genetics (in French : 'maître de conference', a tenure position)

Institution : EPHE, Paris, France. (Ecole Pratique des Hautes Etudes) Research department : 'Origin, Structure and Evolution of Biodiversity' (OSEB) Campus: Jardin des Plantes, in the center of Paris

The population genetics group includes Michel Veuille (Drosophila and Drosophilids) (<http://www.mnhn.fr/-oseb/VEUILLE-Michel>) and Thierry Wirth (Bacteria and other pathogens)

This announcement is for 2010, but we encourage potential candidates to contact us as soon as possible.

The application will begin in February 2010. The job will start in September 2010. Our research group is active in the molecular population genetics of *Drosophila* (including non-melanogaster drosophilids) and in pathogenic bacteria in Humans. Our research focuses on the molecular detection of natural selection (for both research models). We are also interested in using drosophilids to record the signature of the effect of climate changes in the history of ecosystems, and in using commensal bacteria as an indicator of host population migrations

Qualification : a Ph.D. and a post-doc experience, with a publication record demonstrating excellence in the field. The successful candidate should have a background in theoretical and statistical population genetics. The domain of research includes the detection of selective sweeps and the study of population history (including population dynamics) from sequence data. Teaching is moderate, and will be in population genetics.

Michel Veuille <veuille@mnhn.fr>
<mveuille@ephe.sorbonne.fr> +336 3006 1667 (Cell phone) +331 4079 3327 (office phone)

Michel Veuille <veuille@mnhn.fr>

The Genetic Diversity Center at ETH Zurich (Switzerland) has an opening for a Bioinformatics Scientist. The Genetic Diversity Center (www.gdc.ethz.ch) is a newly established knowledge and technology platform that provides scientific and technical support for all research related to genetic diversity in natural and managed populations of a wide range of organisms. One of the key aims of the GDC is to give research groups at ETH Zurich and their collaborations access to up-to-date methods for genotyping populations and processing large sample sizes, e.g. with next-generation sequencing technologies, SNP genotyping, or gene expression analysis. The new methodologies provide many scientific challenges and place a high demand on processing, storing and interpreting genetic data. We therefore seek an innovative person who will be responsible for providing bioinformatics support for GDC, e.g. to handle the processing and analysis of sequence and other genetic data for the study of natural populations. The GDC provides an excellent opportunity for collaboration across a wide cross-section of interests and organisms. In this role, he/she will also be involved in data interpretation and joint publication of the results. The ideal candidate will have a PhD in bioinformatics or related field, or be a biologist with a strong background in informatics, bioinformatic programming/scripting skills, experience with next generation sequence analysis (454, SOLID, Solexa) and a strong interest in the biological questions asked by the users. He/she is motivated to work in a team and enjoys supporting the users of the Genetic Diversity Center in their research projects. The position is initially limited to 2 years and is available starting October 2009. The working language of GDC and the user laboratories is English. Screening of applications will start 10 August 2009 and continue until the post is filled. For more information, contact Dr. Aria Minder (aria.minder@env.ethz.ch) or Prof. Paul Schmid-Hempel (psh@env.ethz.ch). Please apply online: www.jobs.ethz.ch Aria Minder <aria.minder@env.ethz.ch>

**LouisianaStateU LabTech
SalixPhylogeography**

Research Associate 2 Department of Biological Sciences

The Research Associate 2 position is in the lab of Bryan Carstens at Louisiana State University. The ideal candidate will be a recent graduate (B.S. or M.S.) who is planning on continuing with graduate school, but whom would like to take a year off before they start a Ph. D. program. The Carstens' lab currently includes a number of researchers (undergraduate, graduate, post-doctoral) who investigate a broad range of empirical and methodological questions. The technician will have ample opportunity to assist with the analysis of the molecular sequence data and will be included on publications. Required Qualifications: Bachelor's degree or equivalent degree in a biological science or related field; experience with PCR and DNA sequencing, as well other molecular biology techniques. Responsibilities: creates a genomic library; performs PCR and sequencing of multiple genes from western /Salix/ for a phylogeography project. An offer of employment is contingent on a satisfactory pre-employment background check. Application deadline is July 17, 2009 or until a candidate is selected. Apply online at: www.lsusystemcareers.lsu.edu. Position #024178.

LSU SYSTEM IS AN EQUAL OPPORTUNITY/EQUAL ACCESS EMPLOYER Quick link to ad URL: <https://lsusystemcareers.lsu.edu/applicants/-Central?quickFind=50991> Please direct questions to Bryan Carstens: carstens@lsu.edu

<http://www.lsu.edu/faculty/carstens/> Bryan C. Carstens Assistant Professor Department of Biological Sciences Louisiana State University

mail 202 Life Sciences Building Louisiana State University Baton Rouge, LA 70803 USA

e-mail carstens@lsu.edu bryan.c.carstens@gmail.com

web <http://www.lsu.edu/faculty/carstens/> office A114 Life Sciences Annex (225) 578-0960

lab A153 Life Sciences Annex (225) 578-4918

"Bryan C. Carstens" <carstens@lsu.edu>

**Lusignan INRA France
GrassEvolution**

Potential position in Lusignan in France at INRA

We propose a position during 4 years

The candidate must be a senior researcher in a permanent position or not.

The candidate will define his own topic on genetic and morphologic olution of grassland.

The candidate will supervise a Phd and a post doc from second year of the position.

Net salary ~ 3200 euros per month

The person who is interested with this proposition should send an e-mail with CV to isabelle.litrico@lusignan.inra.fr before the end of July 2009.

Thank you, Best regards, Isabelle Litrico

Isabelle LITRICO INRA - Centre Poitou-Charentes Unité de Recherche Pluridisciplinaire Prairies et Plantes Fourragères Route de Saintes 86600 Lusignan BP 6

Tel :00 33 (0)5 49 55 61 48 Fax : 00 33 (0)5 49 55 60 44 e-mail : isabelle.litrico@lusignan.inra.fr

Isabelle Litrico <isabelle.litrico@lusignan.inra.fr>

Lyon Bioinformatician

All the information is available at www.prabi.fr under the Jobs section

Job Vacancy at the INCa-Synergie Bioinformatics Facility for Cancer Genomics, Lyon France

Experienced bioinformatician specialized in biological databases

1-PROGRAMME

1.1- Background Recognizing the new opportunities offered by next generation sequencing technologies in the field of cancer genomics, the French National Cancer Institute (INCa) has pledged to provide a major contri-

bution to the International Cancer Genome Consortium (ICGC- <http://www.icgc.org/>) through the study of two cancer types (hepatocellular carcinoma and HER2 amplified breast tumors). In the near future, INCa is considering contributing more tumor types. The entire sequencing of multiple pairs of tumor and matched germline DNAs has already been completed in France and other pairs are rapidly following. In order to overcome the challenges raised by the massive amount of sequence data that has been and will be generated by such programs, INCa and the Lyon community through the Synergie Lyon Cancer Foundation (<http://www.synergielyoncancer.com/>) are joining efforts to create a dedicated bioinformatics facility. The objective of the bioinformatics facility will be to empower the biomedical teams working in the field of cancer to best exploit the data generated through large scale genomic projects, notably those funded by INCa and in the first place those taking place within the ICGC.

1.2 Context The INCa-Synergie facility is located in a major French comprehensive cancer center (Centre Leon Berard) with a very active research department (http://oncora1.lyon.fnclcc.fr/english_version/index_eng.html). It is in close proximity to the International Agency for Research on Cancer, IARC. The facility is integrated into the "Pole Rhone-Alpes de Bioinformatique, PRABI (<http://www.prabi.fr/>), which federates major bioinformatic teams. Thus the facility benefits both from strong biomedical and bioinformatics environments. It is acquiring a large HPC equipment. The facility will open over the coming months four positions for experienced bioinformaticians who will work under the supervision of the facility director, Pr. Gilles Thomas. This job description corresponds to one of these positions.

1.3 Description of duties Working in a team of experienced bioinformaticians and in close collaboration with French partner groups and international research centers, the candidate will : be in charge of the design, development, implementation and maintenance of a high performance storage database enabling the integration of very large volumes of heterogeneous genomic data using different technologies (row storage, column storage, xml, key-value) while respecting accepted standards. This database, interconnected and in communication with the major genomic databases of the scientific community, will be the core of a platform dedicated to data mining for both local and distant research teams. In addition, the database will offer interfaces (API) which will permit the development of innovative analytic tools. be a major player in providing the organization and implementing the procedures to develop the facility in accordance with the ISO 9001:2000 stan-

dard. develop tools such as ETL (Extract-Transform-Load) in order to import or export data in an automatic or semi-automatic manner. continually evaluate, in the context of the platform, new technologies which may be of interest in the scientific field. bring her/his expertise in managing data to specific requests from the collaborating research teams.

2- REQUIRED QUALIFICATION

2.1 Education: Advanced university degree (Masters, PhD) in bioinformatics.

2.2 Skills design and development of databases for the management and analysis of large heterogeneous data sets. modeling schemes for databases (relational databases, entity-association models, UML,) and associated programs. implementation and optimization of relational database management systems (Oracle, Postgres, MySQL,). knowledge of the major genomic databases and their interfaces. knowledge of querying languages such as SQL. major script, programming and markup languages (shell, awk, perl, python, php, ruby, ajax, javascript, java, c, c++, XML).

2.3 Professional experience At least two years of relevant professional experience at the international level in the field of bioinformatics and/or data base management is required. Prior experience in quality assurance procedures will be highly appreciated.

2.4 Complementary information: Communication in French is not required but advanced English language, excellent communication and interpersonal skills are essential. The candidate should be

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

Lyon StatisticalGenomicist

All the information is available at www.prabi.fr under the Jobs section

Job Vacancy at the INCa-Synergie Bioinformatics Facility for Cancer Genomics, Lyon, France.

Experienced genomicist with statistical expertise

1-PROGRAMME

1.1- Background Recognizing the new opportunities of-

ferred by next generation sequencing technologies in the field of cancer genomics, the French National Cancer Institute (INCa) has pledged to provide a major contribution to the International Cancer Genome Consortium (ICGC- <http://www.icgc.org/>) through the study of two cancer types (hepatocellular carcinoma and HER2 amplified breast tumors). In the near future, INCa is considering contributing more tumor types. The entire sequencing of multiple pairs of tumor and matched germline DNAs has already been completed in France and other pairs are rapidly following. In order to overcome the challenges raised by the massive amount of sequence data that has been and will be generated by such programs, INCa and the Lyon community through the Synergie Lyon Cancer Foundation (<http://www.synergielyoncancer.com/>) are joining efforts to create a dedicated bioinformatics facility. The objective of the bioinformatics facility will be to empower the biomedical teams working in the field of cancer to best exploit the data generated through large scale genomic projects, notably those funded by INCa and in the first place those taking place within the ICGC.

1.2 Context The INCa-Synergie facility is located in a major French comprehensive cancer center (Centre Leon Berard) with a very active research department (http://oncora1.lyon.fnclcc.fr/english_version/index_eng.html). It is in close proximity to the International Agency for Research on Cancer, IARC. The facility is integrated into the "Pole Rhone-Alpes de Bioinformatique, PRABI (<http://www.prabi.fr/>), which federates major bioinformatic teams. Thus the facility benefits both from strong biomedical and bioinformatics environments. It is acquiring a large HPC equipment. The facility will open over the coming months four positions for experienced bioinformaticians who will work under the supervision of the facility director, Pr. Gilles Thomas. This job description corresponds to one of these positions.

1.3 Description of duties Working in a team of experienced bioinformaticians and in close collaboration with French partner groups and international research centers, the candidate will be in charge of : initiating with investigators trained in mathematics, statistics, informatics and genomics and with the collaborating sequence production teams, methods for the efficient processing and analysis of nucleotide sequences, adapted to the huge volume of data produced by genomic technologies and notably by new high throughput DNA sequencing methods (quality control, identification and analysis of correlations, genome reconstruction and characterization algorithms). developing data mining tools to best characterize the reconstructed genomes and generate biological knowledge. testing and developing these

methods and tools to a level that will allow their implementation in standard analytical packages that can be used by biomedical research teams. gaining expertise in developing and applying quality control procedures in accordance with the ISO 9001:2000 standard. continually evaluating new technology, algorithms and publications relevant to the scientific field. bringing his/her expertise in data mining to specific requests from the collaborating research teams.

2- REQUIRED QUALIFICATION

2.1 Education: Advanced university degree (Masters, PhD) in statistics and informatics.

2.2 Skills statistical modeling. descriptive and inferred statistics. simulation methods, model fitting, optimization. knowledge of the major genomic databases and their interfaces. thorough knowledge of the main computing and statistical packages (R, SAS, Stata, Matlab, Maple, Mathematica,). practical knowledge of scripting (Linux/UNIX) and programming languages (awk, perl/bioperl, python, C, C++, java), of database query (SQL) and markup (XML) languages. basic knowledge of web programming (php, html, ajax/javascript).

2.3 Professional experience At least two years of relevant professional experience at the international level in the field of statistical genomics.

2.4 Complementary information: Communication in French is not required but advanced English language, excellent communication and interpersonal skills are essential. The candidate should be self motivated, capable of working both independently and within a closely interacting team of scientists and be able to deliver a quality product with fixed deadlines.

3- CONTRACT AND SUBMISSION PROCEDURE

3.1 Contract :

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

NewSouthWales FieldAssist Honeyeaters

Field assistant/prospective PhD students to study the evolution of family living and cooperation in honeyeaters in Australia

I am looking for two highly motivated field assistants to join me working on a project investigating the evolution of family living and cooperation in three honeyeater species. Since the project is in its start-up phase, initial work will involve locating suitable study sites, and thereafter birding catching and banding. Responsibilities will include catching and colour-banding birds, establishing group membership and home range use (using a GPS), nest-searching and monitoring, behavioural observations and data entry. The study will take place in New South Wales (Australia).

The working conditions will include considerable distances covered on foot, working outside in both cold and hot conditions, long days and the applicants need to be willing to work out outside normal hours.

The positions are available for 4 months - from the end of September 2009 until end of January 2010. I am particularly interested in assistants that would be interested to continue working on the systems as PhD students. These positions will be open from the beginning of next year (2010) onwards.

Qualifications: 1) MSc (or equivalent) in biology with strong interest in evolution of sociality and cooperation 2) Field experience of behavioural observations/experimental work 3) Bird handling and banding experience 4) Sociable personality and highly motivated 5) Willing to work in field with basic facilities 6) Drivers licence would be a plus.

The project will cover transport to study site, accommodation and food. Assistants will be paid a salary of about 500 per month.

Applications received before 27th July 2009 will be given full consideration.

If you have questions, or are interested, send a motivation letter stating why you are interested and your CV, publication list, two contacts for references and short summary of your current research via email to:

michael.griesser@ekol.slu.se

Michael Griesser Department of Ecology Swedish University of Agricultural Sciences Box 7044 SE-75007 Uppsala Sweden

Tel: +46 (0) 18 67 23 54 Fax +46 (0) 18 67 35 37

michael.griesser@ekol.slu.se;

michael.griesser@gmail.com http://www.ekol.slu.se/-ShowPage.cfm?OrgenhetSida_ID=3D10914

michael.griesser@gmail.com

OhioStateU LabTech PlantEvolution

Lab Technician Position in Evolutionary Ecology of Agricultural Plants Mercer Lab at Ohio State University Applications accepted July 18 V August 2

I am seeking a highly motivated individual to fill a full-time lab technician position (Research Assistant II) in a newly established lab at The Ohio State University in the Department of Horticulture and Crop Science. The successful candidate will work on projects related to the evolutionary ecology of agricultural plants V both weedy and cultivated.

In particular, my lab focuses on the evolutionary impacts of crop-wild hybridization in sunflower as it relates to risk assessment for transgenic crops and the effects of climate change on crop genetic resources, in the US and Mexico. The successful candidate will assist in conducting field, greenhouse, and laboratory research, test the validity of research methods and recommend alterations as needed. S/he will also collect and maintain data and experimental records, prepare data in forms appropriate for statistical analysis and tables or figures in forms appropriate for publication. In addition, s/he will provide general supervision to undergraduate students and hourly student employees in the lab, procure and maintain laboratory equipment and supplies, and may execute molecular genetic analysis using microsatellites and design or update the laboratory website.

The position requires someone with a Bachelors degree in Biology, Ecology, Agronomy, or Plant Science who has experience working with plants in the field or greenhouse. Considerable experience with Microsoft Word and Excel is also required. Desired experience includes familiarity with statistical analysis, ability to design and/or update websites, and experience in molecular genetic analysis.

To apply, submit an on-line application through the Ohio State University job website (<http://-jobs.osu.edu/>). The position will be posted from July 18 V August 2. During that period, you can search for it on the website using requisition number 346091. In addition to the standard application form, please include a cover letter indicating why you are interested in the position, as well as a resume or CV. Contact Kristin Mercer (mercner.97@osu.edu or 614-247-6394) with any questions. Salary will depend on experience and range

from \$11.55-\$13.03/hr. Position to start as soon as possible. This is a full-time, regular position with benefits.

Kristin Mercer Assistant Professor Ohio State University Department of Horticulture and Crop Science Columbus, Ohio 43210 (614) 247-6394 mercer.97@osu.edu

KRISTIN MERCER <mercer.97@osu.edu>

RegensburgU Germany PlantEvolSyst

Open Ph.D. position in plant systematics and evolution at the Institute of Botany of the University of Regensburg (Germany)

Position description: A 3-years Ph.D. position funded by the German Science Foundation (DFG) is presently available in the area of plant systematics and evolution at the Intitute of Botany of the University of Regensburg, under the supervision of Prof. Dr. Christoph Oberprieler (<http://www.biologie.uni-regensburg.de/-Botanik/Oberprieler/index.html>) and in co-operation with Dr. Robert Vogt (Botanic Garden & Botanical Museum Berlin-Dahlem). The salary will be according the TV-L E13/2. The Ph.D. project will focus on the evolution of polyploidy in the genus *Leucanthemum* (Compositae, Anthemideae) and will use this genus of around 40 species distributed in southern and central Europe as a model to investigate the genetic, genomic, biogeographical and ecological consequences of polyploidy. Work packages envisaged will comprise (a) the reconstruction of the phylogeny of the genus based on nrDNA and cpDNA marker sequences, (b) the modelling of eco-climatological niches of species using GIS techniques, (c) the phylogeography of species groups of this genus, and (d) expression studies of genes of salt tolerance in diploid and polyploid members. The project will include extensive travelling throughout S Europe to collect plant material in natural populations.

Deadline for application: August 15, 2009. If needed, the position will remain open until a suitable candidate is found.

Starting date: between September 1, 2009 and January 1, 2010.

Requirements: Applicants are expected to have their Masters/Diploma degree by the start of the Ph.D. project. Good knowledge of English and German are highly desirable. The ideal candidate will have doc-

umented experience in one or more of the following areas: molecular biology, expression techniques, phylogeny reconstruction, population genetics, GIS techniques, botanical field work (including the possession of a driver's licence). The selected candidate will be a member of the Regensburg International Graduate School of Biological Sciences (RIGeL; <http://www.biologie.uni-regensburg.de/RIGeL/index.html>).

How to apply: Please send you application including (a) an application letter addressing your motives for application and your career goals, (b) a detailed CV including a detailed list of molecular, analytical, linguistic, and field work skills, presentations at scientific meetings, and publications (if applicable), and (c) addresses of two academic advisors who could comment on your skills, your dedication to science, and your ability to work cooperatively in a team. Please, send applications by email to:

Prof. Dr. Christoph Oberprieler Institut für Botanik Universität Regensburg Universitätsstr. 31 D-93053 Regensburg Germany phone +49-(0)941-9433129 fax +49-(0)941-9433106 christoph.oberprieler@biologie.uni-regensburg.de

Rostock Postdoc Gradstud Evolution of aging

The newly established Independent Research Group Modeling the Evolution of Aging at the MPIDR in Rostock, Germany, is seeking to make appointments at the PhD, Post-Doc, and Research Scientist levels. Starting date as soon as feasible but preferably not later than 01.04.2010

The patterns of life are stunningly diverse, and so are the patterns of aging. Our group on "Modeling the Evolution of Aging" aims to discover the unifying principles and patterns underlying this diversity. We will ask why evolution favored a certain path of aging in a certain species. In particular, we will ask why some species age fast while others age slowly or even seem to escape aging all together. Can we understand aging across animals, plants, fungi and bacteria to a degree that allows us to identify the factors responsible for whether aging is fast, slow, or even reversed? We will develop generic models that capture aging for certain groups of species such as mammals, reptiles, or trees.

Our plan will be the following: 1. Conceptualize/define

“aging” as well as “fast aging”, “slow aging”, “no-aging” in a comparative framework across animals, plants, fungi and bacteria. 2. Discover what species follow what aging patterns. To get a broad view on patterns across species, we will rely on good life table data and textbook knowledge on the phylogeny, physiology and ecology of the various species. To get an in-depth view we will collaborate with experts around the world who can provide us with empirical evidence and expert knowledge on particular species. 3. Running our creative minds, juggling available data and knowledge on the various species thinking outside of conventional boxes we then identify key variables that seem to give us a reasonable species grouping. 4. Based on these key variables, we will develop generic models for these groups. If a model becomes too clumsy with all the key variables included, we will develop several simple models to shed light on different aspects of aging in a single group. 5. What is the evolutionary successful strategy of aging in the various models? Can we develop a general algorithm that solves the various models?

Our team will consist of people with a burning interest in theoretical modeling, a strong preference for revealing and understanding general mechanisms and unifying principles, and a strong interest in studying population dynamics in an interdisciplinary group. Our collective expertise should ideally cover skills and knowledge in theoretical modeling, evolutionary biology, life history biology, comparative biology (with a main focus on basic physiological, phylogenetic and ecological characteristics across the tree of life), demography, ecology, mathematics, dynamic optimization, programming, statistics, non-linear dynamics, complex adaptive systems and principles of self-organization. Our project is likely to cut across all the life sciences.

The group will be established by Dr. Annette Baudisch. The group will be part of the MPIDR in Rostock, a bike-ride away from the Baltic Sea. The institute is very international, with a warm and collegial working atmosphere hosting a diverse range of labs with interdisciplinary topics. The working language of all groups including ours is English.

Applications should include a CV with relevant experience, educational degrees, a list of any publications and the contact details of 3 references. A description of your research interest and why you would enjoy becoming a member of our team would be very helpful. All material should be e-mailed to: appl-irgmea@demogr.mpg.de, preferably in a single pdf file. Applications will be considered and positions will be filled on a rolling basis.

PhD and Post-Doc appointments are made on doctoral and postdoctoral stipends, respectively. Research sci-

entists will be employed up to salary level 14 on the basis of the German TVöD system according to the qualification of the candidate and in accordance with the rules of federal employees in Germany.

The Max Planck Society wishes to increase the share of women in areas where they are underrepresented, and strongly encourages women to apply. The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply.

“Baudisch, Annette” <Baudisch@demogr.mpg.de>

Sapphire Energy

*Sapphire Energy is looking for a Geneticist to work in the Evolution Engineering team.

Job Description: Sapphire Energy is a venture capital backed company developing next generation biofuels based on recent advances in metabolic engineering. The company’s focus is the commercialization of high performance, low cost, and low carbon footprint biofuels that are direct replacements for conventional gasoline, diesel, and jet fuel.

We are seeking an exceptional Scientist to join our Molecular Biology staff in San Diego, CA.

Requirements - Advanced degree in Microbiology, Genetics, Biology, Molecular Biology or a related discipline, and 3 or more years of industrial (or equivalent postdoctoral) experience. - Highly motivated, innovative researcher capable of critical thinking and problem solving

- Demonstrated ability to independently design, execute, troubleshoot and interpret experiments - Management experience and leadership skills. - Creativity and the ability to work in an interdisciplinary team in order to achieve technical and business milestones. -Due to the highly collaborative nature of this position, interpersonal and communications skills will be extremely important. - Proficiency in writing and oral presentations.

Responsibilities include, but are not limited to: - Microbial genetics and directed evolution. Design of selection experiments, genetic screens. Methods development to drive such projects as necessary. - PCR, cloning, and sequence analysis. - Develop assays and criteria for characterization for microbiology and molecular biology teams. * Provide example of professionalism and

proficiency for the laboratory staff

Sapphire offers very competitive compensation packages including bonuses and equity, as well as full benefit packages, which include health, dental, vision insurance, 401k, and paid time off. To apply, please send your CV and cover letter to human.resources@sapphireenergy.com.

Thanks, Kimberly

Kimberly Daniels I Manager, Human Resources Sapphire Energy 3115 Merryfield Row I San Diego I CA I 92121 Office 858-768-4703 I Mobile 619-379-1176 I Fax 858-408-3018 kimberly.daniels@sapphireenergy.com

cute, troubleshoot and interpret experiments * Provide example of professionalism and proficiency for the laboratory staff

Sapphire offers very competitive compensation packages including bonuses and equity, as well as full benefit packages, which include health, dental, vision insurance, 401k, and paid time off. To apply, please send your CV and cover letter to human.resources@sapphireenergy.com.

Kimberly Daniels I Manager, Human Resources Sapphire Energy 3115 Merryfield Row I San Diego I CA I 92121 Office 858-768-4703 I Mobile 619-379-1176 I Fax 858-408-3018 kimberly.daniels@sapphireenergy.com

Sapphire Energy 2

Sapphire Energy is a venture capital backed company developing next generation biofuels based on recent advances in metabolic engineering. The company's focus is the commercialization of high performance, low cost, and low carbon footprint biofuels that are direct replacements for conventional gasoline, diesel, and jet fuel.

Requirements - Experience in phage biology is essential: Culturing, titering, assessing growth characteristics (attachment, latent period, burst size). - Preference given to candidates with the following experience: o Experimental evolution of phage/bacteria interactions, or in other predator/prey model systems o Investigation and understanding of new model systems for predator/prey interactions. o Genetics and molecular genetics of phage/bacteria interactions, or in other predator/prey model systems - Strong leadership skills. - Ability to participate in interdisciplinary teams. - Strong interpersonal and communications skills will be extremely important. - Proficiency in writing and oral presentations.

Responsibilities include, but are not limited to: - Microbiology and characterization of predator/prey interactions. - PCR, cloning, sequence analysis, and vector design desirable. - Design and execute experiments. - Develop assays and criteria for characterization for predator/prey interactions. - Creativity and the ability to work within a team to in order to achieve technical and business milestones are required. - Highly motivated, innovative researcher capable of critical thinking and problem solving

- Demonstrated ability to independently design, exe-

SwanseaU ResTech SalmonGenetics

Research Technician in Genetic Stock Identification of Atlantic Salmon

An EU-funded (SALSEA-MERGE) Research Technician position is available for 20 months starting on September 2009 at the Department of Pure & Applied Ecology (Swansea University; <http://www.swan.ac.uk/biosci/> < <http://www.swan.ac.uk/biosci/> >) in collaboration with the Institute of Biological, Environmental and Rural Sciences (Aberystwyth University; <http://www.aber.ac.uk/biology/> < <http://www.aber.ac.uk/biology/> >).

SALSEA-MERGE combines genetic and ecological investigations to infer the migration and distribution of Atlantic salmon at sea, and seeks to understand the reasons for the high marine mortality and widespread decline of Atlantic salmon across its range (<http://www.nasco.int/sas/salseamerge.htm>).

The successful candidate will be based at IBERS Aberystwyth and will work on the development of a genetic database to support the identification of the region and river of origin of Atlantic salmon captured at sea. The work will involve microsatellite typing, as well as the development of a suite of SNP markers for mitochondrial DNA in collaboration with partners at the FRS Freshwater Laboratory (Pitlochry, Scotland).

Required qualifications: - A first class or upper second BSc in Biological Sciences or related topic - Research experience on the above mentioned topics

Desirable qualifications

- A PhD in population genetics, molecular ecology or

related topic

- Consideration will also be given to previous research experience on salmonids and publication record

Salary will be in the range £20,226 to £ 22,126 per annum, depending on experience and qualifications.

Informal enquiries can be directed to Dr. Carlos Garcia de Leaniz c.garciadeleaniz@swansea.ac.uk <<mailto:c.garciadeleaniz@swansea.ac.uk>>

<http://www.swan.ac.uk/staff/academic/-EnvironmentSociety/BiologicalSciences/-deLeanizcarlosgarcia/> < <http://www.swan.ac.uk/staff/academic/EnvironmentSociety/-BiologicalSciences/deLeanizcarlosgarcia/> >

or Dr. Sonia Consuegra skc@aber.ac.uk

http://www.aber.ac.uk/biology/dept/-sonia_consuegra.html < http://www.aber.ac.uk/biology/dept/sonia_consuegra.html >

Applicants should send a covering letter summarizing their research background and interests, a recent CV, and contact details of two referees. An application form and further details may be obtained from the Personnel Department, Swansea University, Singleton Park, Swansea, SA2 8PP, tel. (01792) 295136 (24 hours) or at <http://www.swan.ac.uk/personnel/Vacancies/> . < <http://www.swan.ac.uk/personnel/Vacancies/.%20> >

The closing date for applications is Thursday 23rd July 2009. Interviews are expected to be carried out on the first week of August 2009

Dr. Carlos Garcia de Leaniz Swansea University Biological Sciences Singleton Park, SA2 8PP Swansea, UK Tel. +44 (0) 1792 295383 Fax. +44 (0) 1792 295447 email. c.garciadeleaniz@swansea.ac.uk <<mailto:c.garciadeleaniz@swansea.ac.uk>>

“GarciaDeLeaniz C.” <C.GarciaDeLeaniz@swansea.ac.uk>

UArizona MouseMaleFertility

Postdoctoral Researcher, University of Arizona

A Postdoctoral Researcher position is available in the laboratory of Dr. Michael Nachman in the Department of Ecology and Evolutionary Biology at The University of Arizona. The position involves studying the evolutionary genetics of male fertility in house mice. The successful candidate will have a background in molecular biology, evolution, and population genetics, includ-

ing both data collection and analytical aspects. Responsibilities include studying fertility of wild caught house mice and identifying candidate genes that may affect mouse fertility.

Michael Nachman and the members of his lab study population, evolutionary, and ecological genetics and genomics. Most work is on mammals with particular emphasis on mice and humans. Research is focused on understanding the forces that shape genetic variation in natural populations, identifying genes that underlie fitness-related traits, and understanding the genetic basis of speciation. Details of the research can be found at <http://www.eebweb.arizona.edu/faculty/-nachman/index.htm> . Qualifications: Ph.D in biology or a related field with an exceptional background in evolutionary genetics. Knowledge of genomics, bioinformatics, and molecular biological techniques preferred. To apply, please send a letter describing your interests and qualifications, a CV, and contact information for three references to: Dr. Michael Nachman (nachman@u.arizona.edu). The University of Arizona is an Affirmative Action / Equal Opportunity Employer.

genomics@email.arizona.edu

genomics@email.arizona.edu

genomics@email.arizona.edu

UCaliforniaDavis MicrobialBioinformatics

A bioinformatics engineer position is available on a microbial metagenomics project called iSEEM (<http://openwetware.org/wiki/ISEEM>) under the direction of

Jonathan A. Eisen (UC Davis) http://128.120.136.15/mediawiki/index.php/Main_Page Jessica L. Green

(U Oregon) <http://biology.uoregon.edu/people/green/>

Katherine S. Pollard (Gladstone Institutes at UC San Francisco) <http://docpollard.com> The engineer will

work in an interdisciplinary research group of evolutionary biologists, ecologists, and statisticians. Applicants should have substantial experience with genome-scale bioinformatics, including comparative genomics, analysis of protein families, multiple sequence alignment, and phylogenetic analyses. Familiarity with SQL, Perl/Python, and standard bioinformatics tools are essential. Typical responsibilities for this position may include designing and managing an in-house MySQL database of metagenomic sequence data; running BLAST, HMMER, and AMPHORA on the Global Ocean Survey and other large metagenomic data sets;

identifying OTUs (operational taxonomic units) based on 16S rRNA or proteins; writing Perl scripts to query databases, process data, or run simulations; distributing data, scripts, and information to project members on all three campuses. Strong project management skills are essential.

We will offer a generous salary and benefits commensurate with experience. The position is available immediately, and the initial appointment will be for one year. The engineer would ideally be located at UC Davis, although other arrangements will be considered.

TO APPLY: Applications should be submitted at

http://jobs.genomecenter.ucdavis.edu/-start_app.php?job_idx and consist of (1) a cover letter describing your interest in the position, (2) the names and contact information for three references, (3) a curriculum vita (including publications). Applications will be reviewed upon receipt, until the position is filled.

jlgreen@uoregon.edu jlgreen@uoregon.edu

a probationary period of five years, with appointment to the retiring age thereafter.

Further particulars and an application form may be obtained from <http://www.gen.cam.ac.uk>, or from the Secretary of the Department, University of Cambridge, Department of Genetics, Downing Street, Cambridge CB2 3EH (E-mail: t.oakley@gen.cam.ac.uk; telephone 01223 333987, fax 01223 333992). Applications should be sent to this address to arrive no later than 28 August 2009 and should include a completed form PD18, a curriculum vitae, a list of publications, and a brief statement of research interests and future plans (no more than two pages). Informal enquiries may be made to the head of department Dr David Summers (Email: dks11@cam.ac.uk).

Closing date: 28 August 2009. Planned Interview dates: Early October 2009.

I am also happy to answer informal questions about this job (Frank Jiggins fmj1001@cam.ac.uk)

fmj1001@cam.ac.uk fmj1001@cam.ac.uk

UCambridge PopGenetics

University Lecturer Quantitative, population or evolutionary genetics Department of Genetics, University of Cambridge

Vacancy Reference No: PC05464 Salary: £36,532-£46,278

Applications are invited for a University Lectureship in the Department of Genetics, from scientists who have demonstrated the potential to become leaders in their field of research. The Department particularly wishes to attract candidates within the areas of quantitative, population or evolutionary genetics. The successful candidate will interact with existing members of the Department in both research and teaching. In addition, the research environment of Cambridge offers opportunities to establish collaborative links with members of other biological science Departments, Faculties (including Mathematics and Medicine) and nearby institutes such as the European Bioinformatics Institute and the Sanger Centre. As a University Lecturer you will be expected to play a full role in the teaching and research activities of the Department, including the training of post-graduate students and post-doctoral Fellows, and undergraduate teaching in the Faculty of Biology. Appointments made at University Lecturer level will be for

UCambridge ResAssist EvolBiol

Research Assistant: Animal coloration, behaviour, and bird vision Department of Zoology, University of Cambridge, UK Salary: £23,449-£26,391 Duration: Up to 5 years Closing date: 3 August 2009 This position is available from 1 October 2009 for a Research Assistant to work with Dr Martin Stevens and other members of the behavioural ecology group. The project will investigate how animal visual signals work, and how they relate to the viewing animal's visual perception. The work will study the types of visual signals associated with preventing predation and with avian brood parasitism. The successful candidate will be expected to divide their time between fieldwork in the UK and abroad, and studies based in the Department of Zoology at Cambridge. For further information and how to apply, please see: <http://www.admin.cam.ac.uk/offices/hr/jobs/vacancies.cgi?job=5414> Dr Martin Stevens Research Fellow, Girton College, Cambridge. Address: Department of Zoology, University of Cambridge, Downing Street, Cambridge. CB2 3EJ. 01223 331759 ms726@cam.ac.uk <http://www.zoo.cam.ac.uk/zoostaff/bbe/Stevens/Martin1.htm> "M. Stevens" <ms726@cam.ac.uk>

UColorado LabTech GeneticPaternityAnalyses

Laboratory Technician Department of Ecology and Evolutionary Biology University of Colorado Boulder, Colorado

The lab of Dr. Rebecca Safran at the University of Colorado is looking for a technician to conduct and analyze genetic paternity analyses. Responsibilities and Duties: Extract and analyze DNA (microsatellites), edit data (maintaining database), ensure lab supplies are on hand, maintain lab equipment, train other laboratory users. Qualifications: BS required, familiar with lab procedures for DNA extraction, PCR amplification (microsatellites), and paternity analyses using ABI Genemapper and related software programs.

Interested applicants should send a cover letter detailing their experience and interests and a CV in pdf or .doc along with the names and contact information of 3 references to Rebecca Safran at Rebecca.Safran@colorado.edu <<mailto:Rebecca.Safran@colorado.edu>>.

Subject line MUST include reference to Lab Technician Position.

The position will remain open until filled but ideally will start in September 2009.

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>

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>

UdelosAndes ComparativeBotany

UNIVERSIDAD DE LOS ANDES

Botánico(a) / Fisiólogo(a) Vegetal

El Departamento de Ciencias Biológicas de la Universidad de los Andes (Bogotá, Colombia) requiere profesor/investigador de planta de tiempo completo en Botánica a nivel de Profesor Asistente o Asociado. Los aspirantes deben poseer título de Ph.D., preferiblemente con experiencia posdoctoral y disposición a proponer y gestionar proyectos de investigación en el campo de la botánica. Son especialmente bienvenidos candidatos con experiencia previa en morfofisiología y/o ecofisiología comparada de plantas tropicales en un contexto evolutivo.

Se espera del candidato seleccionado que interactúe como profesor y orientador de estudiantes de pregrado y posgrado del Departamento de Ciencias Biológicas, dictando cursos básicos y avanzados en Botánica y Fisiología Vegetal.

La Universidad de los Andes se encuentra dentro de las mejores universidades de Latinoamérica. Su Departamento de Ciencias Biológicas alberga 26 profesores de tiempo completo quienes lideran progra-

mas de investigación de la más alta calidad en evolución, ecología, genética, microbiología, botánica y zoología. Para mayor información visitar: <http://cienciasbiologicas.uniandes.edu.co> Candidatos interesados, favor enviar hoja de vida, copia de publicaciones, una breve descripción del programa de investigación y docencia, y dos cartas de recomendación antes del 15 de octubre de 2009 a la siguiente dirección. Aplicaciones por medio electrónico son bienvenidas.

Comité de Contrataciones Profesorales Departamento de Ciencias Biológicas Universidad de Los Andes Carrera 1 No. 18A-10 Apartado Aéreo 4976 Bogotá, Colombia ccontbio@uniandes.edu.co

UNIVERSIDAD DE LOS ANDES

Botanist/Plant Physiologist

The Department of Biological Sciences, Universidad de los Andes (Bogota, Colombia) seeks to fill a full time position in Botany at the Assistant or Associate Professor level. The applicant must possess a Ph.D., preferably with postdoctoral experience, and disposition to propose and manage research projects in the field of botany. Applicants with research experience in comparative morphophysiology and/or ecophysiology of tropical plants in an evolutionary context are especially welcome.

The chosen candidate will be expected to advise undergraduate and graduate students in the Department of Biological Sciences, and teach basic and advanced courses in Botany and Plant Physiology.

The Universidad de los Andes is among the most renowned universities in Latin America. The Biological Sciences department hosts 26 full-time professors with internationally recognized research programs in evolution, ecology, genetics, microbiology, botany and zoology. For more information visit: <http://cienciasbiologicas.uniandes.edu.co> Interested candidates should send curriculum vitae, copies of recent publications, a brief description of research and teaching program, and two letters of recommendation before October 15, 2009 to the following address. Electronic submissions are preferred.

Faculty Search Committee Departamento de Ciencias Biológicas Universidad de Los Andes Carrera 1 No. 18A-10 P.O. Box 4976 Bogota, Colombia ccontbio@uniandes.edu.co

Santiago Madriñán
<samadrin@uniandes.edu.co>

Restrepo

UFlorida ResTech SexualSelection

Research Technician in Evolution, Ecology, and Behavior Dr. Christine W. Miller University of Florida

I am seeking a motivated individual to work as a full-time research technician. The successful candidate will conduct laboratory, greenhouse, and field research on projects related to animal behavior and evolution. Other important responsibilities will be the supervision of undergraduate research assistants and maintaining an orderly laboratory. Opportunities will exist to contribute to experimental design, analysis, and the co-authoring of manuscripts.

Research in my lab explores the expression and evolution of sexually-selected traits and behaviors. In particular I am interested in how natural environmental variation affects the elaborate ornaments and weapons of sexual selection as well as mate preferences and mate choice. Research includes field studies, insect breeding in a greenhouse setting, behavioral observations, and morphometric analysis. My primary research organisms are the leaf-footed bugs, Family Coreidae (Hemiptera).

Minimal Qualifications: A bachelors degree in biology or a related field, prior research experience, the ability to work well with others in a supervisory role, and a good understanding of the fields of animal behavior and evolution. Previous supervisory experiences are desirable, though not required.

To apply: Please email a CV, a cover letter describing your interests and qualifications, and the names and contact information of three references to cwmiller@ufl.edu. Please write "EvoDir: Technician Position" in the subject line. Informal inquiries are also encouraged. More information about the lab can be found at www.millerlab.net <<http://www.millerlab.net>>.

Review of applications will begin August 17, 2009 and continue until an outstanding candidate is found.

Christine W. Miller Assistant Research Scientist University of Florida Entomology & Nematology Department PO Box 110620; Bldg 970 Natural Area Drive Gainesville, FL 32611-0260 Phone: (352) 273-3917 <http://www.millerlab.net> <<http://www.millerlab.net>>

"Miller,Christine Whitney" <cwmiller@ufl.edu>

UNebraska PlantQuantGenet

The University of Nebraska-Lincoln Institute of Agriculture and Natural Resources is in the process of enhancing the molecular biosciences in their maize program. There is an expectation that the successful candidate will translate research discoveries into technologies useable in plant species of economic or ecological interest. The Department of Agronomy and Horticulture invites applications for the following position:

The Plant Quantitative Genetics/Statistical Genomics position (requisition # 090232) is a 9-month, tenure-leading, Assistant/Associate/Full Professor position with an 80% research and 20% teaching appointment. Requires Ph.D. in Plant Breeding, Genetics, Agronomy, or other relevant discipline; postdoctoral or private sector competency in genetics, plant breeding, genomics, and bioinformatics relating specifically to improving selection efficiency in maize or other crop species; demonstrable expertise/experience in quantitative genetics, statistical genomics, and bioinformatic approaches to the study of genes that control quantitative traits influencing crop productivity; publication of previous original research in peer-reviewed journals. Successful candidate will have an internationally-recognized, competitively-funded research program in plant quantitative genetics/statistical genomics relating specifically to improving selection efficiency in maize and other crop species.

To apply: Go to <http://employment.unl.edu> and search for requisition # 090232. Complete the Faculty Academic Administrative Information Form. Attach a letter of application, CV, two personal statements V one describing your research focus/interest and one describing your teaching expertise/experience. Review of applications will begin on August 14, 2009, and continue until the position is filled or the search is closed. Arrange for 3 letters of reference emailed by August 14, 2009 to: cwendt1@unl.edu. 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.

Jeffrey P Mower <jmower2@unlnotes.unl.edu>

UppsalaU AssistantProfessor SystematicBiology

Uppsala University hereby declares the following position to be open for application:

Assistant professor/Research Associate in Systematic Biology (http://www.personalavd.uu.se/-ledigaplats/819forass_eng.html)

At the Department of Evolution, Genomics and Systematics at the Evolutionary Biology Center .

A four year independent research position is offered in the Department of Systematic Biology at Uppsala University . Systematic Biology is one of the oldest and largest departments at the Evolutionary Biology Centre, with teaching and research interests covering a wide range of topics. Current research in the department includes the deep phylogeny of eukaryotes, systematics of ferns, of marine invertebrates and of tropical angiosperms, lichenology and mycology, and ethnobiology.

The Systematic Department is housed in spacious modern facilities, adjacent to the museums of zoology and paleontology, herbarium and botanical gardens at Uppsala University , one of the foremost universities in Scandinavia . For further information on the Department, see www.egs.uu.se/sysbiol/index.htm .

Nature of duties: This is principally a research appointment, including supervision of doctoral students. In addition, there will be some opportunity for teaching at the undergraduate and/or postgraduate levels.

Qualifications required: To qualify for an appointment as Assistant Professor/Research Associate you must have a PhD. Priority is given to applicants who have completed their PhD within 5 years of the application deadline. The ability to teach in Swedish or English is a requirement and Uppsala University 's general employment regulations require that teachers possess the necessary skills and qualifications to carry out their duties proficiently.

Criteria for ranking: In ranking qualified applicants the highest importance will be attached to scientific excellence. When evaluating scientific skill special emphasis will be on the quality of scientific publications and on the potential to develop and strengthen current research within Systematic Biology. In filling this posi-

tion, the university aims to recruit the person who, in a combined evaluation of competence, skills and documented qualifications, is judged most suitable to carry out and develop the work-in-hand and to contribute to a positive development of the department and programme.

Personal circumstances that may be of positive relevance to the application, for example parental leave, should be mentioned in the list of qualifications (CV).

Uppsala University is striving to achieve a more even gender balance in its research and teaching staff and women are especially invited to apply for this position.

How to apply: The application must be written in English and the applicant is required to submit 2 copies of documents according to instructions found on the web site <http://www.teknat.uu.se/cms/en/-/node388> or available from Anders Hårsta, e-mail Anders.Harsta@uadm.uu.se.

For further information about the position, please contact Prof. Sandra Baldauf, phone +46 18 471 6452, e-mail: Sandra.Baldauf@ebc.uu.se. The trade union representatives are Anders Grundström, SACO (the Swedish Confederation of Professional Associations), phone +46 18 471 5380 and Carin Söderhäll, TCO/ST (the Swedish Confederation of Professional Employees), phone +46 18 471 1996, Stefan Djurström, SEKO (the Union of Service and Communication Employees), phone +46 18 471 3315.

Applications should be directed to the Vice-chancellor and mailed so as to arrive at Uppsala University, Registrars Office UFV-PA 2009/819, Box 256, S-751 05 Uppsala, Sweden or fax +46 18 471 2000, or e-mail registrator@uu.se no later than August 17, 2009. A fax or e-mail should be followed by a signed original of the application sent within a week of the deadline.

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Petra Korall Associate Professor/Senior Lecturer

Department of Systematic Biology Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

petra.korall@ebc.uu.se

telephone: +46 (0)18 471 6476

USouthCarolina LabTech

A full-time lab technician position (Research Specialist I) is available in ecological genetics at the University of South Carolina in Columbia. Primary duties include maintenance of plankton cultures (mainly *Daphnia*), work with live organisms, experiments with marine microbes, general genetics techniques and lab management. Minimum Qualifications: Bachelor's degree in a related field. A driver's license and a driving record that qualifies the technician to drive university vehicles is required. Required tasks include lifting 20 kg. The successful candidate will be detail-oriented and have excellent organizational and time-management skills, good communication skills, the ability to work independently as well as part of a team, and an understanding of scientific operations and record-keeping. Preference will be given to candidates with the following characteristics: prior experience working in a live-animal, microbiology, aquatics or genetics lab; working knowledge of freshwater biology and/or marine microbiology; working knowledge of and experience with basic genetics techniques (DNA extraction, PCR, gel electrophoresis); problem-solving skills; ability to supervise undergraduate assistants; and the initiative to become a resource for other members of the lab. Information about the research goals can be found at <http://www.biol.sc.edu/~dudycha/> and <http://www.biol.sc.edu/~rlong/>. Anticipated start date: Aug 15th. The position includes health insurance, leave and retirement benefits.

To apply, go to <http://uscjobs.sc.edu> and search for Requisition #770928.

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Jeffrey L. Dudycha Assistant Professor Dept. of Biological Sciences University of South Carolina Columbia, SC 29208 [dudycha \[at\] biol.sc.edu](mailto:dudycha[at]biol.sc.edu) <http://www.biol.sc.edu/~dudycha> dudycha@sc.edu dudycha@sc.edu

UTexasHouston ResTech Genetics

Job: Research Technician - Requisition Number 094550
Institution: University of Texas Health Science Center at Houston - School of Public Health Location: Brownsville Regional Campus

A position is available for a Research Technician in our lab in the Division of Epidemiology and Disease Control at the University of Texas Health Science Center at Houston, under the supervision of Dr Loubna Tazi (<http://www.sph.uth.tmc.edu/>-

brownsville/faculty.aspx). We are seeking an enthusiastic person who will assist with ongoing research projects, with primary responsibilities to participate in our molecular genetics and gene expression research activities, and to manage day-to-day lab duties including occasional training and supervision of new students and other laboratory personnel working in Dr Tazi's group. This full-time position requires a B.S. degree in biology or related field, and a minimum of 2 years experience in genetics or molecular biology. This position also requires laboratory skills in working with DNA/RNA and analytical skills in working with DNA sequence data. The successful candidate should be motivated, have good organizational skills, and be able to work independently. Experience in working in BSL-2/3 labs will be advantageous, but not required. Salary will be commensurate with experience and will include benefits. Review of applications will begin immediately and the position will remain open until filled. To apply, e-mail a cover letter describing briefly your experience, your research interests, and your career goals, along with your resume and contact information for three references to Dr Loubna Tazi (Loubna.Tazi@uth.tmc.edu). The subject of the e-mail must read ResLabTech - Requisition Number 094550, for consideration. Additional information about our campus and the UT School of Public Health can be found at <http://www.sph.uth.tmc.edu/>. The University of Texas is an equal Opportunity Employer, Affirmative Action Employer, and actively seeks diversity among its employees.

Loubna Tazi Assistant Professor Division of Epidemiology & Disease Control University of Texas Health Science Center at Houston School of Public Health, Brownsville Regional Campus 80 Fort Brown, SPH Bldg Room N2.202F Brownsville, TX 78520 Phone: 956-882-5163 Fax: 956-882-5152 E-mail: Loubna.Tazi@uth.tmc.edu

Loubna.Tazi@uth.tmc.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 Canada's 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

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

Communication

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

Education/experience

Essential Qualifications

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

Assets

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

Work style

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

How to apply Please email a cover letter and 2-page re-

sume 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/>
<e.tillier@utoronto.ca> Elisabeth Tillier

WellesleyCollege ScienceDirector

Director of the Science Center Wellesley College

Wellesley College has a strong tradition of preparing women for leadership roles in the sciences. Wellesley offers majors in astronomy, biological sciences, chemistry, computer science, geosciences, mathematics, physics, and psychology, as well as interdepartmental majors in astrophysics, biological chemistry, cognitive and linguistic sciences, environmental studies, media arts and sciences, and neuroscience. Students have the opportunity to collaborate with faculty on research projects and they may be involved in research as early as their first year. All science departments and programs are located in the Science Center which combines the architecture of Sage Hall, the original science building, with dramatic 1977 and 1991 additions, giving the center a feel that transcends time or era.

The Director of the Science Center will oversee programming and outreach initiatives in the sciences; administer all internal funding for faculty and students; and seek outside funding for Science Center-wide initiatives. He/she will manage a team of administrative, technical and union staff committed to providing the many services necessary to support science faculty, staff and students in their teaching, learning and research. He/she will also manage the physical building, oversee regulatory compliance and safety, and monitor policy for building-related issues. The Director will interact with a broad range of members of the college community and will work closely with the Chair of Science Center Chairs, will be assisted by the Sciences Center Office Manager, and will report directly to the Dean of

the College. The successful candidate will be an enthusiastic, inspiring and collaborative leader with a passion for the sciences.

A Ph. D. in the sciences is required. Management experience, including supervising a varied staff in a scientific setting is preferred. Post-secondary teaching/research that engages students in the sciences is desirable. Experience in securing extramural funding is preferred. Nominations and applicants should submit their materials including a cover letter and resume to the following link: [<https://career.wellesley.edu>] <https://career.wellesley.edu> or send cover letter and resume to: Human Resources Office, Wellesley College, 106 Central Street,

Wellesley, MA 02481. Electronic submissions are preferred. Applications will be reviewed starting August 1 until the position is filled. Wellesley College is an EO/AA educational institution and employer. The College is committed to increasing the diversity of the college community and the curriculum. Candidates who believe they will contribute to that goal are encouraged to apply.

Visit our website at www.wellesley.edu/HR/ Susan Doherty <sdoherty@wellesley.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 compu-

tational, 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@acom.yu.edu
Subject line should be: SCB Faculty Search

Careers <careers@acom.yu.edu>

ZFMK Bonn ColeopteraCurator

The Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Bonn (<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 fund 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 pub-

lication 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: <w.waegele.zfmk@uni-bonn.de>.

w.waegele.zfmk@uni-bonn.de

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10K Trees Website

The 10kTrees Website: A New Online Resource for Primate Phylogeny

We are pleased to announce The 10kTrees Project, which is available at <http://10ktrees.fas.harvard.edu/>.

The goal of the 10kTrees Project is to infer a set of phylogenetic trees from available data in GenBank that is appropriate for comparative research on primates. The website provides a Bayesian inference of primate phylogeny for 189 primate species based on 5 genes. At the site, users can download a consensus tree, or they can download up to at 10,000 trees drawn from the Markov chain sample. Comparative analyses can then be conducted across the tree block to control for phylogenetic uncertainty.

The website provides a way for users to prune the trees to the species of interest. We also provide the full genetic data set and details on the analysis. In the documentation, we give advice for importing the trees into different comparative analysis programs, such as BayesTraits, R, and Mesquite.

The 10kTrees Project is a work in progress and we envision regular updates to the data set, trees and website. For example, we are already working on Version 2 of the dataset, which will most likely include over 220 primate species and 9 genes. We also expect that the website itself will evolve to provide more tools for primate comparative biology, including a taxonomic translation

tool.

We hope you will find this website useful, and we welcome any feedback.

Christian Arnold, Luke Matthews, and Charles Nunn
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

Arlequin and AFLP

Dear colleagues,

I am attempting to analyse an AFLP dataset using Arlequin. I have the file currently set up as a STRUCTURE file (which works) but it doesn't export to Arlequin and many web searches have failed to find a program to do this or even find an example input data file. So, if anybody out there would be willing for me to see an 'example' Arlequin input file for AFLP data I would be very grateful.

With best wishes,

Mark.

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

Arlequin and AFLP answers

Dear Colleagues,

Some expressed that I share what I found from the helpful network. And indeed it was helpful, and I am particularly thankful to the large proportion of students who answered my plea.

I went straight to using AFLPdat, this runs in R, but don't be afraid the AFLPdat user-manual was very helpful and it allowed conversions into many of the currently used population genetic programs...however the link is no longer correct and after a little help from Google the following link is where the program can be found:

<http://www.nhm.uio.no/forskning-samlinger/-forskning/forskningsgrupper/ncb/> 2 other conversion programs were recommended, but I did not try these.

The easiest way for me was using FAMD (<http://www.famd.me.uk/famd.html>) which uses a very simple input file and gives you Structure and Arlequin outputs.

a very convenient data converter you might want to give a try. <http://www.cmpg.unibe.ch/software/-PGDSpider/> HOWEVER, one of the biggest hurdles is getting the data (once scored in GeneMapper, or GeneMarker) into EXCEL and back out again in a useful format (ie format for AFLPdat). If anyone knows a way of extending the number of Columns in EXCEL to more than 256 this would help tremendously, as my datasets were 1440 and 1808...which means 4 blocks of data (not very useful) or having individuals as columns (if that is under 256!)...what I had to do is use the macros in EXCEL to save a text file, this was a very useful function

but I have a 'macro-expert' here.

Anyway, thanks again and hope this is useful to someone.

Best wishes,

Mark.

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

Bionumber questions

Dear all

We would be grateful for values, preferably with references for the following:

- 1)The average time it takes to: - transcribe a gene - translate a protein in E. coli (average gene length 1.1 kbp), S. cerevisiae (average gene length 1.6 kbp) and human (or mammalian cell, average gene length 13 kbp)
- 2)Total number of protein (copies) and number of ribosomes in human (or mammalian) cell.

Thanks in advance, Warm regards, Uri Moran

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

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

Book store closing

Dear Colleagues,

I urge you to please help support the following independent bookstore that is struggling to survive. This

bookstore has several branches around the US and supports many important events centered around getting people to think critically about scientific, social, and ethical issues. The bookstore sponsors such events as "Recent developments in cell biology: functioning in a noisy world" (July 19) and panel discussions on evolutionary biology, "intelligent design", as well as discussions and lectures on current social issues.

This precious resource will soon go the way of other independent bookstores (i.e. toward extinction) if we don't support it this month. Please think seriously about a sustaining membership or at least a one-time contribution.

There are very few resources like this where rational people can get together with the public and discuss how critical thinking can be used practically in society and education. As scientists who depend on public support, it is imperative that we be active participants in such ventures.

For more information, please visit: <http://www.revolutionbooksnyc.org/Sustain-donate.htm>
<http://www.revolutionbooksnyc.org> 146 W. 26th St.
 Open 12 noon to 7pm daily

Many thanks! Dave Fitch

~ David H. A. Fitch ~ \ / / / ~ Associate Professor ~
 \ / / / ~ Department of Biology ~ \ / / / ~ New York
 University ~ [] / / ~ Main Building, Room 1009 ~ \ / / /
 ~ 100 Washington Square East ~ \ / / / ~ New York, NY
 10003 ~ \ / / ~ U S A ~ \ / / ~ Tel.: (212) 998-8254 ~ \ / /
 Fax: (212) 995-4015 ~ \ / / ~ e-mail: david.fitch@nyu.edu
 ~ \ / /

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

Czech basic research

Dear All,

Our Czech colleagues are facing a government determined to drastically cut funding for basic research, in favour of applied research and industry.

As highlighted in a recent issue of Nature, the Academy of Sciences of the Czech Republic and Czech academic research as a whole is endangered by planned severe cuts in funding, reaching up to 50% in 2012.

< <http://podpisova-akce.avcr.cz/en/index.php> > If you have benefited from the resurgence of Czech sci-

ence in the international literature, or you simply feel that this issue is one that concerns us all, please take a moment to find out more and perhaps add your signature to a petition in support of our colleagues:

<http://podpisova-akce.avcr.cz/en/index.php> Stuart
 J.E. Baird

Stuart Baird <stuartj.e.baird@gmail.com>

DNA recleaning answers

Dear All, I'd like to thank everyone who responded to my query. I haven't had the chance to try all of the suggestions, but I have had some success (all posted below).

I've tried the following without success (in addition to the list on the original post): - DMSO - BSA - Gene Releaser - DNA Ligase (not conclusive yet) (in combination or isolated, different volumes, etc.)

The only thing that seemed to work for some samples was incubation in Proteinase K for 2 hours at 60°C. There seems to be also an additional quality problem that was not evident in the beginning. After denaturing the re-digested samples at 95°C for 5 minutes I ran them on an agarose gel again and they looked smeary (degraded). It became obvious the double stranded DNA had nicks. I incubated a bunch of samples in different conditions to test for endonucleases and that did not seem to be the case. The best explanation I have so far would be degradation by some physical agent. These DNA samples were shipped by FedEx and might have been X-rayed.

Has anyone had any problems with X-rayed DNA samples before? Is there a better and safer way to ship DNA samples?

Thanks, Hugo

This was the original post: I am having trouble getting PCR amplifications from some of my samples. I have not access to more tissue sample, so I have tried re-cleaning the genomic DNA in solution using different methods with *very* little success, usually losing much of the DNA in the process. I've tried: - Phenol-chlorophorm-isoamyl + chlorophorm-isoamyl + ethanol precipitation; - Heating them in NaOH+SDS for 20 minutes (following Shi et al. 2004) followed by Phenol-chlorophorm-isoamyl + ethanol precipitation; - Promega Wizard Genomic DNA Purification kit;

- Qiagen DNeasy Tissue kit; - Qiagen DNeasy Plant kit. I have plenty, long non-degraded DNA in solution (checked on Nanodrop and on agarose gel). I've also tried diluting the samples with no success. When co-amplifying these samples with ones that work, I still get amplifications (that sequence well) which means whatever it is, it's not something in solution but most likely bound/cross-linked to the DNA. I must add that these samples were originally extracted from fish muscle tissue preserved in ethanol or frozen, using an ammonium acetate protocol and isopropanol precipitation. I'd be grateful if you could suggest some alternative method that has worked for you, including modifications of the above (as they are typically meant for extraction from tissue and not from aqueous solution).

A compilation of mostly unique answers:

I'm not sure what taxa you're looking at but have you tried CTAB in the initial step. We use it with molluscan tissues and it seems to take out the PCR inhibitors.

>>>>>>

probably you have some proteins in your DNA extraction that inhibit PCR amplification. You could try to add some small amount of Proteinase K to your solution. This breaks up these proteins. We use Qiagen Proteinase K of 10-20 μ l (at the moment i have my Lab-book not here, so i cant tell you the concentration, but i could look up). Then use 50-60C for about 30min till 3h and then retry the amplification. An other point is to add more Taq-Polymerase or use a better Polymerase, like Phusion (sometimes you have to raise the concentration of MgCl₂ in your PCR cocktail then). Normally this will help.

Good luck,

>>>>>>

Is there a difference in molecular weight/quality of the DNA that works versus the DNA that does not amplify? Depending on the size you are attempting to amplify, something else you could try, unrelated to DNA purification, is cutting your DNA with a restriction enzyme. I've had limited success doing that when I have problems amplifying extremely high MW DNA samples. You might also try an extra long denature on your PCR cycles to see if that works.

>>>>>>

you might try treating the extracted DNA (from any of the methods listed) with (v/v) 1:1, 1:2 or 1:3 10% Chelex resin (BioRad). Basically, for 1:2, you mix 1 part DNA with 2 parts 10% chelex, heat to 100 C for 10 minutes, spin down and use the supernatant in your PCR reaction. You can scale this up to 96-well (or

greater) by filtering the DNA+Chelex through a millipore plate to remove the chelex from solution (it can inhibit PCR). this works well for us with problematic templates (DNA extracted from blood, tissues, feathers, etc.). In fact, we treat all of our samples this way, since it is inexpensive. you might also give the DNA Clean and Concentrator (Zymo) kits a shot, but that is probably not going to have a terribly different effect from running another Ethanol precip., although you may not lose quite as much DNA.

>>>>>> How much have you tinkered with the PCR reaction? You've probably tried this, but are you using Bovine Serum Albumin (BSA) in your PCR reactions? It non-specifically binds to just about everything except DNA and if you're not

— / —

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>

DNAsp geneflow

Dear community,

Does anyone has a step-by-step protocoll on how input sequences to analyse geneflow and genetic differentiations at the DNAsp software??

I tried to follow the examples provided by the software (i.e. Apes.fas) but probably my problem is related on how separate groups o sequences to be analysed. Does anyone may help me?

Thanks a lot and best regards.

– Prof. Dr. Rodrigo A Torres Laboratório de Genômica Evolutiva e Ambiental Departamento de Zoologia Centro de Ciências Biológicas Universidade Federal de Pernambuco Av. Prof. Moraes Rego s/n Cidade Universitária Recife, PE, Brazil 50670-420 +55(81) 2126-8353 +55(81) 9692-9547

rodrigotorres@ufpe.br

Dear colleagues,

In my courses I've often used the series by University Of Chicago Press on classic papers in different areas ("Foundations of Ecology", "Foundation of Biogeography" and "Foundations of Animal Behavior"). I always wondered why don't we have a similar series on Evolutionary Biology, given that I think it'd be a great teaching tool.

So I decided to contact you and ask for what you think would be the most influential papers in the field of Evolutionary Biology. I'll compile the list, rank the papers and provide the list back to EvolDir.

Looking forward to your contribution,

Marcio Pie

Marcio R. Pie Departamento de Zoologia Universidade Federal do Paraná C.P. 19020 81531-980 Curitiba, PR Brazil Phone: +55(41)3361-1558

pie@ufpr.br

Graph to Newick

Dear EvolDir members, I am curious if anyone has developed software or knows of any that exists that can convert a graphical representation of a phylogenetic tree (e.g., .pdf/.ai/.ps file created from a phylogeny in a published manuscript) to a text format (e.g., newick or phylip). I know there are lots of programs to go the other way (e.g., from newick format to a graphical representation), which is why I am thinking that it might be possible to convert a tree back to a text format.

From discussions with those in my local academic community, there is interest in whether such a conversion is possible. I will also compile and post any comments I receive.

Any information or suggestions would be greatly appreciated and thanks for your time, James

James B. Pettengill Behavior, Ecology, Evolution and Systematics 2174 Plant Sciences Building University of Maryland College Park, MD 20742 USA

jpetteng@umd.edu jpetteng@umd.edu

Graph to Newick answers

Thanks to everyone who shared their knowledge about programs that can convert a graphical representation of a phylogenetic tree into a text format (e.g., newick). It seems as though there is a lot of interest in such software but really only two programs that can get the job done. They are:

TreeSnatcher by Laubach and von Haeseler: <http://www.cibiv.at/software/treesnatcher/>

TreeThief by Andrew Rambaut: <http://microbe.bio.indiana.edu:7131/soft/iubionew/molbio/evolution/phylo/TreeThief/main.html> Below is the original question:

Dear EvolDir members, I am curious if anyone has developed software or knows of any that exists that can convert a graphical representation of a phylogenetic tree (e.g., .pdf/.ai/.ps file created from a phylogeny in a published manuscript) to a text format (e.g., newick or phylip). I know there are lots of programs to go the other way (e.g., from newick format to a graphical representation), which is why I am thinking that it might be possible to convert a tree back to a text format.

From discussions with those in my local academic community, there is interest in whether such a conversion is possible. I will also compile and post any comments I receive.

Any information or suggestions would be greatly appreciated and thanks for your time, James

jpetteng@umd.edu jpetteng@umd.edu

Mixture models

Dear all,

Do any of you know of a software that implements phylogenetic mixture models for mixed topologies (or at least mixed branch length sets)? I couldn't find that in BayesPhylogenies or PhyloBayes, but perhaps I'm missing something...

thanks,

John

sanders_john99@yahoo.com

John Sanders <sanders_john99@yahoo.com>

Number of Ecoli LargeGenomes

Dear all

Would any one know:

1)How many E. coli or yeast cells in a colony (a white dot that develops on agar)? The method of measurement and a reference would be highly appreciated. Mashimo et al 2004 PubMed ID 15351721 < http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list_uids=15351721 >give value of 3.3e+9 but donot specify how.

2)The largest sequenced bacterial genome is 13.7 Mbp of soil bacterium Sorangium cellulosum.

Would anyone happen to know of a larger sequenced or unsequenced bacterial genome, i.e. Is there a larger bacterial genome measured or estimated by methods other than sequencing (electrophoresis, etc.)?

Thanks in advance

Uri

BioNumbers, the database of useful Biological Numbers. www.bionumbers.org < <http://bionumbers.hms.harvard.edu/default.aspx> >

< <http://bionumbers.hms.harvard.edu/bionumber.aspx?s=y&id=104469&ver=1> >

Uri Moran <moranuri@gmail.com>

Parsing sequences by distance

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 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

Polymerase for SmartRace

Dear all,

For 5'RACE and 3'RACE I am using the SMART RACE cDNA amplification kit from Clontech. However, the kit does not contain the DNA polymerase required for the last step, PCR on cDNA. For this reaction Clontech recommends their Advantage 2 polymerase, which is quite expensive (300 euros for 100 reactions or 180 euros for 30 reactions), especially when one already has Promega and Roche DNA polymerases in the lab. A Clontech technical representative told me that most commercially available DNA polymerases will not amplify the cDNA, only a few of them work. But of course she couldn't tell me which ones...

Has anybody tried any other DNA polymerase with this SMART RACE kit?

Thank you for your answers,

Virginie

- Virginie Orgogozo UMR7622 Université Pierre et Marie Curie 9, quai Saint Bernard 75005 Paris www.virginie.orgogozo.org vorgogoz@snv.jussieu.fr vorgogoz@snv.jussieu.fr

Question about LD analysis

Dear colleagues

I am researcher at the Universitat de Barcelona, working with chromosomal inversion polymorphisms in *Drosophila subobscura*. I have been using the MIDAS software, analysing Linkage Disequilibrium (LD) patterns between microsatellites and chromosomal inversions - through the D' parameter.

However, I was unable to obtain information of LD patterns between three loci (with corresponding D' parameters and significance). I have also tried POWERMARKER but, as far as I know, this only provides the p-value of the exact test for the multilocus LD test (and not the D' and their significance). Anyone knows a software package that could perform this analysis (D' parameters and their significance for multilocus LD analysis)?

Thanks in advance Pedro Simões

Departament de Genètica Universitat de Barcelona Espanya

pmsimoes@fc.ul.pt

Renaturing Proteins IEF

Dear EvoDirers,

I apologize for the double posting, but the previous one ended up with a file extension that made the text unreadable.

I am trying to adapt immobilized pH gradient (IPG) strips with a basic narrow range (pH 7-10) to screen for presence and activity of S-RNases in *Solanum*. The problem is that the rehydration and sample preparation buffers that the BioRad Protean cells require cause protein denaturing, hence forbidding me from running the RNase activity test. I read somewhere that one can successfully renature the proteins in the IPG strips by rinsing the strip in a particular buffer after the IEF is done and directly test for RNase activity in the strip, but I can't seem to find specific instructions anywhere. Has anyone done this renaturing and testing in these kind of strips? If so, could you share your protocols/recipes? Any insight will be greatly appreciated

Best,

Jorge

Jorge Mena-Ali, PhD Visiting Assistant Professor Department of Biology Franklin & Marshall College PO Box 3003 Lancaster PA 17604 717-358-4867

jorge.mena-ali@fandm.edu jorge.mena-ali@fandm.edu

Rickettsiaceae DNA

Dear evoldir users,

I am looking for Rickettsiaceae and / or Anaplasmaceae DNA, to be included in test experiment for a pcr protocol aimed at detecting Wolbachia bacteria but not other groups.

I would be most grateful if you could get in touch with me if you have in hands DNA for any of the following groups (or close relatives):

- genus Rickettsia - genus Orientia - genus Anaplasma - genus Aegyptianella - genus Cowdria - genus Ehrlichia - genus Neorickettsia - genus Xenohalictis - genus Neoehrlichia

Many thanks in advance.

Sylvain Charlat.

Sylvain Charlat <charlat@biomserv.univ-lyon1.fr> CNRS (UMR 5558) - University of Lyon Lab. Biometrie & Biologie Evolutive Bat. Mendel, 43 bd du 11 novembre 69622 Villeurbanne - FRANCE Tel: +33 4 72 44 81 01 Fax: +33 4 72 43 13 88 Home: +33 4 79 85 15 07 Mobile: +33 6 87 18 52 21

sylvaincharlat@gmail.com

Software Concatpillar

Dear EvoDir members,

We have just released version 1.4 of Concatpillar. Concatpillar implements a hierarchical likelihood-ratio test for phylogenetic congruence, as described in Leigh JW et al 2008, "Testing congruence in phylogenomic analysis" (Syst. Biol. 57:104-15). Concatpillar was written in Python and uses RAxML for phylogenetic inference of trees from single genes and pairwise concatenated genes.

Concatpillar takes a set of alignments as input and produces a set of concatenated alignments for which no significant incongruence was identified, as well as trees inferred from these sets and a results file indicating the

order in which genes were concatenated. Alignments need not share all the same taxa but all pairs must share at least 4 taxa for congruence to be assessed. Concatenpillar can read a variety of popular alignment formats, including PHYLIP, FASTA, NEXUS, CLUSTAL, and many others. This latest version can now read the “relaxed” PHYLIP format that is written by Mesquite and RAxML, in which sequence names are not restricted to exactly 10 characters, but must be separated from the sequence by a space (strict PHYLIP formats are still supported).

Other features added to the current release of Concatenpillar include support for nucleotide alignments and a pre-screening step to ensure that all alignment pairs share enough taxa, as well as various minor bug fixes.

Concatenpillar can be downloaded from <http://rogerlab.biochem.dal.ca/Software/Software.htm> Regards, Jessica

– Jessica W. Leigh, PhD Université Paris 6 (Pierre et Marie Curie) 9, Quai Saint-Bernard, 75005 Paris

Jessica Leigh <jessica.w.leigh@gmail.com>

Software FLOCK TRACE

Dear evoldir members,

we wish to introduce the first versions of FLOCK_AFLP (1.0), FLOCK_MSAT (1.0) and TRACE (1.0), three programs written in VBA designed to unravel genetic structure within a collection of genotypes possibly comprising a substantial proportion from admixed specimens. In addition, it is assumed that pure, “source”, samples are not available. The method used to partition the set of genotypes is iterative reallocation. This method allows for very short convergence times. One immediate consequence is that a large number of runs (e.g. 50) may be performed within a reasonable time frame. FLOCK searches for reference genetic groups and thereafter computes admixture levels both on an individual and a sample basis. Combined with TRACE, it allows the computation of distance matrices that are meant to closely reflect the structural relationships between samples. Each distance matrix may easily be fed into a tree/cluster plotter to obtain a visual representation of those relationships. The interface of all three programs are user-friendly and similar to that of AFLPOP. (Duchesne & Bernatchez 2002). Potential users may download free copies of FLOCK_AFLP (1.0),

FLOCK_MSAT (1.0) and TRACE (1.0), directly from Julie Turgeon’s Web Page :

http://www.bio.ulaval.ca/no_cache/fr/departement/-professeurs/fiche_des_professeurs/professeur/11/13/

(scroll all the way down to «Téléchargement:»)

Users are invited to ask questions about those programs, make suggestions and report bugs by sending e-mails to either Pierre.Duchesne@bio.ulaval.ca or Julie.Turgeon@bio.ulaval.ca.

Reference:

P DUCHESNE, J TURGEON. 2009. FLOCK: a method for quick mapping of admixture without source samples. *Molecular Ecology Resources* (Published Online: 25 Feb 2009) (currently available only in pre-press version online on the journal’s web page).

Pierre Duchesne <Pierre.Duchesne@bio.ulaval.ca>

Software NOBLAST

Dear Evoldir members,

NOBLAST (New Options for BLAST, patch for the NCBI BLAST) has recently been updated to version 2.1 and is available for download at: <http://sourceforge.net/projects/NOBLAST> New feature: - “Word size” (blastall option -W) can be as low as 4 nucleotides (instead of 7) for the blastn program. Useful for primers/oligos/probes mapping, e-PCR...

Reference: Lagnel J, Tsigenopoulos CS, Iliopoulos I (2009) NOBLAST and JAMBLAST: New Options for BLAST and a Java Application Manager for BLAST results. *Bioinformatics* 25: 824-826

Comments and suggestions are always welcome.

Best regards,

Jacques

ps: I am currently working on an updated doc, website and bioperl/biojava integration.

Jacques Lagnel

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The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

Jill Pilkington <j.pilkington@ed.ac.uk>

StKilda volunteer SoaySheepProject

Soay Sheep Research - St Kilda

Summer and Rut 2009

Fieldwork Volunteer Assistants

We are currently looking for volunteers for this year's Soay sheep Summer and Rut expeditions to St. Kilda, a group of islands 180 km off the coast of north-west Scotland. The expeditions run from mid July till the end of August and from Mid October until late November 2009.

Activities:

- Population census of sheep using telescopes and hand-held computers
- Mortality searches
- Annual catch up of sheep (August)
- Monitoring of Rut behaviour (November)

Requirements:

- . Must be available for the full period of one of the time periods stated
- . Must be fit, St Kilda has a very demanding terrain; ability to run essential
- . A background in Biological Sciences

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

If you wish to apply for this work please send: a CV with covering letter, contact phone number and details of two referees that can be contacted immediately by email.

Contact: Jill Pilkington

Email: j.pilkington@ed.ac.uk

TDWG PublicReview DarwinCore standard

Apologies for cross posts - and please feel free to distribute this announcement to all relevant communities.

TDWG is pleased to announce the commencement of the Public Review of Darwin Core - a standard for sharing biodiversity information. You will find the proposed standard is a living document with a history, an anchor in the Dublin Core, and mechanisms to grow and change. Since being officially put forward as a draft standard in February 2009, Darwin Core has undergone a peer review, a review by the TDWG Executive, and multiple revisions.

Open Invitation: We invite all who may contribute and/or consume biodiversity information to examine this proposed standard during the Public Review period from 11th July through at least 10th August 2009.

How to Participate: Visit the Darwin Core Progress site (<http://code.google.com/p/darwincore/wiki/DarwinCoreProgress>) for the latest background information on the process and critical links to content (<http://rs.tdwg.org/dwc/index.htm>) and participation. To discuss ideas with others or offer comments that are not targeted for action, please subscribe (<http://lists.tdwg.org/mailman/listinfo/tdwg-content>) and contribute to the tdwg-content mailing list (tdwg-content(at)lists.tdwg.org). Recommended actions or issues should be submitted to the Issue Tracker of the Darwin Core (<http://code.google.com/p/darwincore/wiki/SubmittingIssues>) so that they may be assigned, prioritized, and tracked. This Public Review process will be archived along with all other documentation in the TDWG Standards Track. Questions about the process should be directed to the Review Manager, Gail Kampmeier (gkamp(at)jillinois.edu).

Please share this opportunity for public comment and review with others you think may be interested.

Acknowledgements: As Review Manager, I would like to express my gratitude to the authors, John Wicczorek, (MVZ), Markus Döring (GBIF), Renato De Giovanni (CRIA), Tim Robertson (GBIF), Dave Vieglais (KUNHM) for the enormous efforts made in bringing

the Darwin Core standard to this point; to the initial anonymous peer reviewers, and to Lee Belbin and the rest of the TDWG Executive for their advice, support, and encouragement in this process; and to GBIF for tipping the scales by bringing together the authors in a workshop that led to this submission.

Links expanded: Darwin Core Progress - <http://code.google.com/p/darwincore/wiki/-DarwinCoreProgress> Darwin Core content - <http://rs.tdwg.org/dwc/index.htm> Subscribe to tdwg-content - <http://lists.tdwg.org/mailman/listinfo/tdwg-content> Issue Tracker - <http://code.google.com/p/darwincore/wiki/SubmittingIssues> Related Links: TDWG: <http://www.tdwg.org/> Other TDWG Standards: <http://www.tdwg.org/standards/> TDWG Standards Track (in OJS): <http://www.tdwg.org/stdtrack/index> Dublin Coreâs Metadata Initiative in Science: <http://ils.unc.edu/spaces/sam/index.php/Main.Page>

Sincerely, Gail E. Kampmeier, Review Manager Illinois Natural History Survey, Institute of Natural Resource Sustainability, University of Illinois at Urbana-Champaign, 1816 South Oak St., Champaign, Illinois 61820 USA email: [gkamp\(at\)illinois.edu](mailto:gkamp(at)illinois.edu)

Lee Belbin TDWG Secretariat

tdwg mailing list tdwg@lists.tdwg.org <http://lists.tdwg.org/mailman/listinfo/tdwg> - Carol L. Spencer Staff Curator of Herpetology & Researcher Museum of Vertebrate Zoology 3101 Valley Life Sciences Building University of California, Berkeley, CA, USA 94720-3160 atrox10@gmail.com atrox@berkeley.edu TEL: 510-643-5778 /FAX: 510-643-8238

<http://www.herpnet.org> <http://mvz.berkeley.edu/>
Carol Spencer <atrox@berkeley.edu>

UltrametricTrees ConstraintTopology

Dear Evoldir members,

I have a known tree topology for which I need to generate a reasonably correct ultrametric tree using likelihood models. I'm looking for a program which can either correctly mathematically scale the branch lengths in a phylogram into an ultrametric tree or a tree reconstruction program which meets the following criteria: 1) Can accept a fully specified constraint topology to optimize 2) Implements both amino acid sequence models and nucleotide models 3) (optional, but preferable) Will

conduct a partitioned analysis with user specified partition data. A fairly basic molecular clock optimization is all I need for this analysis, so the ability to specify multiple fossil calibration points or calculate margins of error on node divergence times is not necessary.

If you have any suggestions, please mail them to jacar-avas@gmail.com

Thank you for your help, Jason Caravas jacar-avas@gmail.com Department of Biological Sciences Wayne State University Detroit, MI

calibos@comcast.net

VanValen articles

Dear colleagues,

I would like to find these two articles:

Leigh Van Valen (1973). A new evolutionary law. *Evolutionary Theory*, 1:1-30. Leigh Van Valen (1976). Ecological species, multispecies, and oaks. *Taxon*, 25:233-239.

If somebody has a PDF copy of one of them... Thank you very much cheers Didier

Didier Aurelle <didier.aurelle@univmed.fr>

Visible Implant Elastomer for reptiles

Dear all,

we are planning to use Visible Implant Elastomer for individual marking in several reptile species in Madagascar (Furcifer, Oplurus, Zonosaurus, Tracheloptychus). As this method is mainly used in fisheries, we are wondering if anyone has experience with using VIE in reptiles? Ideally, we would like to test the usability of the marking in reptiles before we order the kits, so it would be great if we can get in contact with someone who is working with VIE in (northern) Germany?!?

Thanks a lot for your help! Wiebke Berg

- Wiebke Berg University of Hamburg, Germany +49 (0)40-428385648 wiebkeberg@web.de

wiebkeberg@googlemail.com

WOMBAT and bivariate analysis problem

Hi to everyone,

I'm just starting with WOMBAT so my question may be a little bit naive...

I'm trying to code a bivariate model that uses traits measured in two different environments as the distinct traits. Below you can find the listing of my .par file:

```
ANAL MUV 2 DATA ./resp.dat TRNOS 1 2 traitno 2
animal 0 sire dam fact1 2 ran3 79 ran1 79 ran2 40 fix1
2 fix2 2 NAMES meas1 meas2
```

end data

```
MODEL RAN ran1 1 2 RAN ran2 1 2 RAN ran3 1 2
TR meas1 1 TR meas2 2 END
```

[and here go covariance matrices]

the structure of the DATA section was double checked with the number and content of all the columns in my data file (in this analysis I'm not using sire and dam infos), however when trying to run the analysis I'm getting the following error message:

Error reading parameter file : No trait no. found! Current line : "TRNOS 1 2"

Currently I have no idea what's wrong and here goes my question. Did anybody have problems like this? Can different Linux/Windows coding result in WOMBAT not being able to read the par/dat files? My data file was saved to ASCII by Excel, but this doesn't seem to be a problem since an usual analysis (a univariate one) runs without any problems and yields proper results.

I'd be grateful for showing what's wrong or what I'm missing.

szymek

– Szymon Drobniak Group of Population Ecology Institute of Environmental Sciences Jagiellonian University ul. Gronostajowa 7, 30-387 Kraków, POLAND tel.: +48 12 664 52 19 fax: +48 12 664 69 12 e-mail: szymek.drobniak@uj.edu.pl www: esz-de.blogspot.com geralttee@gmail.com

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Antwerp InfectiousDiseaseEvolution

Dear colleagues, Our team in Antwerp (Evolutionary Ecology Group + Centre for Health Economics Research & Modeling Infectious Diseases) is starting a project entitled "Infectious disease models: wildlife ecology, ecological disturbance and transmission to humans." For this project, two post-doc positions (4 years) and one PhD-fellowship (4 years) are currently available. Could you please forward this information to potential candidates? A project summary and links to the position announcements are given below.

Project summary

Since almost two decades, there is a strong interest in the ecology and epidemiology of infectious diseases, especially the so-called re-emerging or new diseases. Many of those infections are caused by pathogens that have a natural wildlife reservoir (sometimes still unknown) or where an arthropod vector is necessary for the transmission between humans. It is often suggested that environmental disturbances play a major role in the spreading of these diseases. In this project we investigate mechanisms through which this may happen. The two major pathways that are thought to contribute to the importance of these diseases are 1) pathogen jumps between animal and humans leading to the emergence of a really new infection and 2) changing environmental conditions that favour the expansion of populations of the natural reservoir species or that allow faster, more frequent and/or more efficient transmission between hosts. Changes in the environment, however, could also have more complex effects if they for example cause more abundant populations of hosts but at the same time reduce transmission (e.g. warmer winters lead to higher rodent numbers, but some viruses remain infectious for a longer time under cold conditions). For this project, we selected five different model systems where we anticipate likely environmental disturbances (e.g. plausible climate change scenarios, or vaccinations that create opportunities for new pathogens) that would lead to combinations of pos-

itive or negative effects on transmission and positive or neutral effects on host populations (the effects of reductions of host populations are already well studied). Those systems are Puumala hantavirus in bank voles in Belgium, plague in gerbils in Kazakhstan, Mopeia arenaviruses in multimammate mice in Tanzania, the mosquito-transmitted dengue fever in humans (mainly in Asia), and rotaviruses that cause gastro-enteritis in humans (mainly in children) in Belgium. The participating groups have considerable and internationally well-reputed experience with these model systems, but the main reasons for selecting them are that there are sizeable pre-existing long-term data and that clear hypotheses can be formulated about what could happen under very specific ecological conditions. The systems will be studied using a combination of existing observational data, new prospective field data, field and laboratory experiments and mathematical modelling. Mathematical models are a very powerful tool in understanding the ecology of infection and for the development of optimal disease control strategies. At the same time, however, they often remain very theoretical because of lack of field data to parameterise and validate them. The present proposal will provide data to do exactly this and will thus allow to test different basic epidemiological assumptions. This will provide new insights in transmission dynamics that were hitherto impossible to verify, it will allow predictions about what can be expected under different environmental conditions and it will also contribute directly to new approaches in disease management.

More information can be obtained through the following links:

Evolutionary Ecology Group: Ph.D.-student in the field of Ecology of Infections (http://www.ua.ac.be/main.aspx?c=*VACATURES&n=26394&ct=c025734&e=7771) Postdoctoral position for Theoretical Biologist/Mathematical modeler (http://www.ua.ac.be/main.aspx?c=*VACATURES&n=26394&ct=c025734&e=7769) Centre for Health Economics Research & Modeling Infectious Diseases: Postdoctoral position for infectious disease modeler (http://www.ua.ac.be/main.aspx?c=*VACATURES&n=42572&ct=43038&e=207766)

Many thanks and best wishes Herwig

– Prof. dr. Herwig LEIRS Evolutionary Ecology Group, Universiteit Antwerpen Groenenborgerlaan 171, B-2020 Antwerpen, Belgium phone: +32 (0)3 2653469 fax: +32 (0)3 2653474 <http://www.ua.ac.be/herwig.leirs> Herwig Leirs <herwig.leirs@ua.ac.be>

CIBIO Portugal PopulationGenomics

POSDOC: One post-doctoral position in the research group (Gene, Population Genomics and Traits) at Research Center in Biodiversity and Genetic Resources, University of Porto (CIBIO-UP) Portugal. * * We are searching for a post-doc interested in animal domestication genomics and population genomics of domestics and their wild relative species/subspecies. Our long-term goals are to (i) understand the genomic impact of animal domestication and selection (including artificial and natural selection), and (ii) address key unresolved questions in animal domestication history and processes (e.g., how many species/subspecies are needed to create one domestic species). The grants are for 3 years and would start as early as January, 2010. The successful applicants will be integrated in the team of the currently ongoing projects using re-sequencing and next-generation sequencing data, including SNP discovery and the sequencing of polymorphism data using next generation sequencing, SNP genotyping, and data analysis (association mapping and population genetics), funded by The Portuguese Foundation for Science and Technology, and can also propose their own research projects. The main working place will be at Research Center in Biodiversity and Genetic Resources, University of Porto (CIBIO/UP), Campus Agrário de Vairão, near Porto, Portugal. CIBIO/UP is ranked by FCT (Portuguese Foundation for Science and Technology) as excellent, based on the evaluation of an independent international panel of juries. The CIBIO has a very cosmopolitan atmosphere with researchers and postgraduation students from several different countries and continents.

We are searching for an outstanding candidate, highly motivated, capable of independent work, and holding a PhD degree in population genetics, genomics or related subjects. The applicant must have a strong interest in population and evolutionary genetics. They should also be familiarized with bioinformatics approaches relating to population and evolutionary genetics as well as experience analyzing next generation sequencing data would

be desirable. A background in computational and/or statistical methodologies as well as experience in statistical and programming languages is desired. Finally, the candidate is expected to be able to write a research grant application to be submitted to the FCT (Portuguese major funding body for basic research).

Deadline for application: July 28, 2009

The interested candidates should submit their application as soon as possible. Please submit a cover letter, CV, statement of research interests, and the names and contact details of three academic references as a single pdf file by e-mail to Albano Beja-Pereira using the following address posdoc09@gmail.com

To know more about research lines in our group at <http://cibio.up.pt/main.php?lang=en> posdoc2009 cibio <posdoc09@gmail.com>

CIBIO UPorto PlantEvolution

I am looking for a Ph.D or postdoc who is interested to apply for a postdoc fellowship to work in the Plant Evolution Group at CIBIO, University of Porto, in Northern Portugal. CIBIO had recently been rated as “excellent”, by our national evaluation system and provides a stimulating, international research environment. The position can be embedded in one of our projects but would be also a good opportunity to develop or pursue own research lines. Also, it is possible to include a co-advisor from abroad. Deadline for the proposals is September 1st, 2009 and if funded, positions can start in January 2010 or later, generally for three years. All nationalities can be considered.

If interested send me an email for further information: meimberg@mail.icav.up.pt <<mailto:meimberg@mail.icav.up.pt>>

Harald Meimberg, CIBIO, UP

meimberg@mail.icav.up.pt

CornellU PopulationGenomics

* Postdoctoral positions in human population genomics and next-generation sequencing analysis at Cornell Uni-

versity*

Two postdoctoral positions are available with Alon Keinan in the Department of Biological Statistics and Computational Biology at Cornell University. The focus of the group is on human population genomics and on method development for medical genetics. Potential research areas for the positions include human population genetics and evolutionary history, method development for analysis of next-generation sequencing data sets, natural selection detection and characterization, population genetic theory, and method development for genome-wide association studies. Research projects will be closely aligned with the interests of the successful candidates.

The ideal candidate will be enthusiastic, highly motivated, will have both a strong statistical, computer science, or mathematical background and an interest in population genetics or medical genetics, and will have a strong record of accomplishment in research. The starting date is flexible and can be as early as Aug 2009. Applications will be accepted until the positions are filled. Competitive salaries commensurate with experience and skills will be offered, and full benefits plans are available (see <http://www.postdocs.cornell.edu/-benefits.contract.php> for details).

Alon Keinan is building a new research group at Cornell that is closely associated with those of Carlos Bustamante, Andy Clark, Chip Aquadro, and Adam Siepel. The Keinan lab is part of the larger population genomics community at Cornell and is a member of the recently launched Cornell Center for Comparative and Population Genomics (<http://www.news.cornell.edu/-stories/Oct08/PopGenCtr.kr.html>). The lab is located in the Department of Biological Statistics and Computational Biology (<http://www.bscb.cornell.edu/>) that occupies a key position at the interface between the quantitative and biological sciences at Cornell and that has broad strengths in comparative, evolutionary, quantitative, and population genomics, Bayesian and computationally intensive statistics, and machine learning. The lab is also a member of the 1000 Genomes Project (<http://www.1000genomes.org>) and offers rich opportunities for international collaborations on emerging sequencing technologies and data sets.

Interested applicants should send a PDF with CV, a brief description of research interests and experience, and contact information for three references to ak735@cornell.edu, indicating "position 202" in the subject line. Informal inquiries are welcome.

Alon Keinan, PhD Assistant Professor, Department of Biological Statistics & Computational Biology Weill Hall 102A | Cornell University | Ithaca,

New York 14853 ak735@cornell.edu | 617-432-5992
phone <http://genepath.med.harvard.edu/~akeinan/>
<http://genepath.med.harvard.edu/%7Eakeinan/> >

alon.keinan@gmail.com

CornellU SpeciationGenetics

Postdoctoral position in behavioral evolutionary genetics and speciation

P.I.: Dr. Kerry Shaw, Cornell University

Research Project:

A postdoctoral position is available to join an NSF-funded project in the laboratory of Kerry Shaw to study the evolution and genetics of traits involved in reproductive incompatibility and speciation in the Hawaiian cricket genus *Laupala*. *Laupala* species are recently diverged and ecologically and morphologically similar, but differ in acoustic and cuticular hydrocarbon phenotypes. Behavioral evolution involving these traits is thought to have played a large role in the rapid and extensive diversification of this genus. Pre and postzygotic reproductive incompatibilities will be quantified and parallel evolution and genetic architectures of the constituent traits will be evaluated between multiple species pairs.

Requirements:

The desired candidate will possess an interest in / experience with quantitative genetics, experimental design, behavioral observation, and associated statistical analyses. Knowledge of basic molecular laboratory skills (such as DNA/RNA extraction and PCR) is desirable but not essential. An interest in the neurological basis of behavior and/or the evolution of premating isolation would be beneficial but no prior knowledge in these areas is required.

Cornell University has many labs dedicated to the study of behavior and ecology of speciation, speciation and evolutionary genetics. As such, it provides a rich academic environment for those interested in proximate and ultimate causes of behavioral evolution and speciation.

The position can be filled immediately and at least two years of funding are available. To apply, email a statement of research interests, a curriculum vitae, and the email addresses of three references to Kerry Shaw (KLS4@cornell.edu).

kls4@cornell.edu kls4@cornell.edu

CSIRO Hobart MarinePopulationGenomics

CSIRO Marine and Atmospheric Research in Hobart Australia has a three year postdoctoral position in marine population genomics.

The postdoc will play the leading role in a project developing SNP arrays for population genomics in exploited marine species. They will conduct SNP array genotyping of specimens across environmental and exploitative gradients. In collaboration with other CSIRO scientists, and international collaborators the postdoc will conduct population genomics analyses of data to identify non-neutral and neutral SNPs for the study of selection signals and oceanscape genetics.

This work will pioneer the application of population genomics approaches in Australian marine systems.

Before tax salary \$67k-\$76k per annum.

Application deadline July 17 2009.

Enquiries to Phillip England PhD Senior Research Scientist CSIRO Marine & Atmospheric Research Castray Esplanade, Hobart TAS 7000 GPO Box 1538 Hobart TAS 7001 +613 6232 5116 phillip.english@csiro.au

CSIRO is Australia's premier research body, delivering innovative science for the benefit of Australians.

For further details including selection documentation and details on how to apply visit www.csiro/careers or call 1300 301 509 within Australia.

Phillip.England@csiro.au Phillip.England@csiro.au

ETH Zurich PlantPathogenicFungi

Advanced Postdoctoral (\$B!H(BOberassistant\$B!I(B) Position Available at ETH Zurich: Evolutionary biology and ecology of plant pathogenic fungi.

We seek applicants who have a PhD in Plant Pathology or a related science, including Microbiology, Genetics, Biology, or Ecology. Applicants should have demonstrated an ability to work independently and to pub-

lish research in international, peer-reviewed journals. Applicants should have effective communication skills, both oral and written and be able to lead and coordinate a research team of 2-4 people. Applicants should have finished at least one postdoc and have knowledge in one or more of the following fields: population genetics, evolutionary ecology, genetic epidemiology, phylogeography, and bioinformatics. Women candidates are especially encouraged to apply. Experience with fungi is desirable, but not required. A good publication record is essential. The successful applicant will be granted a high degree of flexibility in research direction and approach. Applicants who have experience with plant pathogens, coalescent analyses of sequence data and bioinformatics will have an advantage. Our major areas of research are population genetics, evolutionary biology, evolutionary ecology, experimental evolution, and phylogeography. Our primary experimental organisms are the plant pathogenic fungi *Mycosphaerella graminicola*, *Phaeosphaeria nodorum*, *Rhynchosporium secalis* and *Rhizoctonia solani*. The position is renewable annually for up to six years.

Our research focuses on the evolutionary biology of plant pathogenic fungi. We have global collections of 1000s of strains for all four of our model pathogens. A significant number (12-20) of microsatellite markers have already been developed for each fungus, as well as suites of sequence loci comprising introns in housekeeping genes, known or suspected pathogenicity genes, and anonymous sequences in both nuclear and mitochondrial genomes. Genome sequences are available for all four fungi.

The ETH and the Institute of Integrative Biology possess advanced infrastructure for data collection and analyses including the Genetic Diversity Center (<http://www.gdc.ethz.ch/>) and the Functional Genomics Center Zurich (<http://www.fgc.ethz.ch/>) as well as large computer clusters (<http://www.asgard.ethz.ch/>). Zurich is consistently rated as one of the most livable cities in the world. The Plant Pathology Group (<http://www.path.ethz.ch/>) is currently composed of ~30 people from 12 countries, and English is the working language of the group. But knowledge of German or French is useful outside of the university.

Applications consisting of a CV, publication list and statement of research interests, with names and contact information for 3 references should be sent by email before 1 September 2009 to Prof. Bruce A. McDonald at bruce.mcdonald@agrl.ethz.ch. The position could be filled beginning 1 January 2010 but will remain open until a suitable person has been found.

Bruce McDonald Plant Pathology Institute of Integra-

tive Biology, Zurich (IBZ) ETH Zurich, LFW B16 8092 Zurich Switzerland

Office: +41 44 632 3847 FAX: +41 44 632 1572
 Assistant: +41 44 632 3848 (Ulrike Rosenberger)
 Email: bruce.mcdonald@agrl.ethz.ch Web (Group):
<http://www.path.ethz.ch> Population Genetics of
 Plant Pathogens: <http://www.apsnet.org/education/AdvancedPlantPath/Topics/PopGenetics/top.htm>
 Bruce McDonald <bruce.mcdonald@agrl.ethz.ch>

GeorgetownU DiapauseAdaptation

Postdoc in Molecular Genetics of Adaptation (Diapause).

A two-year NIH-funded postdoctoral position is available to investigate transcriptional components of photoperiodic diapause in the invasive and medically important mosquito, *Aedes albopictus*. The position is part of a collaborative project between the Armbruster and Elsik labs in the Department of Biology at Georgetown University. The work will focus on utilizing 454 sequencing, bioinformatics analyses, quantitative RT-PCR and physiological experiments. This position will involve both wet-lab (approx. 75%) and bioinformatics analyses (approx. 25%). The successful applicant will have opportunities to develop independent lines of research related to molecular evolution and the molecular basis of adaptation.

We seek a collegial and highly motivated individual with a PhD in Molecular Physiology, Genetics, Bioinformatics or Evolutionary Biology. Experience with molecular analysis and strong written and oral communication skills are essential. Experience with the linux/unix operating system and Perl programming are preferred, or the individual must be willing to learn linux/unix and Perl. Salary is \$39,000 per year plus benefits. Anticipated start date is between August-September of 2009.

The Department of Biology at Georgetown University is a collegial and interactive environment. Washington D.C. provides an exceptionally rich cultural and research environment, with opportunities to interact with researchers at the National Institutes of Health, the Smithsonian Institution, the USDA and various other local universities and research institutions.

Application should be sent to Peter Armbruster (paa9@georgetown.edu)

<mailto:paa9@georgetown.edu>) and include the following: (1) a cover letter describing research interests and qualifications (no more than 1 page), (2) a CV, (3) contact information for three references, and (4) up to three representative publications Please include postdoctoral application in the subject line of the e-mail. Review of applications will start immediately and continue until the position is filled. Informal inquiries are welcome.

Georgetown University is an Equal Opportunity/Affirmative Action Employer.

 Peter Armbruster, Ph.D. Assistant Professor Dept. of Biology, Reiss 406 Georgetown University 37th and O Streets NW Washington, DC 20057-1229

Office Phone: 202-687-2567 Lab Phone: 202-687-1741
 Cell: 301-512-9202 Fax: 202-687-5662

Germany HostParasiteCoevolution

Several Postdoc / Research Associate Positions will be available from October 2009 within the recently started DFG Priority Program 1399 -Host-Parasite Coevolution - Rapid Reciprocal Adaptation and its Genetic Basis' Research areas include Evolutionary Biology, Parasitology, Genomics, Immunology, Bioinformatics, and more. The priority program offers cutting edge, cross-disciplinary research. Host-parasite coevolution is used as a powerful and versatile model for analysing the causes and processes of evolutionary adaptation across scales (from genomes to ecosystems). The program is funded by the German Science Foundation (Deutsche Forschungsgemeinschaft, DFG) across various locations in Germany: Berlin, Bonn, Gießen, Halle, Hamburg, Heidelberg, Kiel, Köln, Leipzig, München, Münster, Osnabrück, Plön, Regensburg. We invite applications from highly qualified candidates of any nationality. Women are especially encouraged to apply. Preference will be given to disabled applicants in case of equivalent qualification. The application deadline is August 15, 2009. Information on the various projects and application procedure can be found at: <http://ieb.uni-muenster.de/spp/jobs> Prof. Dr. Joachim Kurtz

University of Muenster Institute for Evolution and Biodiversity, Animal Evolutionary Ecology Group Hueffer-

str. 1, D-48149 Muenster, Germany Phone: + 49 251 83 24661 Fax: + 49 251 83 24668 joachim.kurtz@uni-muenster.de <http://www.uni-muenster.de/Evolution/-joachim.kurtz@uni-muenster.de> joachim.kurtz@uni-muenster.de

Graz Cichlid Quantitative Genetics

Research scientist position in Christian Sturmbauer's group in Graz

The Department of Zoology at the Karl-Franzens-University Graz offers the position of a

Post-doctoral scientist (40 hours per week; for an employment of 2 years, starting November 1st 2009)

Tasks: To join the research group of Christian Sturmbauer for research work on African cichlid fish populations, financed by research grant No. P20994-B03 of the Austrian Science Fund "Natural selection - driving force of adaptive radiation", to carry out quantitative genetic analyses on African cichlid fish populations, and pond-bred offspring. See also <http://www.kfunigraz.ac.at/-zoowww/> Qualification: Ph.D. in Zoology, Genetics or Evolutionary Biology. Experience in quantitative genetics targeting natural populations and breeding experiments. The candidate must have experience in the use of ASReml and similar tools, adequate number of scientific publications and conference contributions corresponding to the applicants experience, team spirit and interest to work in Africa.

Job application: Please apply per e-mail to Prof. Christian Sturmbauer, christian.sturmbauer@uni-graz.at <<mailto:christian.sturmbauer@uni-graz.at>> with the following documents: CV, letter of research interests, list of publications, contact coordinates of two persons for reference.

Univ. Prof. Dr. Christian Sturmbauer Department of Zoology University of Graz Universitaetsplatz 2 A-8010 Graz Austria

christian.sturmbauer@uni-graz.at
christian.sturmbauer@uni-graz.at

ILRI Liverpool Viralevolution

ILRI 2 Post Doc positions available - high throughput sequencing for viral evolution.

Dear All

Please see here

<http://www.genomics.liv.ac.uk/tryps/-AVIDpostdocs.pdf>

for two post-doc positions at ILRI, Nairobi.

If you are interested, or know anyone good who wants an exciting and challenging post doc position please let me know.

I am happy to have an informal email exchange with anyone interested. We are prepared to be flexible on experience as we realize that not many young post-docs will have experience of high throughput sequencing of environmental samples. The positions are available immediately but we will hold them open until we find the right people.

Thanks

Steve Kemp

S J Kemp School of Biological Sciences Biosciences Building Liverpool L69 7ZB UK

and

ILRI P.O. Box 30709, Nairobi, 00100 Kenya Office direct +254 7110 33360 mobile +254 7354 41419

kempsj@liv.ac.uk www.genomics.liv.ac.uk/tryps/
"Tapio, Miika (ILRI)" <M.Tapio@cgiar.org>

IndianaU Bloomington InsectEvoDevo

POSTDOC IN INSECT EVO DEVO (Indiana University, Bloomington)

A full-time NSF-funded postdoctoral position is available in Armin Moczek's lab, Department of Biology, Indiana University, Bloomington. Our lab conducts research in evolutionary developmental (evo-devo) and ecological developmental (eco-devo) biology, focusing on the genetic, developmental and ecological mechanisms that mediate the origins and diversification of novel complex traits in insects such as the horns of beetles or the lanterns of fireflies.

The position advertised will focus on identifying the genes and pathways underlying the origin and diversi-

fication of beetle horns in particular and morphological diversity in general, in the horned beetle genus *Onthophagus*. Specifically, the work will investigate the role of candidate developmental mechanisms in the origin of horn development and how evolutionary changes in these mechanisms have mediated diversification of horn expression between and within species. The postdoctoral candidate will also have opportunity to develop independent lines of research in these and related areas.

We seek a collegial, self-motivated, and intellectually curious individual with a PhD in Evolutionary Biology or Developmental Biology, or related fields. Applicants must have strong bench skills and familiarity with techniques such as immunohistochemistry, cloning, qPCR, and RNA interference is strongly desirable. In addition, candidates must have demonstrated written and oral communication skills. Experience working with insects is a plus but is not required. The position is initially available for 12 months, with possible extension for at least 1 additional year. Salary will be commensurate with experience, and full benefits are included.

Indiana University has a large and interactive group in evolutionary developmental biology and allied fields. Bloomington is situated in scenic, hilly southern Indiana, near several parks and wilderness areas. The cultural environment provided by the University is exceptionally rich in art, music, and theater.

To apply, please send a letter of interest, resume and contact information for 3 references to Dee Verostko (dverostk@indiana.edu), using 'Moczek Postdoctoral Fellow' as the subject line. Review of applications will start immediately and will continue until the position is filled. Inquires about the position can be directed to Armin Moczek (<file:///mailto:lmoyle@indiana.edu>armin@indiana.edu). Additional information about research in the Moczek lab can be found at www.bio.indiana.edu/~moczeklab/index.html Indiana University is an Equal Opportunity/Affirmative Action Employer.

Armin P. Moczek Associate Professor Department of Biology, Indiana University

web1: <http://www.bio.indiana.edu/facultyresearch/faculty/Moczek.html>
 web2: <http://www.bio.indiana.edu/~moczeklab/index.html>
 Evo-devo IGERT at IU: <http://www.bio.indiana.edu/~igert/index.htm>
 Armin Moczek <armin@indiana.edu>

Ipswich MA Comparative Genomics

Postdoc:

Postdoctoral Research Associate (Job Code: OGL-LC, posted 06/15/09) The Ocean Genome Legacy Laboratory for Marine Genomic Research (www.oglf.org) seeks a postdoctoral research associate to investigate lignocellulose degradation by wood boring marine bivalves of the family Teredinidae (shipworms) and their bacterial endosymbionts. The successful candidate will be knowledgeable and experienced in genomics, proteomics, and bioinformatics and must have excellent laboratory skills in molecular biology and microbiology. Knowledge of microscopy and enzymology of lignocellulose degradation is also desirable. OGL seeks an employee with excellent organizational, communication and laboratory skills, who pays strong attention to detail and has the desire and ability to work well in a collaborative group setting. The position is available immediately and offers exciting opportunities for broad research training, publication, competitive salary and benefits, and the potential for advancement within a new academically oriented non-profit research institution. Applicants should submit a cover letter, resume, list of publications, and contact information for at least three references by email to careers@oglf.org (referencing job code OGL-LC in the subject line) or by regular mail to the address below.

Ocean Genome Legacy, Inc. is a publicly supported non-profit research organization dedicated to exploration, description, documentation, and preservation of the genomic diversity of the oceans. Located on the campus of New England Biolabs in Ipswich, MA, OGL is an equal opportunity employer that receives support from the National Science Foundation, the Department of Energy, and the National Institutes of Health.

Please direct all inquiries to: Daniel L. Distel, Ph.D. Executive Director, Ocean Genome Legacy 240 County Rd., Ipswich, MA 01938 careers@oglf.org

<http://www.oglf.org/> —

Job:

Research Assistants - Full and Part Time (Job Codes: OGL-FTRA09 and OGL-PTRA09, posted 06/23/09) The Ocean Genome Legacy Laboratory for Marine Genomic Research (www.oglf.org) seeks research assistants to aid with all aspects of operation of the Ocean

Genome Resource DNA repository and its associated research projects. The successful candidates will have experience and general knowledge of collection management, basic techniques of molecular biology and microbiology (e.g., DNA extraction and handling, gel electrophoresis, PCR amplification, cloning, sterile technique, bacterial cultivation techniques, etc.), and excellent computer and data management skills. Experience and knowledge of protein biochemistry is also desirable. Full- and part-time positions are available immediately.

Applicants should submit a cover letter, resume, list of publications, and contact information for at least three references by email to careers@oglf.org (referencing job code OGL-FTRA09 for full-time or OGL-PTRA09 for part-time in the subject line) or by regular mail to the address below.

Ocean Genome Legacy, Inc. is a publicly supported non-profit research organization dedicated to exploration, description, documentation, and preservation of the genomic diversity of the oceans. Located on the campus of New England Biolabs in Ipswich, MA, OGL is an equal opportunity employer that receives support from the National Science Foundation, the Department of Energy, and the National Institutes of Health.

Please direct all inquiries to: Daniel L. Distel, Ph.D. Executive Director, Ocean Genome Legacy 240 County Rd., Ipswich, MA 01938 careers@oglf.org

<http://www.oglf.org/> —

Job:

Administrative Assistant - Part Time (Job Code: OGL-AA, posted 06/24/09) The Ocean Genome Legacy Laboratory for Marine Genomic Research (www.oglf.org) seeks a part-time administrative assistant to aid in general operations, including editing and formatting an online quarterly newsletter using web forms, summarizing and distributing monthly and quarterly financial reports using QuickBooks and Excel, processing incoming donations and sending out acknowledgements, coordinating shipment and receipt of genomic sample deposits, and assisting with various administrative functions, such as maintaining meeting schedules, entering data, electronic and paper filing, copying, and ordering supplies. The successful candidate will be detail-oriented, accurate, and efficient with a working knowledge of web forms and the ability to navigate the Web, proficiency in MS Office and QuickBooks, a basic understanding of accounting principles, and 1-2 years administrative experience. This position will start at 5-10 hours a week and is available immediately. Applicants should submit a cover

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>

KansasStateU GrassDroughtStress

POSTDOCTORAL OPPORTUNITY AVAILABLE:
Ecological Genomics of Drought Stress in Prairie Grasses, Kansas State University

We have a position available for a post-doctoral research associate to study the ecological genomics of drought stress. The project will include studies of the responses of natural prairie ecosystems to variation in precipitation using the ecologically dominant prairie grass big bluestem as a model. The work is part of a project funded by the USDA Plant Biology Abiotic Stress program. The project will include common garden transplant experiments and genomic approaches to test for the signature of adaptive genetic differentiation among natural populations of big bluestem across the precipitation gradient of the Great Plains.

This specific research assembles investigators with complementary expertise in Plant Ecological Genomics (Johnson www.ksu.edu/johnsonlab, Garrett www.ksu.edu/pdecology), Genomics (Akhunov eakhunov@ksu.edu), Evolutionary Genetics (Morgan <http://www.ksu.edu/morganlab>) and Restoration Ecology (Baer, SIU www.plantbiology.siu.edu/Faculty/Baer/index.html) to elucidate the response and adaptation of prairie grasses to abiotic stresses. This work will take place in the laboratories of Drs. Johnson, Akhunov, and Garrett and in field sites across the Great Plains, with close collaboration with Drs. Morgan and Baer. There will also be opportunities to interact with other researchers in the context of the KSU Ecological Genomics Institute (www.ecogen.ksu.edu).

For this postdoctoral position, we seek candidates with a Ph.D. in the biological sciences with interest in evolutionary and ecological genetics. Preference will be given to individuals with experience in functional genomic approaches, including next-gen sequencing, custom microarray development based on 454 screens, using custom arrays to screen patterns of gene expression among ecotypes in response to drought stress and VIGS techniques. Importantly, applicants should have the interest and willingness to cross disciplines. The successful candidates must be able to design and con-

duct independent experiments. Excellent oral and written communication skills and the ability to work well in a team-based/collaborative research atmosphere are essential.

Applications will begin to be reviewed on Aug 15, and will continue until the position is filled. Start date for the post-doctoral position is Sept 6, 2009. A complete application must consist of:

- 1) A cover letter detailing your qualifications and how they relate to the advertised position.
- 2) A professional resume
- 3) Reprints/preprints of publications
- 4) Names and contact information for three referees

Send a complete application package by e-mail to:

dmerrill@ksu.edu

Complete applications can also be mailed to: Doris Merrill, Program Coordinator Ecological Genomics Institute Division of Biology, Kansas State University 104 Ackert Hall, Manhattan, KS 66506-4901 Phone: (785) 532-3482 Fax: (785) 532-6653

KSU is an Equal Opportunity Employer, and actively seeks diversity among its employees. Background check is required.

dmerrill@ksu.edu dmerrill@ksu.edu

MiddleTennStateU LepidopteraSystematics

Postdoc - molecular systematics of butterflies

Position available immediately (previous postdoc got a permanent job). 18 months of funding available at \$2500/month + benefits.

Middle Tennessee State University Dept. Biology seeks a Postdoctoral Associate to assist with molecular systematics of Pronophilina (Lepidoptera: Nymphalidae: Satyrinae), a diverse neotropical subtribe of montane butterflies (see www.tolweb.org/Pronophilina). Applicants must have Ph. D. in systematics, evolutionary biology or related field, good lab skills and experience in genomic DNA extraction, PCR and sequencing. Entomological background and facility with methods of sequence assembly and phylogenetic analysis are also desirable.

Applicants should submit a CV, a brief statement

of research interests and description of past research experience, PDFs of relevant publications and/or manuscripts, and contact information for two references. Application materials should be submitted as email attachments. Review of applications will begin immediately and continue until a suitable candidate is chosen.

Middle Tennessee State University, in its educational programs and activities involving students and employees, does not discriminate on the basis of race, color, national origin, religion, or sex as required by Titles VI and VII of the Civil Rights Act of 1964, as amended in 1972. Furthermore, MTSU will comply fully with Executive Order 11246 and any other Executive Order(s) amending or superseding such order; Title IX of the Education Amendments of 1972; the Age Discrimination and Employment Act; the Veterans Readjustment Act; and legislation prohibiting discrimination against disabled individuals, Sections 503 and 504 of the Rehabilitation Act of 1973, and the 1990 Americans with Disabilities Act. Students, employees and others who desire information or clarification pertaining to the application of these acts or regulations of them should communicate with the Director of Equal Opportunity and Affirmative Action at (615) 898-2185.

Professor Andrew Brower Department of Biology Middle Tennessee State University Murfreesboro, TN 37132 USA

(615) 898-2064

abrower@mtsu.edu

Andrew Brower <abrower@mtsu.edu>

Montpellier BacterialComparativeGenomics

Postdoc

Postdoc in Bacterial comparative genomics. 12 month contract with IRD (start in september/october 2009), in Montpellier, France at LSTM (Laboratory of tropical and Mediterranean symbioses), in the "Biodiversity and evolution of symbioses" research group. The Postdoc will perform comparative genomics on Bradyrhizobium and Burkholderia genomes by in silico analyses. We seek a bioinformatician/biologist with strong skills with comparative genomics softwares. The applicant must know the MAGE software (MAGnifying GenomE) from Genoscope (www.genoscope.cns.fr/agc/-

mage/wwwpkgdb/MageHome/index.php?webpage=mage). Skills in programming with PERL / java and others languages will be appreciated. The aim of the study is to identify the core genome/ accessory genome in various plant-symbiotic bacteria, and specific adaptations towards their symbiotic abilities. Most of the work will be analyses of genomic data. Gross salary is 1700 euros/month (after taxes; 2150 without taxes). More information on the lab at www.mpl.ird.fr/lstm. Send cv and a letter of application to lionel.moulin@mpl.ird.fr.

Dr Lionel Moulin, Chargé de Recherche IRD Laboratoire des Symbioses Tropicales et Méditerranéennes, TA A-82/J Campus International de Baillarguet, 34398 Montpellier cedex 5, FRANCE Tél: +33 467593763 Fax: +33 467593802 <http://www.mpl.ird.fr/lstm/> lionel.moulin@mpl.ird.fr

NatlUIreland NetworkOfLife

Hi,

There is a post-doc position available in my laboratory at the National University of Ireland, Maynooth, to work on the species concept in prokaryotes and specifically on whether there are meaningful modules in the network of life.

This is a two-year position, funded by Science Foundation Ireland and will be entirely computational. The ideal candidate will have experience working with genomic data, phylogenetic trees and the Network of Life concept. There will be a requirement to develop programs (preferably in Python, but any experience of programming should suffice). Further details of the position, including salary, can be made available on request.

NUI Maynooth is a small university (approx. 7,000 students), situated in a village approximately 25 Km from the centre of Dublin.

Thanks,

James.

Recent relevant publications from the group (<http://bioinf.nuim.ie/pubs.html>):

Haggerty, L.S., Martin, F.J., Fitzpatrick, D.A. and McInerney, J.O. (2009) Gene and Genome Trees Conflict at Many Levels. *Philosophical Transactions of the Royal Society of London: B Series.* 364, 2209-2219

Martin, F.J. and McInerney, J.O. (2009) Recur-

ring cluster and operon assembly for Phenylacetate degradation genes. *BMC Evolutionary Biology* 9:36 doi:10.1186/1471-2148-9-36.

McCann, A., Cotton, J.A. and McInerney, J.O. (2008) The Tree of Genomes: An Empirical Comparison of Genome Phylogeny Reconstruction Methods. *BMC Evolutionary Biology* 8:312.

McInerney, J.O., Cotton, J.A. and Pisani, D. (2008) The Prokaryotic Tree of Life: Past, Present...and Future? *Trends in Ecology and Evolution* 23 (5) 276-281.

McInerney, J.O. and Pisani, D (2007) Genetics: Paradigm for Life. *Science* 318:1390-1391.

– James McInerney, Senior lecturer, Institute for Chemical Biology, NUI Maynooth, Co. Kildare, Ireland. P: +353 1 7083860 F: +353 1 7083845 W: <http://bioinf.nuim.ie/>

NewMexicoStateU SymbiosisEvolution

The Department of Biology at New Mexico State University invites applications for a postdoctoral research associate interested in the evolution and specificity involved in bacterial/animal symbiosis. A Ph.D. in biology, bacterial genetics, or molecular biology is recommended. Experience with bacterial mutagenesis, recombinational cloning, and gap repair are highly desirable. Send a curriculum vitae and contact information for at least three references to: Dr. Michele Nishiguchi, Biology Department MSC 3AF, Box 30001, Las Cruces, NM. 88003. E-mail: nish@nmsu.edu. Screening of applications will begin on August 15th, 2009 and will continue until filled. New Mexico State University is an equal opportunity/affirmative action employer. Offer of employment is contingent upon verification of individual's eligibility for employment in the United States and upon completion of a criminal history check. Requisition # 2009005978 330350 Biology. –

Michele K. Nishiguchi, PhD Professor Department of Biology - MSC 3AF New Mexico State University PO Box 30001 Las Cruces, NM 88003-8001 575-646-3721 (office) 575-646-4123 (lab) 575-646-5665 (FAX) email: nish@nmsu.edu <http://biology-web.nmsu.edu/nish/Nishiguchi.htm> "Michele K. Nishiguchi" <nish@nmsu.edu>

NTNU Trondheim ReefFishColoration

Postdoctor/researcher position on Reef Fish Coloration (NT-43/09)

A 3-year postdoctor/researcher position to investigate coloration in coral reef fishes is available at the Department of Biology, Norwegian University of Science and Technology (NTNU), Trondheim, Norway. The position is related to the project «Coral Reef Fish Coloration: Sexual Selection, Diversity and Speciation», funded by the Research Council of Norway. The project involves field and lab experiments at Lizard Island, GBR, Australia, and comparative work on reef fish coloration based on published material and databases held by the project team. Most of the empirical work will use the damselfish *Neoglyphidodon nigroris* as a model organism. Field work at Lizard Island will typically take place during October-December each of 2009-2011. The project is managed by Trond Amundsen at the NTNU, with collaborators Elisabet Forsgren (NINA, Trondheim), Ivar Folstad (U Tromsø), Alexandra Grutter (U Queensland), Justin Marshall (U Queensland), and Ian Owens (Imperial College).

The postdoctor/researcher will have a main responsibility for the field and lab studies of the project, in collaboration with the manager and project team, and supported by field/lab assistants.

Applicants should hold a PhD in ecology, evolution, behaviour or other relevant subjects, and should have experience from relevant empirical work with animals, and an ability to work independently and as a field team leader. Experience from fish work, and/or work on coral reefs, is a relevant but not required qualification. As the project involves collection of fish and also some field study of the fishes (<10 m depth), applicants need to hold a Divemaster or higher diving certificate in order to meet Australian legal requirements for scientific diving. Ideally, applicants should combine the abovementioned qualifications with knowledge of modern comparative methods. However, this is not an absolute requirement and candidates without a background in comparative work but else well qualified will be considered. Ability to carry out goal-oriented work, ability to deliver, oral and written presentation of research results, and good co-operation abilities will be emphasized.

The postdoctor/researcher will be formally employed by the Faculty of Natural Sciences at the NTNU, and will become a member of the Department of Biology. The Department of Biology has 36 members of faculty (professors and associate professors), 22 research scientists and about 70 PhD students and post docs. The department has research programs in evolutionary biology, population genetics, aquatic and terrestrial ecology, conservation biology and biodiversity, ethology, molecular biology, cell biology, plant and animal physiology, toxicology, aquaculture, and marine biology. There is considerable collaboration between the disciplines. More information about the Department of Biology can be found at: www.ntnu.no/biologi/english. The appointment will be made according to Norwegian guidelines for universities and university colleges and to the general regulations regarding university employees in Norway.

The starting annual salary of the postdoctor/researcher position is NOK 435.500 per year (level 57, according to the government pay-scale for university employees). There is 2 % deduction for superannuation.

Please contact professor Trond Amundsen for further information about the position (tel + 47 918 97 293, email: trond.amundsen@bio.ntnu.no), and in case of questions regarding the application procedure.

Applicants should describe why they want the position and why they are well suited for it. Applications should also include a CV with a complete publication list, 3 selected publications (or manuscripts), documentation of educational background and other relevant experience, and 3 named references (incl. email and phone no.). Please include a brief description of the applicants contribution in cases of multi-authored publications (submitted or listed in the CV) where the applicant is not the first author.

Applications should be submitted electronically through [jobbnorge.no \(https://secure.jobbnorge.no/-visstilling2.aspx?stillid=59273\)](https://secure.jobbnorge.no/-visstilling2.aspx?stillid=59273). CV, recommendations and transcripts of grade certificates and other documents should be attached electronically, preferably as one document. Application deadline: 2 August 2009. Reference number: NT-43/09. Please refer to where you first saw this position.

Trond Amundsen Professor Department of Biology Section for Ecology, Ethology & Evolution Norwegian University of Science and Technology NO 7491 Trondheim Norway Tel +47 918 97 293 Email: trond.amundsen@bio.ntnu.no

Trond Amundsen <trond.amundsen@bio.ntnu.no>

Paris Comparative genomics and metagenomics

Postdoc: Paris.Comparative_genomics_and_metagenomics
 The team "Modélisation des Systèmes Dynamiques Intégrés (UMR CNRS 7138, UPMC, Paris)", located by the Seine river and next to the "Jardin des Plantes", specializes in comparative genomics and comparative metagenomics via the reconstruction of phylogenetic trees and networks. In particular, we study the impact of mobile elements (viruses, plasmids and integrons) on the evolution of prokaryotic genomes (bacteria and archaea), looking at the rules that influence lateral gene transfer between these entities, with a focus on the influence of the environment on gene flow. These questions are hot topics in evolutionary biology and they are highly debated. Molecular data from complete genomes and from environmental DNA projects are both increasingly abundant. Their study opens new avenues to gain original knowledge on the evolutionary processes acting on prokaryotes. At the same time, the classical model of a single evolutionary tree appears too rigid to successfully account for the fact that contemporary bacteria regularly exchange genetic material, even when they are not closely related. As a result, the universal tree model is being replaced by more reticulate models. This major transition must be followed by the development of new methods to detect clusters of genes that share the same phylogenetic history in order to fully study the evolution of prokaryotic genomes. We are offering a postdoctoral position to compare the evolutionary history of genes in the presence of multiple lateral gene transfers, for very large molecular datasets. The methods will aim at (i) clarifying the rules of lateral gene transfer between mobile elements and bacterial genomes and (ii) achieving a systematic identification of the adaptation resulting from lateral gene transfer in the 3 domains of life. To this end, the candidate will benefit from existing datasets comprising (i) hundreds of thousands of genes from mobile elements and of prokaryotic genes, and (ii) thousands of eukaryotic genes. This postdoctoral work (one year to two years, starting in November 2009 at the latest) will be part of a large ongoing international collaboration with well-known specialists of phylogenetic networks (including T. Dagan and W. Martin (Germany), and F.J. Lapointe (Canada)). Gross salary will be at least

2150 euros/month without taxes. The candidate must be a recognized computer scientist (with programming and algorithmic skills), and ideally knowledge in the mathematics of networks, and/or in statistics. A background in molecular evolution will be strongly appreciated. Please, do apply and send your resume to : eric.bapteste@snv.jussieu.fr

Dr. Eric Bapteste Chargé de Recherche CNRS Laboratoire "Modélisation des Systèmes Dynamiques Intégrés" UMR CNRS 7138 Université Pierre et Marie Curie Paris, 75005 France Tél: +33 44 27 21 64 Fax: +33 44 27 58 01 Keywords : Network, Lateral gene transfer, Adaptation, Evolution, Large molecular datasets

Eric.Bapteste@DAL.CA Eric.Bapteste@DAL.CA

PennStateU HumanPopulationGenetics

- Postdoctoral position in comparative evolutionary genomics/human population genomics/statistical genomics at Penn State -

A postdoctoral position is available immediately in the laboratory of Kateryna Makova (<http://www.bx.psu.edu/makova.lab/>) at Penn State. The current focus of the lab is on deciphering molecular mechanisms of different mutations via whole-genome comparisons and on sex chromosome evolution.

As a successful candidate, you will come to our lab with relevant bioinformatics expertise, including some combination of programming experience, previous use of the R statistical package, and working knowledge of molecular evolution or population genetics. Once hired, you will analyze next-generation sequencing data sets and vertebrate genome alignments, and perform statistical and evolutionary modeling. You will work in close collaboration with statisticians to develop computational models, with wet-lab biologists to validate model predictions, and with the GALAXY team (<http://g2.bx.psu.edu>) to implement our computational tools. You will be joining a dynamic group with an established record (<http://www.bx.psu.edu/makova.lab/Publications.php>). We are part of the Center for Comparative Genomics and Bioinformatics (<http://www.bx.psu.edu/>) and of the newly established Center for Medical Genomics at Penn State. Penn State is a vibrant scientific community with particular strengths in computational genomics and molecular

evolution.

The starting date is flexible, with an earlier date preferred. Due to the nature of our projects, we would prefer a candidate who can commit for at least two years, but an extension of a contract for up to four years is possible.

Interested applicants should send pdfs with CV, a statement of research interests, and contact information of three references to kmakova@bx.psu.edu, indicating \$B!H(Bpostdoctoral position\$B!I(B in the subject line.

Kateryna Makova

Associate Professor Center for Comparative Genomics and Bioinformatics Department of Biology 305 Wartik Lab Penn State University University Park, PA 16802 Tel: 814-863-1619 Fax: 814-865-9131 E-mail: kmakova@bx.psu.edu Web: http://www.bx.psu.edu/makova_lab/ Kateryna Makova <kmakova@bx.psu.edu>

Portugal PopulationGenetics

POSTDOCTORAL PROPOSAL Selection of candidates for a grant proposal to submit to the Portuguese Foundation for Science and Technology.

We are inviting applicants for a Postdoctoral grant proposal to be submitted to the Portuguese Foundation for Science and Technology (FCT) in populations genetics and modeling of propagule transport in surface waters. The successful applicant will work with teams from the Centro de Ciências do Mar (CCMAR - <http://ccmar.ualg.pt/>), at the University of the Algarve (<http://www.ualg.pt>) and from the Eco-Ethology Research Unit (<http://www.ispa.pt/ui/uie/>) at ISPA, Lisbon, Portugal.

We are looking for a scientist with a strong research focus at the interface of biology, physics and informatics, with experience in both populations genetics and modeling of propagule transport in surface waters in particular. Applicants should hold a Ph.D. in biology, bioinformatics or in another relevant subject and have a strong publication record in the field. Expertise in the following areas is expected: modeling approaches, population genetics and multi-platform software programming. Very good written and oral communication skills in English and the interest in joining a multidisciplinary team are required. Participation in university teaching and an active role in the acquisition of external

funds is highly desired.

The position is available for 3 years from January 2010 and is open to all nationalities. The researcher will receive a salary of 1495 euros/ month. Applications should be submitted before 15th August 2009 to Rita Castilho (rcastil@ualg.pt) with the subject: POSTDOC-PROPAGULE. Applicants should send a cover 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.

The Biogeographical Evolution and Ecology group of CCMAR-CIMAR LA, and the Eco-Ethology Research Unit of ISPA, are currently interested in research that couples population genetics and modeling of larval transport in surface waters. This coupling stems from the growing need to integrate patterns of larval dispersal in research on the phylogeography and historical demography of marine organisms.

CCMAR is located on the Gambelas campus, 4km from Faro, the capital city of the Algarve and close to Faro International Airport (FAO) (map). ISPA is located in the right margin of the river Tagus.

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

Prof. Vítor Almada ISPA - Eco-Ethology Research Unit Rua Jardim do Tabaco, 34 1149-041 Lisboa Portugal Phone: + 351 21 8811226 Fax: + 351 21 8860954 E-mail: valmada@ispa.pt

Dr. Rita Castilho BEE - Center for Marine Sciences University of Algarve Campus de Gambelas 8005-139 Faro Portugal Phone: + 351 918397282 Fax: + 351 289800069 E-mail: rcastil@ualg.pt

Rita Castilho <rcastil@ualg.pt>

RIKEN ComparativeGenomics

One Researcher or one postdoctoral Researcher Position available in Comparative Genomics (Kousuke Hanada), Gene Discovery Research Group, RIKEN Plant Sciences Center, Japan

Area of Research The research program contributes to RIKEN Plant Science Center activities. A successful applicant will belong to one of programs which is Comparative and evolutionary genomics based on bioinformatics. This program performs the development

of exhaustive search method to identify novel genes by multiple genome data and the functionalization of duplicate genes in plant. For more information, <http://labs.psc.riken.jp/gdrg/English/index.html> Job Description A successful applicant will take part in a project which is to find novel functional genes in *A. thaliana* and *O. sativa*. The project succeeded to identify several thousands of small open reading frames (sORFs) with coding potential in intergenic regions of *A. thaliana* and *O. sativa* (Hanada et al., Genome Research 2007). To examine functionality of each sORF, experimental collaborators will perform the microarray and over-expression analysis for newly identified sORFs. Main job of the applicant is to generate the database of sORF and examine its evolutionary origin by comparative genomics approach. The ideal candidate will have a strong background and experience of genome analysis by Python, R, Perl, C++ or Java.

Contract Conditions One-year, full-time contract, renewable annually by evaluation until 31st of March 2012. Salaries are determined on an annual basis subject to the applicants' experience and performance. Commuting and housing allowances will be paid, and social security premiums will be deducted. Holidays: Saturdays and Sundays, national holidays, end-of-year holidays (Dec. 29-Jan. 3), and RIKEN Founding Day.

Application and required documentation All other provisions will conform to RIKEN rules and regulations. Application and required documentation (1) Curriculum vitae (with photo and e-mail address) (2) List of publications and other research achievements (3) Brief description of previous research and future research plans (4) Contact information of at least two reference persons (5) A recommendation letter from an immediate supervisor (or if impossible, from a third person) The recommendation letters should be addressed to "Director of the Plant Science Center." (6) Certificate of graduation or copy of Ph.D. diploma **INote:** Provided documents are strictly protected under the RIKEN Privacy Policy and will be used only for the purpose of applicant screening. Personal information will not be disclosed, transferred or loaned to a third party under any circumstances without legitimate reason.

Selection Process Applicants who pass the first document screening will be interviewed. Applications will be considered until the position is filled. Start of Employment August 1, 2009 or later.

Inquiry/Contact address Kousuke Hanada Gene Discovery Group, Plant Sciences Center (PSC) RIKEN (The Institute of Physical and Chemical Research) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, 230-0045 JAPAN Tel: +81-45-503-9575 Fax: +81-45-503-9591

e-mail: kohanada@psc.riken.jp

Send application documents to Sachiko Owada Yokohama Research Promotion Division RIKEN (The Institute of Physical and Chemical Research) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, 230-0045 JAPAN e-mail sowada@riken.jp

RutgersU Statistical Population Genetics

Postdoctoral Position in Statistical Population Genetics at Rutgers University

A postdoctoral position in population genetics is available in the lab of Jody Hey, at Rutgers University. The research will involve adapting coalescent models to problems in population divergence, as well as developing statistical methods for fitting divergence models to data sets. These methods will be used to study problems in the divergence of human populations, as well as in other systems including Malawi cichlids and Chimpanzees.

This position is NSF funded for three years.

Candidates with research experience in any the following will be considered:

- Population Genetics Theory - Coalescent modeling
- The use of stochastic methods for likelihood and Bayesian computation (e.g. MCMC, Gibbs Sampling etc)
- Statistical Phylogeography - Divergence Population Genetics

In addition candidates should have experience in programming using C/C++ or a similar low-level language.

The position can begin as early as Fall, 2009.

Applications should email a CV and any other relevant information to Jody Hey

hey@biology.rutgers.edu

The Hey lab is on the Busch Campus of Rutgers University. This is in central New Jersey, just outside of the city of New Brunswick - a small cosmopolitan city within commuting distance (by car or train) of Manhattan.

Jody Hey Professor, Department of Genetics Rutgers University Nelson Biological Labs (rm B326) 604 Allison Rd. Piscataway, NJ 08854-8082

732-445-5272 fax 732-445-5870 hey@biology.rutgers.edu
<http://lifesci.rutgers.edu/~heylab/>
 Hey@Biology.Rutgers.Edu

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/canghai.htm>),

Berndt van Rensburg (website: <http://www.up.ac.za/zoology/staff.php?person=164>).

Berndt Janse van Rensburg
 <bjvanrensburg@zoology.up.ac.za>

StonyBrook 3 EvolutionaryGenetics

Three Postdoctoral Positions in Evolutionary Genetics at Stony Brook

NSF and NIH-supported postdoctoral positions are available in the laboratory of Walt Eanes at Stony Brook University. The first position is to work on the physiological genetics of insect flight metabolism using *Drosophila melanogaster* as a model (see Eanes et al. 2006. Flux control and excess capacity in the enzymes of glycolysis and their relationship to flight metabolism in *Drosophila melanogaster*. Proc. Natl. Acad. Sci. USA 103: 19413-19418). The second position (a collaboration with Pal Schmidt at Penn) will study the population and functional genetics of the couch potato gene, diapause and life history variation in *D. melanogaster* (see Schmidt et al. 2008. An amino acid polymorphism in the couch potato gene forms the basis for climatic adaptation in *Drosophila melanogaster*. Proc. Natl. Acad. Sci. U.S.A. 105:16207-16211.). The third position, in collaboration with the lab of John True, will study the role that the major central metabolic and dopamine pathways play in the mechanism of nutrient or energy-state sensing and life history adaptation in *Drosophila*.

All three positions are available this fall, and there is flexibility in start dates. All three have an initial term of two years with the possibility of renewal.

Successful applicants should possess a Ph.D. and

could possess skills in any of several areas including *Drosophila* genetics, molecular evolution, and population, or physiological genetics.

If interested please contact Walt Eanes, Department of Ecology and Evolution, Stony Brook University, Stony Brook, NY 11794 or e-mail walter@life.bio.sunysb.edu.

Walter F. Eanes Professor Dept. of Ecology and Evolution Stony Brook University Stony Brook, New York 11794

weanes@notes.cc.sunysb.edu

Tours France InsectVirusEvolution

Post-doc position available (2 years) at the Insect Biology Research Institute funded by an ANR grant (Agence nationale pour la Recherche) from october 2009.

Please send detailed CV, publication list, summary of PhD research project, technics and people to contact for references

Contact : Jean-Michel DREZEN

CNRS Research Director

drezen@univ-tours.fr

tél: 33 (0)2 47 36 73 57

Institut de Recherche sur la Biologie de l'Insecte, UMR CNRS 6035

Faculté des Sciences, Parc de Grandmont

37200 Tours

Project :

Parasitic wasps from the braconid family and their lepidopteran hosts have antagonistic relationships : wasps introduce their eggs in the caterpillar together with virus particles to alter host immunity and development. The genes encoding virus particle components have recently been identified in the wasp genome in collaboration with the National Center for Sequencing- Genoscope (Bézier et al. Science 2009). These genes originated from a nudivirus (nudiviruses are related to baculoviruses) whose genome was captured by an ancestor wasp that lived 100 million years ago. Since this integration event the nudivirus genes have lost the ability to be encapsidated in virus particles. The particles are used to deliver wasp genes into the lepidopteran host to manipulate host physiology. The post-doctoral research project aims at drawing a more complete pic-

ture of the viral ancestor by isolating and sequencing the genomic regions containing nudivirus genes from wasps belonging to phylogenetically distant braconid subfamilies. A second part of the project will analyze gall-forming wasps of oak and roses, these species form a clade suggesting the ability to produce complex and species-specific galls may have been acquired by a unique evolutionary event. Sequencing of cDNAs from ovaries, venom glands and salivary glands will allow the identification of genes potentially involved in gall induction and eventually of viral cDNAs (collaboration with the Genoscope).

Candidat : Evolutionary Biologist having a molecular biology technical background, good communication skills are also required since the project involves national and international collaborations (Switzerland, Italy, Canada, USA).

Localisation : The laboratory is very well equipped and is situated in a new building on a very pleasant wooded campus close to the city centre. Tours is only one hour from Paris by TGV train, in the Loire Valley region, listed as a world heritage site by UNESCO.

Jean-Michel DREZEN Directeur de Recherche CNRS tél: 33 (0)2 47 36 73 57 Institut de Recherche sur la Biologie de l'Insecte, UMR CNRS 6035 Faculté des Sciences, Parc de Grandmont 37200 Tours

TulaneU PlantAnimalInteractions 2

Post-Doctoral Position: Molecular Evolutionary Ecology

A two-year postdoctoral position is available in the Karubian lab in the Department of Ecology & Evolutionary Biology at Tulane University. Research in the lab incorporates evolution, ecology and animal behavior, and applicants with relevant laboratory experience are broadly encouraged to apply. The primary line of research tests how seed dispersal by rainforest birds affects gene flow in plants, with the goal of linking variation in disperser behavior to genetic consequences for the plant. The study system is a mutualism between the endangered Long-wattled Umbrellabird (*Cephalopterus penduliger*) and the canopy palm *Oenocarpus bataua* in northwest Ecuador. The successful candidate will expand this work to assess gene flow via seed and pollen movement in fragmented and continuous habitat. Independent research that complements this central objective is encouraged, and

additional research opportunities related to avian behavior and phylogeography also exist within the lab.

Preference will be given to candidates with extensive experience in laboratory methods including sample preparation, microsatellite screening, and sequence analysis in plants and/or birds. GIS and remote sensing skills are also a plus. A start date of January 2010 is preferred. Initial appointment will be for one year, with continuation for an additional year dependent upon performance. Salary will be commensurate with experience and qualifications. Send via email attachment a letter of application, curriculum vitae, statement of research interests, and names and addresses of three references to Dr. Jordan Karubian at jk@tulane.edu. Tulane University is an Affirmative Action/Equal Employment Opportunity/ADA Employer. Women and minorities are encouraged to apply.

Jordan Karubian <JORDANK@ucla.edu>

– Douglas G. Scofield, Ph.D. Ecology & Evolutionary Biology University of California, Los Angeles
dgscofield@ucla.edu douglasgscofield@gmail.com

Jordan Karubian <jordank@ucla.edu>

TulaneU PlantGeneFlow

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Jordan Karubian <JORDANK@ucla.edu>

UCambridge SkeletalMammalEvolution

Research Associate à Mammalian Skeletodental Development The Mammal Evolution and Morphology Group LoT applies* Grade 7, Salary range: £27,183 - £35,469 per annum

We invite applications for a postdoctoral Research Associate to work in the Department of Zoology, University of Cambridge, UK, on the cranioskeletal ontogeny of placental mammals, focusing on afrotherians and xenarthrans. We seek to test the hypothesis that these two major placental mammal clades differ from other mammals in terms of their patterns of skeletal ossification and dental development, both pre- and post-natally. The project, funded by the Leverhulme Trust, will ideally start in October 2009.

The candidate should have a PhD (or equivalent) in evolutionary biology, be well-acquainted with vertebrate cranioskeletal anatomy, development of the skeleton and dentition, concepts in heterochrony, and research in a collections-based environment. Experience with noninvasive imaging technology (e.g., microCT) is highly desirable.

*The appointment will be for a period of up two years in the first instance.

Informal email enquiries may be made to Dr Robert Asher using the email address posted at his website: <http://people.pwf.cam.ac.uk/rja58/>
To apply see: <http://www.zoo.cam.ac.uk/zoone/-administration/vacancy.html> Closing date 17 August

2009. Interviews are scheduled to take place in the first week in September 2009.

UCLouvain ConservationGenetics

POSTDOC GRANT APPLICATION IN CONSERVATION GENETICS

As part of an ongoing project funded by the Belgian National Fund for Scientific Research (FNRS), and realized by three Belgian labs (located in Univ. Mons-Hainaut, UCLouvain-la-Neuve, and National Botanic Garden), it is possible for non-Belgian young postdoc researchers to APPLY for a three-year FNRS postdoc grant. The topic of the project is “Key factors for the persistence of fragmented populations of rare or declining plant species and their preferential pollinators: pollination patterns, inbreeding depression, gene flow and available resources”. Four insect-pollinated plant species from fens are studied: *Comarum palustre*, *Menyanthes trifoliata*, *Vaccinium oxycoccos* and *V. uliginosum*, as well as the diversity and efficiency of their pollinators. The study sites are located in two regions in southern Belgium (Upper Ardenne and Lorraine). They are protected areas (EU Natura 2000 zones and natural reserves) and ecologically managed fens. This project is realized in collaboration with the local nature managers and aims to contribute to the long-term preservation of viable populations of fen species in these highly threatened habitats.

We are looking for a plant population geneticist, who will investigate population structure, outcrossing rates and realized pollen flow using DNA microsatellite markers. Therefore, training and experience in development and use of microsatellite markers and in genetic data analysis is required; experience in spatial or landscape analyses would be an advantage. Being able to work within a research team including PhD students and international postdoc(s) is very important. The candidate will be based at the National Botanic Garden of Belgium (Meise; Olivier Raspe, Fabienne Van Rossum; see <http://www.br.fgov.be/-RESEARCH/PROJECTS/floraofbelgium.php>).

The grant is for a full-time position, salary of 37000 euros/year, which represents a net monthly salary of roughly 1900 euros, with social security cover.

IMPORTANT: to be qualified to apply to this grant, the candidate must have obtained his /her PhD after 1 January 2004 (= max. 6 years at 1 January 2010),

have a good CV (several publications in ecological, conservation or evolutionary journals) and did not stay in Belgium for more than 24 months during the last 3 years.

If you are interested, please send an e-mail and attach a cover letter outlining your interest and motivation to join us, along with your curriculum vitae (including all obtained diplomas, with exact titles, dates, number of years of study, mentions, and the name of issuing university, a publication list, and contact information for two reference scientists) as a separate document, to Olivier Raspe (raspe@br.fgov.be) BEFORE 31 AUGUST 2008. The selected candidate will be informed during the second week of September. The deadline of the application to the FNRS grant (done by the promoter of the project) is 15 September. IF GRANTED, the starting date is 1 January 2010.

Best regards,

Olivier Raspe

– Dr. Olivier Raspé

NATIONAL BOTANIC GARDEN OF BELGIUM
Domein van Bouchout B-1860 Meise Belgium

Tel: +32(0)2 260.09.37 Fax: +32(0)2 260.09.45

e-mail: raspe@br.fgov.be

Belgian Journal of Botany available online at
<http://www.ingentaconnect.com/content/rbsb/bjb>
raspe@br.fgov.be raspe@br.fgov.be

UofArizona BehavioralEvolution

POSTDOCTORAL POSITION IN BEE LEARNING

POSITION AVAILABLE: Postdoctoral opportunity studying bee learning and foraging behavior in relation to floral complexity with Dan Papaj, Anna Dornhaus, and Anne Leonard at the University of Arizona in Tucson, Arizona.

PROJECT DESCRIPTION: The goal of this NSF-funded project is to understand why flowers use complex stimuli in multiple sensory modalities to signal to pollinators. Bumblebees will be used as a model system in assays that manipulate the complexity of floral stimuli and quantify bee learning and floral choice. Special emphasis will be given to analysis of speed-accuracy tradeoffs with respect to predictions derived from eco-

nomic and neural decision-making theory.

QUALIFICATIONS: Ph.D. in animal behavior or allied field. Training in the area of animal learning is preferred, but not required. Ability to think independently and well developed skills in oral and written communication are essential.

START DATE: As early as September 1st, but negotiable. Starting salary will be commensurate with experience; the position includes medical insurance and benefits. The initial appointment will be for one year, with funding available for two additional years, contingent upon satisfactory progress.

ACADEMIC SETTING: The University of Arizona has strength in ecology and evolutionary biology, animal behavior, cognitive science, neurobiology, and entomology. It is particularly well represented in insect science across a variety of disciplines.

DAILY LIFE: Tucson, Arizona is known for its cultural diversity, Southwest lifestyle, and close proximity to natural areas of biological and geological significance. The distinctive fauna and flora of the Sonoran desert make the region especially appealing to biologists.

For inquiries or to apply, please email Dan Papaj (papaj@email.arizona.edu <<mailto:papaj@email.arizona.edu>>). Applications should include: (1) cover letter indicating relevant experience and interests, and possible starting date; (2) CV; (3) publication reprints or preprints in electronic form and; (4) names and contact information for three references.

For more information on labs and research programs, please visit the following links:

Dan Papaj, <http://www.eebweb.arizona.edu/faculty/papaj> Anna Dornhaus, <http://www.eebweb.arizona.edu/faculty/dornhaus> Anne Leonard, <http://cis.arl.arizona.edu/PERT/people/Leonard/index.htm>

Daniel R. Papaj Professor and Associate Head Department of Ecology & Evolutionary Biology University of Arizona Tucson, AZ 85721

papaj@email.arizona.edu Office: 520-621-8988 Fax: 520-621-9190

papaj@email.arizona.edu papaj@email.arizona.edu

UOslo EvolutionaryBiol

Post-Doctoral Research Fellowship in Paleobiology/ Macroevolution/ Macroecology/ Statistics/ Modelling

Ref. No: 2009/6996 Published Apr 29, 2009

ONE POSITION AS POST-DOCTORAL RESEARCH FELLOWSHIP in paleobiology / macroevolution / macroecology / statistics / modelling

is available at The Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo. The appointment is for two years with the possibility of extension and is funded by the Norwegian Research Council.

Start date September 1, 2009

We seek a highly motivated postdoctoral research fellow to contribute to current paleobiological research projects running at our centre (macroevolutionary dynamics, occupancy modelling using fossil occurrence data) and to develop independent project(s) pertaining to understanding long-term evolutionary patterns and processes as seen in the fossil record. The successful candidate will be strongly independent but simultaneously an active contributor to team work carried out with scientists from disciplines such as population ecology, geology, and mathematics. We seek candidates with expertise in two or more of the following areas: paleobiology / macroevolution / macroecology / statistics / mathematical modelling.

The CEES is a national centre of excellence for integrative biological research and is well-funded. It provides a stimulating research environment with many young international and Norwegian scientists working on a variety of theoretical and empirical topics within ecology, evolution, population genetics, genomics, phylogenetics, molecular biology, and statistical methodology. The CEES is chaired by Nils Chr. Stenseth and currently employs 20 faculty, 43 postdocs/researchers, 36 PhD students and 36 MSc students.

Information about the centre can be found at: <http://www.cees.uio.no/> Please contact Nils Christian Stenseth or Lee Hsiang Liow for more details on the project.

Applicants must hold a degree equivalent to a Norwegian PhD/doctoral degree. The main purpose of our

post-doctoral research fellowships is to qualify successful candidates for top academic positions within their disciplines. The position is available from 1 September 2009 (negotiable) for a period of two years with the possibility of extension.

Applicants should submit i) a cover letter including a statement of interest, summarizing the applicants scientific work and interests and describing how she/he fits the description of the person we seek and how she/he may fit in the CEES general setting, ii) a CV including a list of published and unpublished works, iii) four set of copies of certificates, iv) and copies of at most five representative publications.

Alternatively the application may also be submitted by e-mail to apply-to@matnat.uio.no, The mail must contain all necessary documents as pdf-files. Applicants may be called in for an interview.

Applications should be addressed to the Faculty of Mathematics and Natural Sciences, (marked with the REF:NR. 2009/6996), Attn.: Senior Executive Officer Bente Schjoldager, P.O.Box 1032, 0315 OSLO, NORWAY.

Please also refer to the regulations pertaining to the conditions of employment for post-doctoral fellowship positions: <http://www.matnat.uio.no/-/internt/administrasjonen/personal/Forskriver-phd-postdoc-eng.pdf> The University of Oslo is an equal opportunity employer and seeks in particular to increase its number of female scientists. Women are therefore particularly encouraged to apply.

The University of Oslo has an agreement for all employees aiming to secure rights to research results.

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Lee Hsiang Liow, Ph.D Centre for Ecological and Evolutionary Synthesis (CEES) Dept. of Biology, University of Oslo P.O. Box 1066 Blindern 0316 Oslo Norway phone: +47 22855078 email: l.h.liow@bio.uio.no

<http://www.cees.uio.no/about/staff/homepage/-lee-hsiang-liow.html> Lee Hsiang Liow
<l.h.liow@bio.uio.no>

UParisSud AlimentarySelection

Detection of multilocus selection in genes involved in alimentary processes.

We propose a postdoctoral position financed by the

French Agence Nationale de la Recherche, project NUTGENEVOL. This position is opened for two years, with a beginning between September and November 2009. The NUTGENEVOL project consists in studying the selection pressures that occurred on genes involved in alimentary processes and associated with type II diabetes.

Before the major Neolithic transition (~10.000 yBP), our hunter-gatherer ancestors certainly had a meat-based diet, poor in carbohydrates and rich in protein. Therefore, genes favouring insulin resistance and gluconeogenesis were selected for, in order to constantly maintain sufficient level of glucose in the blood. These potentially thrifty genes may now be detrimental in urbanized societies, because under the present high carbohydrate diet, insulin resistance and gluconeogenesis may lead to metabolic disorders such as type II diabetes, obesity, and hypertension. To detect the selective pressures that occurred on these genes, we have compared the genetic diversity of pastoralist and agriculturist populations in Central Asia, for which differences in diet may have lead to different selective pressures on such genes (current project of a PhD student, L. Segurel). Classical single-locus test have been performed by this student for 11 candidate genes.

However, all the traits involved in this study are polygenic traits involved in gene networks, and a multilocus approach would seem especially appropriate. Therefore, the postdoctoral position within this project would consist in developing methods for jointly analysing combination of SNP in different genes, as obtained in Central Asia but also from public databases as HAPMAP, in order to detect multilocus signals of selection. These methods will be applied to both simulated and real data, the simulated data being produced by a software developed by another PhD student (J.-T. Brandenburg), but to which the postdoctoral fellow may also contribute. This software will aim to simulate as accurately as possible the evolution of genes involved in this network.

Another aspect of the postdoctoral position will consist in analysing finely the position and level of involvement of each gene in the network, in order to test whether the position in the network could influence the level of selection occurring on these genes. A particular emphasis will be put on studying the level of pleiotropy of these genes, as selective pressures may differ for genes involved in one vs. several different functions. This research on gene networks will be mostly performed through searches in public databases.

The ideal candidate for this postdoctoral position should have solid knowledge in population genetics,

bioinformatics, statistics, and use of databases.

This project is a joint collaboration between the laboratories Ecologie, Systématique et Evolution located at the Université de Paris-Sud in Orsay near Paris and Eco-Anthropology located at the National Museum of Natural History in Paris. The postdoctoral fellow will be based in the first laboratory but with frequent interactions with the other laboratory (team of Evelyne Heyer). Salary should be around 1900 euros per month. Interested candidates should send their application, preferentially by email, to Frédéric Austerlitz (see coordinates below). Please include a CV, a brief letter explaining your motivations and the coordinates of two or three potential references. Applications should be sent before July 31st, 2009. Please also do not hesitate to ask for further details at this address.

Frédéric Austerlitz Laboratoire Ecologie, Systématique et Evolution UMR CNRS/Université Paris Sud/AgroParisTech 8079 Université Paris-Sud, Bâtiment 360 F-91405 Orsay cedex, France Tel : +33 1 69 15 77 20 / Fax : +33 1 69 15 46 97 frederic.austerlitz@u-psud.fr

– Frederic Austerlitz

Charge de Recherche CNRS / CNRS researcher Laboratoire Ecologie, Systematique et Evolution UMR CNRS/Universite Paris Sud/AgroParisTech 8079 Université Paris-Sud, Batiment 360 F-91405 Orsay cedex FRANCE tel: + 33 1 69 15 77 20 / fax: + 33 1 69 15 46 97 webpage: http://www.ese.u-psud.fr/pages_perso/spip.php?article26 frederic.austerlitz@u-psud.fr frederic.austerlitz@u-psud.fr

UPenn Microbe Evolution

Post Doc Department of Biology, University of Pennsylvania

A three-year postdoctoral position is available in the group of Dustin Brisson at the University of Pennsylvania to study evolution of infectious microbes. The main focus of the projects involves the bacterial cause of Lyme disease, *Borrelia burgdorferi*. The major aim of the projects concentrates on molecular evolution and immune evasion at the genetic and systemic level. All projects in the lab intellectually integrate multiple scales of biological complexity (i.e. molecular-level, organism-level, and population-level) potentially using laboratory, field, and computational studies.

The positions require highly motivated, enthusiastic, and enquiring individuals with strong backgrounds in evolutionary biology and statistical analysis. Strong molecular genetic skills are highly advantageous. Quantitative skills are essential.

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 January 2010. Starting dates are flexible and I will wait for outstanding candidates. Salary is commensurate with experience based on the NIH guidelines.

Informal enquiries and formal applications (curriculum vitae, a 1-2 page statement of research interests, and two letters of reference (by email if possible)), 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

UPennsylvania TheoPopGenetics

POSTDOCTORAL FELLOWSHIP, U. Penn

A postdoctoral fellowship (2 years) is available in the mathematical biology group of Dr. Joshua B. Plotkin at the University of Pennsylvania (<http://mathbio.sas.upenn.edu/>).

The specific research project is flexible and can be tailored to the interests of the individual, but it will fall under the broad purview of evolutionary and ecological theory. Areas of interest in the Plotkin lab include theoretical population genetics, the evolutionary ecology of viral populations, the evolution of robustness and adaptability, and the evolution of language and social norms.

Requirements for the position include: a proven record of self-motivated research; a PhD in mathematics, statistics, physics, biology or related area; excellent communication skills. The ideal candidate should also be familiar with scientific programming.

The postdoctoral fellowship provides a competitive annual stipend (minimum \$38,000) plus benefits and health insurance. Start date and term are negotiable. Applications are welcome from candidates of any nationality, and will be reviewed starting August 15, 2009.

The Penn Genome Frontiers Institute offers an outstanding intellectual environment. Research at the Institute addresses basic questions in biology through genomic, computational, and modeling approaches. Collaborations among research groups and across the broader Penn community are common. The Institute is housed in the newly constructed Lynch research building.

Applicants are encouraged to email a statement of research interests, CV, and contact details for three references to [jplotkin \(at\) sas.upenn.edu](mailto:jplotkin@sas.upenn.edu). Informal inquiries are also welcomed.

Joshua B. Plotkin Martin Meyerson Assistant Professor of Interdisciplinary Studies Department of Biology University of Pennsylvania <http://mathbio.sas.upenn.edu/> jplotkin@sas.upenn.edu

URhodeIsland ShellfishGenomics

Postdoctoral Fellowship in Oyster Genomics

The University of Rhode Island (www.uri.edu) is seeking a postdoctoral fellow to participate in a USDA funded project involving the use of high-throughput sequencing to identify novel molecules involved in oyster immunity.

Applicants must have a PhD in biology, molecular biology, bioinformatics, or related fields. Experience in the analysis of high-throughput sequencing data, sequence variation, annotation, or functional genomics (microarray, QPCR) is preferred, as well as experience in shellfish biology. Applicants should also have excellent communication skills and be able to work in a team environment.

This is a 20 month position at a competitive salary. Applicants should include submitted in the form of a covering letter and resumé to the address below, and should include the e-mail address of three people willing to act as referees. Review of applications will begin September 1st.

For further information or to submit an application please contact: Dr. Marta Gómez-Chiarri, University

of Rhode Island, 169 CBLS, 120 Flagg Road, Kingston, RI 02835, USA. Telephone: +1-401-874-2917, email: gomezchi@uri.edu

clane@mail.uri.edu clane@mail.uri.edu

UUppsala PlantGenomics

Post-doc in plant genomics at Uppsala University

One Post doc position is available at the Department of Evolutionary Functional Genomics at Uppsala University starting summer/autumn 2009. The department is part of the Evolutionary Biology Centre, EBC. A major focus of the department is the genetic basis of plant adaptation, combining information on gene function from model organisms with studies of variation in adaptive traits in different species. The aim is understand the mechanisms behind populations and species divergence. Our strategy is to integrate traditional ecological and phylogeographic studies with genomics and population genetics, at both theoretical and experimental levels. For more information: <http://www.genetik.uu.se/>

The successful applicant will take part in a project on the genetics of quantitative traits in *Salix* species. A major focus will be on association mapping in recently established mapping populations, but will also include comparative population genomics of *Salix* and *Populus*. The work will include SNP discovery and generation of sequence polymorphism data using next generation sequencing, SNP genotyping, generation of phenotypic data, and data analysis (association mapping and population genetics).

The project is a collaboration between Uppsala University, the Swedish Agricultural University (SLU), and Rothamsted Research (UK). The work will mainly be conducted at the Evolutionary Biology Centre, but partly also at SLU as the project is run in close collaboration with groups at SLU in Uppsala.

We are looking for an applicant with a strong interest in population and evolutionary genetics. The applicants PhD degree must have been obtained no more than three years prior to the application date. A PhD in molecular biology, genomics, genetics, or a related subject is required and experience in molecular genetics (for example Sanger and New Generation Sequencing), bioinformatics and statistics is an advantage.

The application should include curriculum vitae, degree certificate, a copy of the PhD thesis and other publi-

cations, contact information of at least two reference persons, a short description of the applicant and his / her experience and interests.

For further information contact: Ulf Lagercrantz, +46 18 471 64 18 Ulf.Lagercrantz@ebc.uu.se

Please send your application to: Registrar's Office, UFV-PA 2009/1167, Uppsala University, Box 256, 751 05 Uppsala, e-mail registrator@uu.se or fax +46 18-471 2000 no later than July 9, 2009. If the application is sent by e-mail or fax the original papers should be sent to the Registrar within a week of the application deadline.

Ulf Lagercrantz Dept. of Evolutionary Functional Genomics Evolutionary Biology Centre Uppsala University Norbyv. 18D SE-752 36 Uppsala Sweden T: 46 18 471 6418 F: 46 18 471 6457 New email: ulf.lagercrantz@ebc.uu.se

UZurich ComparativeFunctionalGenomics

Postdoctoral position available in Comparative Functional Genomics in the Zoological Museum at the University of Zurich in Switzerland

The research group in Evolutionary Biology and Biodiversity led by Professor Tony Wilson in the Zoological Museum at the University of Zurich (<http://www.zm.uzh.ch/agwilson/>) is seeking a postdoctoral associate for a position in comparative functional genomics. This position is funded for 1.5 years, beginning in September 2009, with a yearly salary of ca. 80,000 Swiss Francs (\$75,000US).

The postdoctoral associate will work on a project which is using next-generation sequencing technologies to study the development and elaboration of a novel reproductive trait, male pregnancy, in syngnathid fishes (BioEssays 29: 884-896). Seahorse and pipefish males have reproductive structures for brooding developing embryos, but the complexity of these structures varies across the group, from the simple ventral attachment of eggs in some species of pipefish to the fully enclosed pouch of the seahorse, in which males aerate, osmoregulate and provision embryos during their development (Evolution 57: 1374-1386). The high degree of reproductive variation in this group offers exceptional opportunities to study the genetic regulation of male pregnancy in a comparative evolutionary framework.

The candidate will develop a custom Agilent microarray based on a 454 screen of the seahorse transcriptome and will use this array to screen patterns of gene expression in a set of syngnathid species that differ in the complexity of their brooding structures. By comparing patterns of gene expression across species, we aim to clarify how changes in the spatial and temporal expression of genes have paralleled the development of the morphological, physiological and hormonal traits that characterize the most complex forms of male pregnancy in this group.

The ideal candidate will have experience in functional genomics methodologies and familiarity with microarray development and analysis in non-model organisms. Bioinformatics experience would be an asset. Interested candidates should submit a Curriculum vitae and statement of research interests, along with a list of three references, by email or post to Dr. Wilson (tony.wilson@zm.uzh.ch) before August 1, 2009.

Tony Wilson Assistant Professor, Evolution and Biodiversity Zoological Museum University of Zurich Room Y44J55 Winterthurerstrasse 190 CH 8057 Zurich Switzerland Tel: 41 44 635 4790 Fax: 41 44 635 4780 tony.wilson@zm.uzh.ch <http://www.zm.uzh.ch/agwilson> tony.wilson@zm.uzh.ch

Vienna PopGenomics

Vienna: Career Track Postdoc Position In Population Genomics

Research profile:

We are searching for an outstanding candidate with a strong background in population genetics, who is interested in using next generation sequencing (NGS) for population genetic inferences. We encourage experimentalists with a strong aptitude for NGS data analysis as well as theoreticians to apply for this position. Preference would be given to candidates with interest in population genetics of epigenetic programming.

Background about the position:

The University of Veterinary Medicine in Vienna (VUW) offers a new funding scheme to attract outstanding postdocs to Vienna. The position has two funding phases. In the first phase the candidate is expected to carry out preparatory work for a full research grant application to be submitted to the FWF (Austria's major funding body for basic research). Based on a successful evaluation after two years, the post-

doc will be promoted to a group leader with approx. 80k base funding for research/year. After 2-3 years the group leader will be reviewed and upon positive review s/he could be offered a tenured faculty position at the VUW.

The post will be based at the Institute of Population Genetics (<http://i122server.vu-wien.ac.at/pop/index.html>). The Institute hosts research groups in experimental population genetics (C. Schlötterer), functional population genetics/evodevo (A. McGregor), life history evolution (T. Flatt), conservation genetics (P. Burger) and evolutionary modeling (C. Kosiol). The Vienna research area offers many additional possibilities for collaborations in population genetics: Nick Barton, Reinhard Bürger, Andreas Futschik, Ines Hellmann, Joachim Hermisson, Magnus Nordborg, and Claus Vogl.

Deadline for application:

The official closing date for applications is 10 November 2009. Please submit a cover letter, CV, statement of research interests, and the names and contact details of three academic references as a single pdf file by e-mail to Dr. Thomas Flatt: thomas.flatt@vu-wien.ac.at

Dr. Thomas Flatt Veterinärmedizinische Universität Wien Institut für Populationsgenetik Veterinärplatz 1 A-1210 WIEN, Austria

VOX +43(0)1-25077-4334 FAX +43(0)1-25077-4390 E-mail: Thomas.Flatt@vu-wien.ac.at

http://i122server.vu-wien.ac.at/pop/Flatt_website/flatt_home.html flatt.thomas@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/ destroyed 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 Europe's 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@mf-n-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@mf-n-berlin.de>

Two NSF-funded postdoctoral research positions available to study evolution of sexual development in perithecium-producing ascomycetes. One position is at Michigan State University with Dr. Frances Trail, the other is at Yale University with Dr. Jeffrey Townsend. The positions will involve comparative transcriptomics and functional genomics, and candidates will gain experience in computational biology. Candidates should have a solid background through coursework and (preferably) lab experience in molecular biology. Experience with fungi will be considered a plus.

Funding available for up to three years. Interested candidates should send a letter of interest describing research experience and interests to Dr. Frances Trail at trail@msu.edu or Dr. Jeffrey Townsend at Jeffrey.Townsend@Yale.edu . Please include 3 references and a list of publications.

<http://www.plantbiology.msu.edu/faculty/faculty-research/frances-trail/>

<http://www.yale.edu/townsend/>

townsend.yale@comcast.net

**YaleU MichiganStateU
EvolExpSexDevFungi**

WorkshopsCourses

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Montana PopulationGeneticsDataAnalysis Aug31-Sep4			

Albuquerque InvasiveSpecies Aug2

Are Invasive Species Different? (NB: Space has been added for additional participants)

A workshop on the ecology and evolution of invasive species

Ecological Society of America Annual Meetings Sunday, August 2, 2009: 1:00 PM-6:00 PM San Miguel, Albuquerque Convention Center ESA Workshop - WK 15

The ecological impacts of some of the world's most notorious invaders are well-documented. However, the impacts of the majority of invaders may be small, whilst native species can also have large ecological effects. This raises two important questions. First, are introduced species fundamentally different from natives, or do they have similar ecological impacts? Second, do native and introduced species differ in key ecological relationships or evolutionary processes, such as abundance-impact, species-area or diversity-productivity?

Invited Talks:

Are non-native species different than natives? Comparisons of species distribution and abundance within regions Dov F. Sax, Brown University

Comparing phylogenetic patterns of native and exotic community assembly Marc W. Cadotte, National Center for Ecological Analysis and Synthesis Are exotic plants more chemically noxious and less nutritious than native plants?

Variation in native species influences invader impacts John L. Maron, and Marilyn Marler University of Montana

Mutualisms: Key drivers of invasions . . . key casualties of invasions David Richardson, Stellenbosch University and Anna Traveset, Institut Mediterrani d'Estudis Avançats

Escape of invasive plants from herbivory: How different is different enough? Peter M. Kotanen, University of Toronto

John D. Parker, Smithsonian Institution, Eric M. Lind, Smithsonian Environmental Research Center, Wendy Morrison, Georgia Tech, Mark E. Hay, Georgia Institute of Technology

rob.colautti@utoronto.ca

Ecological Genomics Sponsored by ESF ConGen and co-sponsored by ThermAdapt Summer School 2009

October 19 ? 24, 2009 Centro Residenziale Universitario di Bertinoro Bertinoro (FC), Italy <http://www.centrocongressibertinoro.it/> DNA sequencing technology is undergoing exceptional improvements. Next-generation parallel sequencers can generate millions of DNA sequences overnight at reduced costs. SNP detection technology is evolving fast from massive microarray to a variety of lower scale and less expensive technologies. These methods are changing the way of planning research and experimental protocols in theoretical and applied evolutionary and population genetics, and bioinformatics. Aim of the Summer School is to introduce the new genomic approaches into the field of ecological and conservation genetics. Genomic methods have been developed and applied mainly to the study of human populations or model organisms. However, genomic approaches are very well suited to the study of natural populations, as well. Classical population genetics in the last two decades made extensive use of very limited numbers of "neutral" markers (mainly microsatellites and mtDNA sequences), while the study of functional genetic systems has been substantially limited. Consequently, it has been problematic (or even impossible) to correlate such kind of population genetic data with the main domains of functional population genetics, that is the dynamics of whole genome heterozygosity and the genetic control of phenotypic variation. Genome sequencing and the very first population genomic data clearly indicate that a significant proportion of the population DNA diversity have been selected and functionally diverged in response to evolutionary adaptive pressures. Genomic methods might straight overcome the limitations of classical genetic marker approaches. Parallel sequencing and genome scanning technologies allow genotyping thousands of genes, covering both mutational diversity at the DNA level, regulatory mechanisms and patterns of qualitative or quantitative gene expression. In this way it is now feasible to understanding the functional role of genetic systems, the dynamics of selection processes and the adaptive potential of natural populations to changing climate and environments.

The Summer School is dedicated to design the role of next-generation sequencing and other genomic technologies as applied in the field of population and conservation genetics. Particular emphasis will be given to the study of functional genes and adaptation in natural non-model organisms. Aim of the School will be to show how the new perspectives offered by genomics could be applied to solve theoretical and practical ecological and conservation genetics problems. The School

will provide updated overview on major genomic methods, introduce case-studies in ecological genomics, and in this way it will stimulate the audience to develop new perspectives in the application of genomic methods in the study of natural plant and animal populations. Participants will be asked to share information and discuss genomic research approaches in wildlife species to gain a more profound understanding of the variation of genes and their functions in evolution, ecology and conservation. The School will emphasize the use of bioinformatic tools and software, and will further stimulate collaboration among international research groups within the field of ecological genomics.

The School, organized by Ettore Randi (Bologna) and Cino Pertoldi (Aarhus), consists in four full-day sessions with an adequate balance between theory and computer practice, oriented to handle genomic data bases, solve problems and hypothesis testing. There will be morning and afternoon sessions featuring invited speakers, practical computer sessions, and evening poster session dedicated to the students' own research projects. The School is primarily intended for young researchers at the doctoral and post-doctoral stages. Participants must have their own laptop computer and have software applications installed (information regarding the software will be provided by the organizers in advance). Candidates should preferably have some background in genomics and conservation genetics, as well as some experience in bioinformatics, and molecular evolutionary biology.

Invited speakers: Robert K. Wayne (UCLA, Los Angeles, California) Fyodor Kondrashov (Barcelona, Spain) Joop Ouborg (Nijmegen, The Netherlands) Thierry K.S. Janssens (Amsterdam, The Netherlands) Jacek Radwan (Kracow, Poland) Remy Bruggmann (Zurich, Switzerland) Pierre Taberlet (Grenoble, France) Eric Coissac (Grenoble, France) Michael M. Hansen (Silkeborg, Denmark) Ditte Demontis (Aarhus, Denmark) Christian Schlötterer (Wien, Austria) Christopher W. Wheat (Helsinki, Finland)

— / —

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>

**ColdSpringHarbour
ComparativeGenomics Nov4-10**

Course announcement - Application deadline, July 15, 2009

Cold Spring Harbor COMPUTATIONAL & COMPARATIVE GENOMICS November 4 - 10, 2009 Application Deadline: July 15, 2009

INSTRUCTORS:

Pearson, William, Ph.D., University of Virginia, Charlottesville, VA Smith, Randall, Ph.D., SmithKline Beecham Pharmaceuticals, King of Prussia, PA Lisa Stubbs, Ph.D., University of Illinois, Urbana, IL

Beyond BLAST and FASTA - Alignment: from proteins to genomes - This course presents a comprehensive overview of the theory and practice of computational methods for extracting the maximum amount of information from protein and DNA sequence similarity through sequence database searches, statistical analysis, and multiple sequence alignment, and genome scale alignment. Additional topics include identifying signals in unaligned sequences, integration of genetic and sequence information in biological databases. This year, there will be a focus on metagenomics and functional prediction.

The course combines lectures with hands-on exercises; students are encouraged to pose challenging sequence analysis problems using their own data. The course makes extensive use of local WWW pages to present problem sets and the computing tools to solve them. Students use Windows and Mac workstations attached to a UNIX server.

The course is designed for biologists seeking advanced training in biological sequence analysis, computational biology core resource directors and staff, and for scientists in other disciplines, such as computer science, who wish to survey current research problems in biological sequence analysis and comparative genomics.

The primary focus of the Computational and Comparative Genomics Course is the theory and practice of algorithms used in computational biology, with the goal of using current methods more effectively and developing new algorithms. Cold Spring Harbor also offers a "Programming for Biology" course, which focuses more on software development.

For additional information and the lecture schedule and problem sets for the 2008 course, see:

<http://fasta.bioch.virginia.edu/csh/> To apply to the course, fill out and send in the form at:

http://meetings.cshl.edu/course/-courseapp_instr.shtml Bill Pearson

wrp@virginia.edu

Florida Conservation Genetics Feb7-20

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.

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 <johnsonw@ncifcrf.gov>

Montana Population Genetics Data Analysis Aug31-Sep4

4th ConGen - Population Genetics Data Analysis
Course/Workshop

Recent Approaches for Estimation of Population Size, Structure, Gene flow, Selection Detection, and 454 sequence analysis

31-Aug/4-Sep 2009, Flathead Lake Biological Station, Montana, USA

APPLICATIONS FOR 2009 WILL CLOSE SOON!

Objective: To provide training in conceptual and practical aspects of data analysis for population genetics, molecular ecology, conservation genetics, and the management of populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches and software. This course will cover analysis methods including the coalescent, Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology.

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location (Lakeside cabins) will allow for extensive exchange and facilitate learning. Participants will receive the instructors' PowerPoint slides, example exercises, meals, lodging, transportation to/from airport, & a visit to Glacier National Park guided by expert wildlife (bear) ecologists and geneticists.

For detailed information on instructors & course see <http://popgen.eu/congen2009/> <<https://messaging.umt.edu/exchweb/bin/redir.asp?URL=http://popgen.eu/congen2009/>>

Instructors: Fred Allendorf, University of Montana, USA Sam Cushman, US Forest Service, Missoula, USA Jonathan Pritchard, The University of Chicago, USA Robert Lacy, Chicago Zoological Society, USA Oscar Gaggiotti, University Joseph Fourier in Grenoble, France Gordon Luikart, CIBIO, Portugal & University of Montana Albano Beja-Pereira, CIBIO, Portugal Tiago Antao, Liverpool School of Tropical Medicine, UK Mike Schwartz, US Forest Service, Missoula, USA Robin Waples, Northwest Fisheries Science Center of the National Marine Fisheries Service, USA

congen@popgen.eu

“Luikart, Gordon” <gordon.luikart@mso.umt.edu>

Montana
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Aug31-Sep4 2

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Instructors: Fred Allendorf, University of Montana,

USA Sam Cushman, US Forest Service, Missoula, USA
 Jonathan Pritchard, The University of Chicago, USA
 Robert Lacy, Chicago Zoological Society, USA
 Oscar Gaggiotti, University Joseph Fourier in Grenoble, France
 Gordon Luikart, CIBIO, Portugal & University of Montana
 Albano Beja-Pereira, CIBIO, Portugal
 Tiago Antao, Liverpool School of Tropical Medicine, UK
 Mike Schwartz, US Forest Service, Missoula, USA
 Robin Waples, Northwest Fisheries Science Center of the National Marine Fisheries Service, USA

congen@popgen.eu

“Luikart, Gordon” <gordon.luikart@mso.umt.edu>

UAberdeen
Evolution Stress Responses Sep18-19

First announcement - EPSRC workshop: Evolution of Stress Responses, 18-19 September 2009, University of Aberdeen, UK

This EPSRC funded workshop will bring together experimentalists and theoreticians and will broadly cover eukaryotic and prokaryotic stress responses at both cell and population levels under the following general themes:

1. molecular mechanisms governing biochemical, genetic and physiological responses
2. the ability to sense and respond to the environment

For more details and to register please go to: <http://www.mmems.org/> For all scientific enquiries contact Ivana Gudelj (i.gudelj@imperial.ac.uk). For administrative enquiries e-mail Ann Linfield (masadl@bath.ac.uk)

Ivana Gudelj <i.gudelj@imperial.ac.uk>

UFreiburg Forest Genetics Oct7-9

I would like to bring the following workshop to your attention: “Opportunities, challenges and limitations of genomics-based technologies in forest tree breeding and forest genetics”. This workshop will be held from October 07 until October 09 2009 in Freiburg and is organised by the Forest Research Institute of Baden-

Württemberg (FVA), the Institute of Tree Physiologie at the University of Freiburg, and the regional office EFICIENT of the European Forest Institute (EFI).

The goal of this workshop is to provide a forum for population geneticists, evolutionary biologists and molecular ecologists to evaluate the state of the art in forest tree genetics and genomics and to discuss how to apply that information to genomics-based research in gene conservation, selection and breeding.

A detailed programme including a list of invited speakers, details on the registration and further information can be obtained at http://www.efi.int/portal/news_events/events/extra/2009/-workshop_forest_genetics/ Registration already ends by August 31 2009. Please note that the total number of participants is limited to 50 in order to make this an efficient workshop with intensive discussions.

Thanks in advance,

Ingo

Dr. Ingo Ensminger

Abteilung Waldökologie Forstliche Versuchs- und Forschungsanstalt Baden-Württemberg (FVA) Wonnhaldestr.4, 79100 Freiburg

Department of Forest Ecology Forest Research Institute Baden-Württemberg (FVA) Wonnhaldestr. 4, 79100 Freiburg, Germany

Tel +49 (0)761 40 18 17 7 Fax +49 (0)761 40 18 33 3

ingo.ensminger@forst.bwl.de

& ingo.ensminger@ctp.uni-freiburg.de & <http://www.fva-bw.de> & <http://www.uwo.ca/biology/Faculty/ensminger/index.htm>

Ingo.Ensminger@Forst.bwl.de

ULiege Belgium StatisticalGenetics Aug31-Sep9

The Summer Institute in Statistical Genetics will offer a series of short courses at the University of Liege, Belgium, between August 31 and September 9, 2009. Details are available at <http://sisg.biostat.washington.edu>
Bruce Weir

bsweir@u.washington.edu

UManchester Morphometrics Nov9-Dec18

I am pleased to announce this year's morphometrics course from the University of Manchester. This year's course will run in the six weeks from 9 November to 18 December 2009.

The course information can be found on the following we site: <http://www.flywings.org.uk/MorphoCourse>
Course content: * Data acquisition: the kinds of data and the equipment used to collect them. * Definitions of size and shape * Geometric methods to characterise shape from a configuration of landmark points (Procrustes superimposition) * Statistics of variation, scatter plots, basic multivariate statistics * Principal component analysis * Measurement error and outliers * Shape transformations and 'warping' – the thin plate spline * Analysis of outline shapes * Distinguishing between groups (taxonomy, clinical diagnosis, etc.) * Allometry and size correction * Influence of external factors on shape (ecomorphology, dose-response studies) * Symmetric forms and measurement of asymmetry. * Morphometric inferences on developmental processes, morphological integration, modularity * Genetics of shape: analyses of resemblance between relatives, QTL analyses. * Phylogeny: reconstructing the evolution of shape

Practice examples: As far as possible, practical exercises are provided to accompany the course content. These practice exercises consist of data sets and explanations on how to run the respective analyses using the MorphoJ software (http://www.flywings.org.uk/MorphoJ_page.htm). Participants who already have their own data are encouraged to use those and to discuss them as part of the course. I hope there will be a bit of a 'workshop' feel to the course unit.

Group work: Participants will work in small groups to prepare web presentations of possible morphometric studies. This activity stimulates discussion and provides a broad overview of questions that can be addressed with morphometric methods.

The fee for the course is GBP 190.00 (I'm afraid it's gone up a bit from last year – but the UK pound has dropped against most other currencies...).

All prospective participants need to pre-register for the course. The deadline for this is the *31 August 2009*.

For further details, see the course web page: <http://www.flywings.org.uk/MorphoCourse> Best wishes,
Chris

Christian Peter Klingenberg Faculty of Life Sciences
The University of Manchester Michael Smith Building

Oxford Road Manchester M13 9PT United Kingdom
Telephone: +44 161 275 3899 Fax: +44 161 275
5082 E-mail: cpk@manchester.ac.uk Web: <http://www.flywings.org.uk> Skype: [chris.klingenberg](https://www.skype.com/user/chris.klingenberg)
cpk@manchester.ac.uk cpk@manchester.ac.uk

Instructions

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

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

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as \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 formatted) 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 preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.