
E v o l D i r

June 1, 2011

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.

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Adelaide Barcode 2

Latest News on the Adelaide Conference. * [1]Registration is now open for the Fourth International Barcode of Life conference in Adelaide, Australia! + Register before 15 September to benefit from the Early Bird discounted rate. + Register for the Pre-Conference Training Event, 28-29 November. + Secure specially-discounted conference rates on hotels and [2]half-day excursions. * The [3]Exhibitor Form is now available. Organisations should apply soon for one of the limited number of exhibition booths. * Your organization or project can be highlighted at the conference through one of the [4]Sponsorship Opportunities. * Have you [5]submitted your abstract yet? Be sure to do so before the [6]new deadline. Links:

For all links see <http://barcodeoflife.us1.list-manage2.com> View of the [7]South Australia Museum along North Terrace, near the University of Adelaide, site of the Adelaide Barcode Conference.

Belfast ArthropodSystematics Jul4-8

Arthropod systematics: are morphology, palaeontology and molecules coming together? is the title of our symposium at the upcoming Systematics Association biennial meeting at Queen's University Belfast (Northern Ireland) on 4-8 July 2011. Our symposium is one of four main symposia scheduled for the biennial meeting, and is planned to take place on Thursday and Friday 8 and 9

July. For those interested to attend the meeting and our symposium, registration is now open via [www.systass](http://www.systass.org) < [http://www.systass](http://www.systass.org) > (early bird registration closes at 5 pm UK time on 23 May 2011). We invite those interested in contributing a talk or poster to our symposium to please submit your abstract by 1 June 2011 via www.systass.org < <http://www.systass.org> > .

The backbone of our symposium will be a series of invited talks given by an exciting selection of internationally renowned experts on the biology and palaeontology of arthropods, including Thorsten Burmester, Jason Dunlop, Greg Edgecombe, Georg Mayer, Alessandro Minelli, Jerome Regier, Björn von Reumont, Angelika Stollewerk, and Max Telford. These speakers will cover recent advances in our understanding of arthropod evolution from the perspectives of developmental biology, comparative morphology, the fossil record, and phylogenomics.

We have reserved significant time for contributed talks and discussions in our symposium, which we anticipate will be filled with lively discussions about the present and future of arthropod systematics. We look forward to welcoming you in Belfast in July 2011!

Omar Rota-Stabelli (IASMA Research and Innovation Centre, Edmund Mach Foundation, Trento), Davide Pisani (National University of Ireland, Maynooth), Ronald Jenner (The Natural History Museum, London)
r.jenner@nhm.ac.uk

of Ubiquitous Genomics - Arthropod Systematics: are Morphology, Palaeontology and Molecules Coming Together? - Algal Systematics: Where Next? - Advances in Using Museum Specimens and Ancient DNA in Systematics Research.

The Biennial also presents excellent opportunities for contributed papers on any aspect of systematics. It is a great forum for students and young researchers to present their work and compete for prizes. We are also offering a number of student bursaries (see <http://www.systass.org/> for details of how to apply for a student bursary). You can attend on a daily basis if you wish.

Details of the biennial, how to register, submit your abstract (deadline 1st June 2011) and how to apply for a bursary can be found at <http://www.systass.org/-biennial2011/> and details are below.

On behalf of the conference organisers, we hope to see you there!

Juliet Brodie, President James Cotton, Programme Officer Peter Olson, Treasurer Christine Maggs, Local Organiser

Sponsors: The Linnean Society of London, British Phycological Society, Cambridge University Press, Genetics Society, Queen's University Belfast
james.cotton@sanger.ac.uk

Belfast Systematics Jul4-8 EarlyRegistrationExtended

Dear Colleagues,

8th Systematics Association Biennial, 4-8 July 2011, Queen's University Belfast

***** EARLY REGISTRATION EXTENDED TO 1ST JUNE 2011*****

Early bird registration for the 8th Systematics Association Biennial, 4-8 July 2011 at Queen's University Belfast, has been extended to June 1st 2011.

All details can be found at <http://www.systass.org/-biennial2011/>

We have a very exciting scientific programme

Scheduled symposia include: - Next Generation Systematics - Studying Evolution and Diversity in an Era

BucknellU MultitrophicInteractions

Conference: Multitrophic Interactions, Warren Abrahamson

Early registration and a call for posters have been extended until May 15 for an international conference to be held at Bucknell University in Lewisburg, Pennsylvania, USA on Monday, June 13 and Tuesday, June 14, 2011, entitled “*Evolutionary Ecology across Trophic Levels* - A Symposium in Honor of Warren Abrahamson.”

Registration is available from the conference website: <http://www.bucknell.edu/x65430.xml> Registration costs have been reduced to \$15 for students and postdocs and \$35 for others. Evening meals are no longer included in this price, and can be selected separately if desired. Registration fees will increase on May 16.

The conference will feature roughly twenty scientific talks to be given by alumni, collaborators, and friends of the Abrahamson Lab. Confirmed speakers include:

- Doug Allchin, University of Minnesota Twin Cities
- Catherine Blair, Bucknell University
- Jackie Brown, Grinnell College
- Timothy Craig, University of Minnesota-Duluth
- Sarah Diamond, University of North Carolina
- Netta Dorchin, Museum Koenig
- Micky Eubanks, Texas A&M University
- David Hartnett, Kansas State University
- Christine Hawkes, University of Texas at Austin
- John Horner, Texas Christian University
- Jason Irwin, Central Washington University
- Ann Johnson, Florida Natural Areas Inventory
- Eric Menges, Archbold Biological Station
- Patricia Peroni, Davidson College
- Peter Price, Northern Arizona University
- Otto Solbrig, Harvard University
- John Stinchcombe, University of Toronto
- Hilary Swain, Archbold Biological Station
- Mizuki Takahashi, Bucknell University
- Art Weis, University of Toronto
- Michael Wise, Roanoke College

Tentative titles are available on the symposium website. Topics will address the diversity of subjects and approaches taken by Abe over his career, from the ecology and evolution of plant-insect interactions to community and ecosystem approaches to fire ecology, restoration, and conservation of natural landscapes.

A contributed poster session is also planned, and can be selected as part of the registration. Activities will include a banquet, picnic, and talent show, as well as regional natural history excursions. Events will be held in the Elaine Langone Center on the Bucknell University Campus.

Conference fees include daytime meals and snacks, but not lodging. Additional tickets to the picnic and banquet are available for attendees and guests. Lodging in Bucknell dormitories is available for \$38/night single and \$30/night double occupancy, with a one-time key charge of \$10. There are many high-quality hotels, inns, and B&Bs in the region as well.

The Bucknell University campus provides easy access to the downtown shopping, dining, and entertainment district of Lewisburg, a town noted for its historical preservation and vibrant culture. Details can be found at: <http://www.lewisburgpa.com/> This conference will celebrate Warren Abrahamson's 38 years of service to Bucknell University and the scientific community in anticipation of his upcoming retirement in the summer of 2012. During his career, Abe has supervised approximately 200 undergraduate research students, 18 Master's recipients, and 21 postdoctoral fellows, many of whom have remained active in science. In 2009 he was named a AAAS fellow. His main research interests include 1) multitrophic plant-insect interactions using the goldenrod system and 2) fire ecology and plant demography in Florida's upland communities.

For more information on Warren Abrahamson and his work, please visit his lab website: <http://www.facstaff.bucknell.edu/abrahmsn/> Questions and comments can be addressed to steve.jordan@bucknell.edu
sdjordan@bucknell.edu

Galway RECOMB Comparative Genomics Oct8-10

Dear colleagues: This is a second call for papers for RECOMB Comparative Genomics 2011 and reminder that the paper submission deadline is approaching next week. Best, Aaron Darling and Cathal Seoighe

RECOMB-CG, 2011 October 8-10, 2011 Galway, Ireland <http://recombcg.org> CONFIRMED KEYNOTE SPEAKERS

* Ed Green (UC Santa Cruz, USA) * Kateryna Makova (Penn State University, USA) * Julian Parkhill (Sanger Institute, UK) * Nikolaus Rajewsky (Max-Delbrück Center for Molecular Medicine, Germany) * Christopher Greenman (TGAC, UK) * Jerome Salse (INRA, France)

KEY DATES Paper submission deadline June 03, 2011 Notification of paper acceptance June 24, 2011 Poster submission deadline September 20, 2011 Workshop October 8-10, 2011 More details available at <http://recombcg.org> THEME AND SCOPE

The continuing advance of DNA sequencing technol-

ogy has produced an avalanche of genome sequence and genome structural information across the evolutionary spectrum. Transforming that information into biological knowledge requires creative and innovative new computational and statistical methods for comparative genomics.

The RECOMB Satellite Workshop on Comparative Genomics aims to provide the premier forum for new computational developments applied to all aspects of comparative genomics. We solicit contributions on topics including comparison of genome structure and organization, genome function, and evolution. We particularly encourage contributions that use new computational methods to acquire new insight into biological processes. Advances in computational theory are welcome, though all submissions should include genome-scale analyses informed by comparative data.

New for 2011, all peer-reviewed and accepted RECOMB-CG manuscripts will be published in a supplement to BMC Bioinformatics as open access, author subsidized, articles.

Specific topics of interest include but are not limited to:

Gene and genome duplication
Gene family evolution
Genome structural variation
Algorithms for comparative genomics
Genome rearrangement
Ancestral genome reconstruction
Multiple genome alignment
Genome sequence comparison
Modeling genome evolution
Comparative genomics for genome annotation
Gene tree reconciliation
Species and gene tree inference
Comparative metagenomics
Comparative genomics linked to proteomics, metabolomics, and other 'omic data
Comparative genomics and gene expression and regulation
Applications of comparative genomic methods

CALL FOR PAPERS

Papers should be submitted via the EasyChair system. Submissions must be received in electronic form by 11:59pm (Samoa time), June 3rd, 2011.

Submissions should be typeset as double-spaced A4 pages with 1-inch margins all around in a minimum of 10 point font. Submissions should be limited to 16 pages, everything included (title, authors, addresses, abstract, references, figures, tables). Exceptions to this limit may be granted by consultation with the Program Committee Chairs. Authors are encouraged to use the BMC document templates when preparing manuscripts. Templates are available in Microsoft and LaTeX formats. Submitted manuscripts must be rendered to PDF format prior to upload into EasyChair at the review stage. Submissions must include the cor-

responding author's email address. Papers submitted for review should represent original, previously unpublished work. At the time the paper is submitted to the conference, and for the entire review period, the paper should not be under review by any other conference or scientific journal.

At least one author per each successful submission is required to register and present the paper at the workshop. The paper will be included in the conference proceedings, which will be published in BMC Bioinformatics. Address any questions to the program committee chairs: Aaron E. Darling (aaron.darling at ucDavis.edu) and Cathal Seoighe (cathal.seoighe at nuigalway.ie)

CONFERENCE CHAIR

Cathal Seoighe (National University of Ireland, Galway, Ireland)

PROGRAM COMMITTEE CHAIRS

Aaron E. Darling (University of California, Davis, USA) Cathal Seoighe (National University of Ireland, Galway, Ireland)

PROGRAM COMMITTEE

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Gerton Lunter, Oxford University, UK

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Hawaii Biocomputing Jan3-7 MicrobiomePapers

REMINDER:

Submissions for this special session are due 11 July!

We invite high quality manuscripts for publication and presentation at a special session on Microbiome Studies

at the Pacific Symposium on Biocomputing, 3-7 January in Hawaii. Papers will be refereed by top names in the field, and accepted papers will be published in the PSB proceedings, which are indexed in Medline.

For details (new URL): <http://psb.stanford.edu/cfp-ms/index.html> james a. foster university of Idaho

foster@uidaho.edu

Jyvaskyla Coevolution Oct4-7

Symposium on CoEvolution 4th - 7th October 2011, Jyväskylä, Finland

We are pleased to announce a special symposium on Coevolution in Jyväskylä, Finland (October 4th 7th, 2011).

Our keynote speakers will be Dr. Sheena Cotter from Queens' University (Belfast), Dr. Mario Vallejo Marín from University of Stirling (Scotland) and Dr. Dagmar Voigt from University of Kiel (Germany) in addition to contributions from local professors.

We are accepting oral presentations and posters covering all aspects of coevolution with emphasis on the following themes:

1. Mutualism 2. Insect-plant interactions 3. Predator-prey interactions 4. Multitrophic interactions 5. Sexual conflict 6. Virulence evolution 7. Gene-gene interactions

Please go to <https://www.jyu.fi/bioenv/en/divisions/eko/coevolution/coevolution-symposium> for more information and online registration or contact as at coevo.symposium@jyu.fi. Registration deadline is August 31st and deadline for abstract submission is July 31st.

The symposium is organized by the post-docs of the Centre of Excellence in Evolutionary Research and the Division of Ecology and Evolutionary Biology from the University of Jyväskylä. We are particularly keen to give postdocs a chance to present and discuss their work on coevolution together with other interested researchers.

Looking forward to meeting you in Jyväskylä!

On behalf of the organising committee.

— Dr. Sandra Varga Postdoctoral Researcher Department of Biological and Environmental Science PO Box 35, FI-40014 University of Jyväskylä Finland

<http://users.jyu.fi/~savarga/> <http://-jyu.academia.edu/SandraVarga> Sandra Varga
<sandra.varga@jyu.fi>

Jyvaskyla Speciation Feb27-28

Event: "Progress in understanding the origins of biodiversity" Date: 27-28 February 2012 Location: University of Jyvaskyla, Finland

We are pleased to invite you to the conference "Progress in understanding the origins of biodiversity" organized by the EU Marie Curie Initial Training Network SPECIATION. The event will be held 27-28 February 2012, Jyvaskyla, Finland. The conference will consist of plenary sessions, four symposia and posters covering recent advances in speciation and adaptation research. Registration and abstract submission will be open in October. There will also be limited space available for talks by the participants.

Confirmed speakers:

Mark Kirkpatrick, University of Texas, USA Mohammed Noor, Duke University, USA Daven Presgraves, University of Rochester, USA Kerry Shaw, Cornell University, USA Patrik Nosil, University of Colorado, USA Ilkka Hanski, University of Helsinki, Finland

Organisers: Anneli Hoikkala, Emily Knott, Maaria Kankare, Venera Tyukmaeva and Jackson Jennings on behalf of the Marie Curie ITN

Information about the meeting will be available later on our website <http://sites.google.com/site/itnspeciation/>. Also for more information contact Venera Tyukmaeva venera.v.tyukmaeva@jyu.fi

– Venera Tyukmaeva Evolutionary Genetics Group Centre of Excellence in Evolutionary Research Department of Environmental and Biological Science P.O. Box 35, 40014, University of Jyväskylä, Finland

Tel. +358-14-260-4253 Room: YAC421.1

venera.v.tyukmaeva@jyu.fi

tionary Biology, Harvard University
 Overcoming the gene discovery bottleneck for arthropod evo-devo:
 Creating de novo developmental transcriptomes

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Toni GabaldÃ³n Center for Genomic Regulation (CRG), Barcelona, Spain
 Arthropod genomes as seen through the lens of evolution

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Cheryl Y. Hayashi Department of Biology, University of California, Riverside
 Spider silks: Functional and evolutionary insights into high-performance materials

Â

Mary Ann McDowell Biological Sciences, University of Notre Dame
 A tale of two sand fly genomes: Phlebotomus papatasi and Lutzomyia longipalpis

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Pedro L. Oliveira Instituto de BioquÃªmica MÃ©dica, Programa de Biologia Molecular e Biotecnologia Universidade Federal do Rio de Janeiro and

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Kyoto SMBE 2011 Jul26-30 Ancient DNA Symposium

CALL FOR ABSTRACTS

The DEADLINE for abstract submission for SMBE 2011 in Kyoto is MAY 31*.* http://smbe2011.com/-important_dates.html Please consider submitting an abstract to the ancient DNA symposium described below. / /NEW APPROACHES IN ANCIENT DNA

*Confirmed speakers: *Alan Cooper, Johannes Krause, Ludovic Orlando, Mark Stoneking, Eske Willerslev

With recent advances in DNA sequencing and DNA preparation techniques, the study of extinct and long dead organisms is entering a new era. Previously limited to short segments of mitochondrial DNA, whole nuclear genomes are now available from several extinct species, thus providing new insights into deep evolutionary history. Within the last year for instance - the

Neandertal genome, the Denisovan genome as well as the genome of a Palaeo-Eskimo have become publicly available. Nevertheless, acquiring high quality DNA sequence remains a critical challenge, owing to DNA damage as well as contamination by microbial and contemporary DNA. This symposium aims to highlight current research in ancient DNA with a focus on comparative genomics and population genetics of extinct populations. Methodological and theoretical advancements will be equally presented - promoting a general forum for the advancement of this novel and exciting field.

*Organizers: *Johannes Krause, Anna-Sapfo Malaspinas

Anna-Sapfo Malaspinas <sapfo@berkeley.edu>

Kyoto SMBE 2011 Jul26-30 Registration Deadline

The 2011 meeting of the Society for Molecular Biology and Evolution (SMBE) takes place in Kyoto, Japan, on July 26-30. It is shaping up to be an outstanding international meeting, though some have expressed concerns about the residual effect of the earthquake. We would like to assure you that the conference will go ahead as planned, despite the earlier disruption caused by the earthquake in the eastern portions of Japan. Over 250 people have already registered to attend, and the closing date for early registration at a discounted rate is coming up soon: May 31. You may of course register after that date but at a higher cost.

Kyoto is well served by direct international flights to Osaka airport from many countries, or you can fly to Tokyo and take the bullet train. Kyoto is located in western Japan and was not affected by the earthquake or nuclear accident.

Please visit the meeting website <http://smbe2011.com/> for more information and program details. It promises to be an exciting meeting in one of Japan's most beautiful and historic cities, and I look forward to seeing you there.

Yours sincerely,

Ken Wolfe President, SMBE

===Ken Wolfe Smurfit Institute of Genetics, Trinity College, Dublin 2, Ireland. Tel. +353 1 8961253

Kyoto SMBE2011 Jul26-30 RegistrationDeadline

Friday, May 27, 2011

To evoldir people:

SMBE will have this year's annual meeting at Kyoto, Japan. Conference website is <http://smbe2011.com/>. Early registration deadline is May 31. This is not Japan time, but global time, i.e., only when it turned to be June 1 in all area on earth. But it is ONLY FIVE DAYS left!

As of May 27, 359 persons from 29 countries/regions (including 97 from USA, 15 from Germany, 13 from China, 12 from UK and Taiwan, 9 from France, 8 from Canada and Sweden, 7 from New Zealand, 6 from Australia, Ireland, Spain, and Switzerland, 5 from Denmark, 4 from Austria, 3 from Poland, and 127 from Japan) already registered.

>From "Registration" [<http://smbe2011.com/-registration.html>]: // All payments must be made in Japanese Yen (JPY). ==èrly = JPY 35,000 Late = JPY 45,000 for Regular SMBE member Early = JPY 40,000 Late = JPY 50,000 for Regular non-SMBE member Early = JPY 25,000 Late = JPY 35,000 for Student/Post-doc SMBE member Early = JPY 30,000 Late = JPY 40,000 for Student/Post-doc non-SMBE member ==SMBE banquet: JPY 5,000

Registration fee includes: # Attendance to all Sessions (July 27-31, including SESJ annual meeting) # Program Book # Welcome Reception (evening of July 26) # 3 Lunch boxes (July 27, 28, 29) # Coffee Breaks (July 27-30) * Banquet ticket is not included in the registration fee. //

As many of you are aware, the northeast part of Japan was hit by very strong earthquake on March 11, 2011. Kyoto is located in western Japan, and thankfully was left unscathed. The schedule for the SMBE2011 Kyoto Conference is unaffected. Furthermore, Kyoto is far from the Fukushima nuclear power plants, and radiation level is normal. Please see: http://mextrad.blob.core.windows.net/page/-26_Kyoto_en.html Current Schedule of SMBE2011 Kyoto Conference is as follows; from "Program Overview" [http://smbe2011.com/program_overview.html] —
Tuesday, July 26

Welcome Reception Time: 18:00-20:00 Place: International Hall at Kyoto University Centennial Clock Tower Hall (Building C)

Wednesday, July 27

Morning Sessions (9:30- 12:00) Room C-1: [Symposium 1] Evolution of modern human Room S-1: [Symposium 2] Gene evolution and phenotypic adaptation Room S-2: [Workshop 1] Methods for multiple alignment and phylogenetic tree making for large sequence data set Room S-3: [Workshop 2] Reverse transcriptase as an evolutionary force

Afternoon Sessions (13:30- 16:00) Room C-1: [Symposium 3] Compensatory fitness interactions and genome evolution Room S-1: [Symposium 4] Symbiosis as the source of evolutionary novelties Room S-2: [Workshop 3] Natural selection in human populations: beyond classic sweeps Room S-3: [Workshop 4] Evolutionary diversity revealed by comparative transcriptomics Room C-3: [Workshop 5] Visualizing the geographic and temporal structure of biodiversity

Evening Sessions (16:30- 19:00) Room C-1: [Symposium 5] Genome evolution: surprises from microbes Room S-1: [Symposium 6] Molecular bases of speciation Room S-2: [Workshop 6] Comparative and evolutionary neurogenomics in humans and non-human primates Room S-3: [Workshop 7] Virus evolution Room S-4: [Workshop 8] Modeling protein structural and energetic constraints on sequence evolution

Thursday, July 28

Morning Sessions (9:30- 12:00) Room C-1: [Symposium 7] New approaches in ancient DNA Room S-1: [Symposium 8] Origin and diversification of sensory organs Room S-2: [Symposium 9] Evolutionary systems biology Room S-3: [used for additional workshop or contributed oral presentations] Room S-4: [Workshop 9] Molecular biology and evolution of blood group and MHC antigens in primates Room C-3: [Workshop 10] Selective sweeps in complex demographic and genetic systems

Afternoon Sessions (13:30- 16:00) Room C-1: [Symposium 10] Evolution of genome structure Room S-1: [Symposium 11] Molecular mechanisms governing morphological divergence of arthropod appendages Room S-2: [Symposium 12] Evolution as a stochastic process Room S-3: [Workshop 11] Recombination and the efficacy of selection Room S-4: [Workshop 9; continuation] Molecular biology and evolution of blood group and MHC antigens in primates Room C-3: [Workshop 10; continuation] Selective sweeps in complex demographic and genetic systems

Evening Sessions (16:30- 19:00) Room C-1: [Special Symposium] Honoring late Walter M. Fitch Room C-1: [Special Session] History of MBE

Friday, July 29

9:15- 9:30 Welcome to SMBE 2011 at Kyoto by SMBE2011 Organizing Committees 9:30-10:30 Nei Lecture by Ken Wolfe, SMBE President "Yeast genome evolution and the aftermath of polyploidization" 10:30-11:20 Plenary Talk 1 by Manolo Gouy, CNRS, Lyon

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Linköping Sweden PhenotypeEvolution Jun16-19

Linköping Brain Seminar

*International Workshop *

Perinatal Effects shaping Individual Phenotypes

June 16-19th 2011

Dear colleagues,

We are organizing a workshop on perinatal effects to be held at the Linköping University, Sweden and are happy to welcome our keynote lecturers:*

Frances Champagne*, epigenetic effects of maternal care (Columbia University),

Ton Groothuis, hormone mediated maternal effects (University of Groningen), and

Barbara Tzschentke, perinatal adaptation (Humboldt-Universität zu Berlin)

The evolution of phenotypic variation is determined not only by the underlying genotype but is influenced to a great extent by non-genetic factors. Especially the pre- and postnatal environment has profound impact on an individual's phenotype and can result in short- and long-term modifications even across generations, for example through heritable epigenetic alterations of the genome. In this workshop we want to bring together researchers from various fields such as genetics, endocrinology, physiology, and behavioural biology and discuss the adaptive nature of perinatal programming and underlying mechanisms.

We welcome you to give an oral or poster presentation!

Deadline for abstract submission is *May 23rd, 2011*

Deadline for registration: *May 30th, 2011*

Please check <https://cms.ifm.liu.se/biology/zoology/-avian/brainseminar-1/index.xml> for more information.

E-mail: perinatalBS2011@gmail.com

Vivian Goerlich <vivgo@ifm.liu.se>

Lisbon Phylogeography Nov26-27

CALL FOR PARTICIPANTS in 2-day International Workshop on Biogeography and Phylogeography of Fish from the Atlantic

Date: 26-27 November 2011 Location: Lisbon, Portugal Hosted by Eco-Ethology Research Unit (EERU), ISPA

Over the last several years a number of studies on the phylogeography of Atlantic fish have started to shed light on evolutionary processes in this taxa and in their marine environment. Some reviews of this literature have been published illuminating biogeographic patterns, namely diversity patterns, historical refuges, dispersal routes and barriers, etc. The aim of the workshop is to present and discuss studies and perspectives on major patterns and give updates on the state of the art in Atlantic biogeography and phylogeography of fish and outline directions for future research.

The Workshop is divided into two major sessions: 1) a public session, open to all, on Saturday November 26th 2011, with presentation of oral communications; 2) a session reserved to participants, on Sunday November 27th 2011, with short presentations, and ample time for discussion and exchange of ideas.

Those interested in participating in the Sunday session are required to submit a short CV until the 15th of September. Number of participants in the Sunday session are limited in order to guarantee a workshop environment and a productive exchange of ideas. Unfortunately, we are unable to subsidize travel/stay expenses, but there is no registration fee.

Please send personal information and short CV to : centro.biociencias@ispa.pt

The organizing scientific committee, which will review applications, is composed by

Vítor Almada (EERU/ISPA, PT), Emanuel Gonçalves

(EERU/ISPA, PT), André Levy (EERU/ISPA, PT), Joana Robalo (EERU/ISPA, PT), Giacomo Bernardi, Ricardo Santos (Univ. Azores, PT), Alberto Brito (Univ. Laguna, Canarias), Rita Castilho (Univ. Algarve, PT), Ricardo Santos (Univ. Azores, PT), Sergio Stefanni (Univ. Azores, PT), Giacomo Bernardi (Univ. California Santa Cruz, US), Knutsen Halvor (IMR, Norway), Sérgio Floeter (UFSC, Brazil), Sophie von der Heyden (Univ. of Stellenbosch, South Africa)
andrelevy@gmail.com

LundU EvolutionFlight Aug29-30

This symposium is aimed at evolutionary biologists, albeit not exclusively. We have planned this meeting deliberately as an interdisciplinary event to promote an integrative view on one of the most fascinating behaviours - flight!

We are sure that many EvolDir subscribers would be interested in this event Best wishes on behalf of the organizers, Sophia Engel

Symposium âInsect Flightâ, 29-30th August 2011

CAnMove Centre for Animal Movement Research Lund University, Sweden

Animal flight has evolved only four times in history, in pterosaurs, birds, bats and insects. To date, insects constitute a majority of the worldâs life forms, and flight appears to have contributed to this inordinate evolutionary success story.

Because flight links a series of fundamental processes within both the physical and biological sciences we aim to provide a plenum for scientists from various fields (evolutionary ecology, morphology, physiology, behaviour, biomechanics) to present insight into the different aspects and implications of insect flight and to combine aspects from biology and engineering to an integrated view on insect flight.

Information about CAnMove and the preliminary programme can be found at our homepage: <http://canmove.lu.se/node/715> Registration: Attendance of the symposium is free, if you want to attend, please register by filling in our online-registration form. The deadline for applications is July 15th

We especially encourage Ph.D. students to present and discuss their work here. Should you have any questions regarding the symposium please do not hesitate to con-

tact Sophia Engel (sophia.engel@biol.lu.se).

Local organisers: Sophia Engel, Erik Svensson and Anders Hedenström

Sophia Engel <Sophia.Engel@biol.lu.se>

Montpellier ModelsEvolEcol Jun8-10 May13Deadline

Dear EvolDir colleagues,

We remind you that you have one week (until Friday, May 13) to register for the seminar "Models in Evolutionary Ecology" here: <http://www.seminar-mee.org/-home/inscription> Thank you to register even if you just want to attend the discussions!

Student workshop: "Models in Evolutionary Ecology". Montpellier (France), June 8-10, 2011 <http://www.seminar-mee.org/> < <http://www.seminar-mee.org/> >

Application deadline: May 13th 2011

We are pleased to invite you to the second edition of the workshop "models in evolutionary ecology". This workshop is organized by PhD students and postdocs, and is dedicated to students (PhD students, postdocs, undergrads) but also to researchers interested in theoretical approaches in evolutionary ecology and has three objectives:

- give a broad overview of modelling techniques used in evolutionary ecology and their relationship with experimental work
- encourage dialogue between PhD students using different approaches
- discuss on how to communicate on the models and their meaning to the general public

The workshop is intended to favour exchange as much as possible, and consists in a series of methodological sessions by invited researchers, talks by researchers and students, journal clubs, poster sessions and round-tables. The detailed program is here: <http://www.seminar-mee.org/home/programme> < <http://www.seminar-mee.org/home/programme> > Registration to the workshop is free, but we strongly recommend all participants to present their work or project in a talk or with a poster.

You can register and submit an abstract before May, 13th. <http://www.seminar-mee.org/home/inscription> < <http://www.seminar-mee.org/home/inscription> >

Confirmed faculty:

Thomas Broquet Vincent Devictor Richard Goumulkiewicz

Sonia Kéfi Sébastien Lion Guillaume Martin Denis Roze

We look forward to seeing you in June!

The organizers, Ronan Becheler, François Blanquart, Benoit Goussen, Etienne Loire and Timothée Poisot.

<http://www.seminar-mee.org/>

GOUSSEN Benoit THESARD
<benoit.goussen@irsn.fr> GOUSSEN Benoit THE-
SARD <benoit.goussen@irsn.fr>

Norman Evolution2011 Jun17-21 EvolutionaryMedicine

Evolutionary Medicine Symposium and Luncheon
Sunday, June 19 at Evolution 2011
8:30am-4:30pm

<http://www.evolution2011.ou.edu/symposia.html>
(Scroll down to SSE symposia)

This symposium will explore the role of evolutionary biologists in promoting evolutionary thinking in medical education and practice, as well as introduce some medical questions that are ideally structured for evolutionary research. Speakers from schools of medicine and public health, as well as more traditional evolutionary biology research backgrounds will address various topics where an evolutionary approach is a valuable asset to medical research, where medical data can advance evolutionary research, and where evolutionary principles can be used to improve medical practice. The symposium is part of a larger movement to increase awareness of the role of evolutionary biologists in connecting evolutionary science to the intellectual development of our future physicians and public health practitioners. The symposium is open to all.

You are invited to join the speakers for lunch to discuss this topic further. Space at the lunch is limited and you must register here by June 12: <http://tinyurl.com/-3qgohsk>. For additional information contact Mike Antolin (michael.antolin@colostate.edu) or Kristin Jenkins (kjenkins@nescent.org).

Kristin Jenkins, PhD Education and Outreach Program

National Evolutionary Synthesis Center 2024 W. Main Street, Suite A200 Durham, NC www.nescent.org Cell 919.260.7369 Office 608.203.5390

Kristin Jenkins <kjenkins@nescent.org>

Norman Evolution2011 Jun17-21 ProgramAvailable

Dear Colleagues,

The Evolution 2011 Program is now available for viewing on the main page of the meeting's website. The links are also on the "Latest News/Updates" page.

<http://www.evolution2011.ou.edu/> Also, the direct link to the searchable program is there too (<http://www.evolutionmeeting.org/engine/search/-index.php?func=summary>) We are looking forward to welcoming you all to Norman in a few weeks!

Best wishes!

Larry Weider, Rich Broughton, Ingo Schlupp
Department of Zoology, University of Oklahoma
Tri-Chairs, Evolution 2011 Organizing Committee
"Weider, Lawrence J." <ljweider@ou.edu>

Norman Evolution2011 Jun17-21 Registration

Registration for the Evolution 2011 meeting will remain at the current (early-bird) rates throughout the conference. We will continue to accept talk/poster submissions until 1 June, but those that are not complete by 11:59 pm (CDT) on Thursday 5 May will not appear in the printed program. Instead, they will be placed in a "late-breaking evolution" session.

Thanks!

Larry Weider, Rich Broughton, Ingo Schlupp
Dept of Zoology, U. of Oklahoma
Tri-Chairs, Evolution 2011 Organizing Committee
"Weider, Lawrence J." <ljweider@ou.edu>

Norman Evolution2011 Jun18 EducationOutreach

Outreach workshop at Evolution 2011 This workshop is for conference attendees who are interested in new materials for teaching human evolution and evolutionary medicine. Paul Beardsly of BSCS and Irene Eckstrand of NIH will present the newly developed NIH/BSCS Evolutionary Medicine Module. Members of the Communicating Human Evolution working group at NESCent will lead discussion of resources for teaching human evolution. The workshop is Saturday, June 18 10:30am -11:50am and will include lunch so attendees will be able to attend the Gould lecture at 12:00pm. There is a \$5 fee for lunch. Please register for the workshop and lunch by June 11 here: <http://tinyurl.com/6bpw565> . SSE EVO 101 Workshop: Evolution and You for K-14 Educators

Are you looking for great ways to engage students in evolutionary biology? Join us Friday June 17th at the Convention Center in Norman, OK, to learn about recent developments in evolutionary medicine and human evolution, preview new teaching materials from the National Institutes of Health and the Concord Consortium, and exchange ideas for teaching evolution with other teachers and researchers. A \$25 fee includes coffee and lunch, as well as a variety of materials for teachers to take and use in the classroom such as copies of the journals *Evolution: Education and Outreach* and *American Biology Teacher*. Participants will be eligible to attend the entire Evolution 2011 meeting, including a lecture by Ken Miller, this years recipient of the Gould award for effort in increasing public understanding of evolution. For more information visit this website: <http://www.evolution2011.ou.edu/workshops.html> . Kristin Jenkins, PhD Education and Outreach Program National Evolutionary Synthesis Center 2024 W. Main Street, Suite A200 Durham, NC www.nescent.org Cell 919.260.7369 Office 608.203.5390

Kristin Jenkins <kjenkins@nescent.org>

Norman iEvoBio Informatics Jun21-22

The Call for Lightning Talks is now open for the 2011 conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio), at <http://ievobio.org/ocs/index.php/ievobio/2011>. See below for instructions.

Lightning talks are short presentations of 5 minutes. They are ideal for drawing the attention of the audience to new developments, tools, and resources, or to subsequent events where more in-depth information can be obtained. Please also see our FAQ for more information (<http://ievobio.org/faq.html#lightning>). Lightning talks will be part of the more interactive afternoon program on both conference days.

Submitted talks should be in the area of informatics aimed at advancing research in phylogenetics, evolution, and biodiversity, including new tools, cyberinfrastructure development, large-scale data analysis, and visualization.

Submissions consist of a title and an abstract at most 1 page long. The abstract should provide an overview of the talk's subject. Reviewers will judge whether a submission is within scope of the conference (see above). If applicable, the abstract must also state the license and give the URL where the source code is available so reviewers can verify that the open-source requirement(*) is met.

Review and acceptance of lightning talks will be on a rolling basis. The deadline for submission is the morning of the first day of the conference (June 21). Note that the number of lightning talk slots is finite, and given the high volume of submissions we experienced for full talks, the Lightning Talks track may fill up early. We cannot accept lightning talks until the open-source requirements are met, and so waiting with that until the deadline risks that the track is full by that time.

We ask all submitters of lightning talks to be willing to also serve as reviewers of such, as described above.

Lightning talks are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Full talks (closed), 2) Challenge entries, 3) Software bazaar demonstrations, and 4) Birds-of-a-Feather gatherings. The Call for Challenge entries remains open (see <http://ievobio.org/challenge.html>), and information on the Software Bazaar and Birds-of-a-Feather sessions is forthcoming. There is also a special focus session on Metagenomics, Barcoding, and Biodiversity (<http://ievobio.org/program.html#specialsession>)

More details about the program and guidelines for contributing content are available at <http://ievobio.org>. You can also find continuous updates on the conference's Twitter feed at <http://twitter.com/iEvoBio> . iEvoBio is sponsored by the US National Evolution-

ary Synthesis Center (NESCent) in partnership with the Society of Systematic Biologists (SSB). Additional support has been provided by the Encyclopedia of Life (EOL).

The iEvoBio 2011 Organizing Committee: Rob Guralnick (University of Colorado at Boulder) (co-Chair) Cynthia Parr (Encyclopedia of Life) (co-Chair) Dawn Field (UK National Environmental Research Center) Mark Holder (University of Kansas) Hilmar Lapp (NESCent) Rod Page (University of Glasgow)

(*) iEvoBio and its sponsors are dedicated to promoting the practice and philosophy of Open Source software development (see <http://www.opensource.org/docs/definition.php>) and reuse within the research community. For this reason, if a submitted talk concerns a specific software system for use by the research community, that software must be licensed with a recognized Open Source License (see <http://www.opensource.org/licenses/>), and be available for download, including source code, by a tar/zip file accessed through ftp/http or through a widely used version control system like cvs, Subversion, git, Bazaar, or Mercurial.

robgur@gmail.com

Norman iEvoBio Informatics Jun21-22 2

The conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio) is holding a Challenge, a competition to create a new software tool, or add a new feature to an existing platform. Entries to the Challenge need to respond to its theme, which for 2011 is “Data Integration”.

Improving our understanding of the evolution of life requires combining data sets from a wide variety of disparate sources. Thus, data integration poses a serious challenge for evolutionary research. Entries for the 2011 iEvoBio challenge must enable new approaches to data interoperability or represent an exceptional example of integrating existing sources of data.

Further information on the nature of challenge entries and how to submit them can be found on the iEvoBio website at <http://ievobio.org/challenge.html>. Selected candidates will make short oral presentations to demonstrate their work in a “Challenge session” at the conference, and if suitable will automatically be entered into

the Software Bazaar track of the conference.

Cash prizes will be awarded for first place (\$1,000) and runner-up entries. The winning entries will be selected by a vote of the iEvoBio meeting participants.

Challenge entries are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Full talks (closed), 2) Lightning talks, 3) Software Bazaar entries, and 4) Birds-of-a-Feather gatherings. The Call for Lightning Talks is currently open (see <http://ievobio.org/ocs/index.php/ievobio/2011/>), and the information on Software Bazaar entries is forthcoming.

More details about the program and guidelines for contributing content are available at <http://ievobio.org>. You can also find continuous updates on the conference’s Twitter feed at <http://twitter.com/iEvoBio>, or subscribe to the low-traffic iEvoBio announcements mailing list at <http://groups.google.com/group/ievobio-announce>. iEvoBio is sponsored by the US National Evolutionary Synthesis Center (NESCent) in partnership with the Society for the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB). Additional support has been provided by the Encyclopedia of Life (EOL).

The iEvoBio 2011 Organizing Committee: Rob Guralnick (University of Colorado at Boulder) (Co-chair) Cynthia Parr (Encyclopedia of Life) (Co-chair) Dawn Field (UK National Environmental Research Center) Mark Holder (University of Kansas) Hilmar Lapp (NESCent) Rod Page (University of Glasgow)

hlapp@nescent.org

Norman iEvoBio Jun21-22 CallSoftwareBazaar

The Call for Software Bazaar entries is now open for the 2011 conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio), at <http://ievobio.org/ocs/index.php/ievobio/2011>. See below for instructions.

The Software Bazaar features presenters demonstrating their software live on a laptop. At iEvoBio, this session takes the place of a poster session, and will be approximately 2.0 hours in duration. Conference attendees will be able to walk from one demonstration to the next and open a conversation with the presenters. Please also see our FAQ for this information (<http://>

ievobio.org/faq.html#software). The Software Bazaar is part of the interactive afternoon program on the first conference day.

Entries should be software aimed at advancing research in phylogenetics, evolution, and biodiversity, and can include interactive visualizations that have been pre-computed (such as SVGs, or Google Earth-compatible KML files).

Submissions consist of a title, which will typically be the name of the software (or visualization method) being presented, the URL of a website where more information about the software can be obtained, and the license under which the source code is available. The provided website must contain a link to where the source code (and possibly binaries) can be downloaded. If it is not obvious from the provided website, the submission must describe what the software does. Reviewers will judge whether a submission is within scope of the conference (see above), and need to be able to verify whether the open-source requirement(*) is met.

Presenters are expected to bring their own laptops for presentation, and any auxiliary devices necessary (such as a mouse). Power will be available at the presentation tables (110V/60Hz, US-style plugs; international presenters need to bring a suitable adaptor). Please let the organizing committee know as much in advance as possible if you expect to have unusually high demands for wireless network bandwidth, a large display, or other hardware. Note that commercial marketing activities are not permitted - presenters wishing to promote commercial or proprietary services or products should contact the Evolution conference about exhibitor space.

Review and acceptance of Software Bazaar submissions will be on a rolling basis. The deadline for submission is the morning of the first day of the conference (June 21). As the number of Software Bazaar presentation slots is finite, we cannot guarantee the availability of slots up until the day of the conference. We cannot accept submissions until the open-source requirements are met.

We ask all submitters of Software Bazaar presentations to be willing to also serve as reviewers of such, as described above.

Software Bazaar demonstrations are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Full talks (closed), 2) Lightning talks, 3) Challenge entries, and 4) Birds-of-a- Feather gatherings. The Calls for Challenge entries (<http://ievobio.org/challenge.html>) and Lightning Talks (same submission URL as above) remain open, and information on the Birds-of-a-Feather session is forthcoming.

More details about the program and guidelines for contributing content are available at <http://ievobio.org>. You can also find continuous updates on the conference's Twitter feed at <http://twitter.com/iEvoBio>. iEvoBio is sponsored by the US National Evolutionary Synthesis Center (NESCent) in partnership with the Society for the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB). Additional support has been provided by the Encyclopedia of Life (EOL).

The iEvoBio 2011 Organizing Committee: Rob Guralnick (University of Colorado at Boulder) (Co-chair) Cynthia Parr (Encyclopedia of Life) (Co-chair) Dawn Field (UK National Environmental Research Center) Mark Holder (University of Kansas) Hilmar Lapp (NESCent) Rod Page (University of Glasgow)

(*) iEvoBio and its sponsors are dedicated to promoting the practice and philosophy of Open Source software development (see <http://www.opensource.org/docs/definition.php>) and reuse within the research community. For this reason, software to be demonstrated to conference attendees must be licensed with a recognized Open Source License (see <http://www.opensource.org/licenses/>), and be available for download, including source code, by a tar/zip file accessed through ftp/http or through a widely used version control system like cvs, Subversion, git, Bazaar, or Mercurial. Authors are advised that

— / —

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

Paris Morphological Evolution Jun13-15

*** Paris Interdisciplinary PhD symposium - June 13-15th, 2011, Paris - Registration deadline May 15th ***

Dear colleague,

We are pleased to announce the 2nd Paris Interdisciplinary PhD symposium, organized by PhD students of the European interdisciplinary graduate school "Frontiers in Life Sciences".

This symposium aims at gathering young researchers (master and PhD students, post-docs) from diverse fields (biology, physics, chemistry, mathematics, computer science, â) together with eminent researchers to

discuss and interact in a relaxing and friendly atmosphere, at the heart of Paris (France).

The topic of this year is:

“Shapes in living systems”.

During the meeting, speakers will present their research in a way accessible to scientists coming from different backgrounds in order to lay grounds for relevant and exciting discussions. Lectures will be supplemented with thematic round tables, poster sessions and informal dinner discussions. Emphasis will be put on interactions, discussions and exchanges of ideas between all participants, students and lecturers alike, giving an opportunity for young scientists to create networks and get in touch with the international speakers who will be present.

For more information please visit the website of the event: <http://symposium.fdv-paris.org>. In addition, this website will also provide an easily-accessible platform to foster interactions between participants before, during and after the symposium, in particular via a blog section.

The deadline for online registration to the symposium is May 15th, 2011.

Please feel free to forward this information to anyone interested.

We hope to see you in Paris in June!

Best regards,

The Paris Interdisciplinary PhD Symposium 2011 team

<http://symposium.fdv-paris.org> Confirmed speakers: Jean-François Joanny, Institut Curie Jacques Prost, ESPCI Robert D. Goldman, NorthWestern University Dennis Discher, University of Pennsylvania Eshel Ben-Jacob, Tel-Aviv University Ron Eglash, Rensselaer Polytechnic Institute, Audrey Bennett, Rensselaer Polytechnic Institute Botond Roska, Friedrich Miescher Institute Kumaran Ramamurthi, US National Cancer Institute Patrick Eichenberger, New York University Nicolas Thoma, Friedrich Miescher Institute Anthony Herrel, Muséum National d'Histoire Naturelle Kerwyn Casey Huang, Stanford University Linda Smith, Indiana University

and others

– Paris Interdisciplinary PhD Symposium 2011 ED 474 *Frontiers in Life Sciences* <http://symposium.fdv-paris.org/> Movies of last edition of PIPS (2009) : <http://vimeo.com/album/1554718> Facebook < <http://www.facebook.com/event.php?eid=157704287619668> >, Linked In < <http://events.linkedin.com/Paris-Interdisciplinary-PhD-Symposium/pub/634597> > and

tweets on @fdvPIPS

Paris Interdisciplinary PhD Symposium
<symposium@fdv-paris.org>

Porto Portugal Ancient Human DNA Nov23-25

Dear Evoldir Members,

We are happy to announce that the ***call for abstracts*** concerning the international conference “COMPARING ANCIENT AND MODERN DNA VARIABILITY IN HUMAN POPULATIONS” to be held in Porto (Portugal), November 23-25, 2011 is now open!

The aim of the conference is to compare the results emerging everywhere about the genetic variability of ancient populations with the modern variability of their supposed descendants, or with populations inhabiting the same region. Contemporary ancient DNA technology allows the typing of several specimens and a population genetics approach of ancient and remote populations is now emerging. With this meeting we want to give emphasis to this new dimension of ancient DNA studies that equally challenges scholars working with modern or ancient material.

For more details we invite you to check the following website: http://www.mnhn.fr/mnhn/-ecoanthropologie/Porto2011/Porto2011_index.html
Thank you!

Franz Manni and Jorge Rocha, convenors

Franz Manni <manni@mnhn.fr>

Queens University Belfast Systematics Jul4-8

***** EARLY REGISTRATION CLOSES IN ONE WEEK *****

8TH SYSTEMATICS ASSOCIATION BIENNIAL QUEEN'S UNIVERSITY BELFAST 4-8 JULY 2011

Dear Colleagues,

We are pleased to announce that registration is open for the 8th biennial conference of the Systematics As-

sociation, held for the first time in Northern Ireland!

There is an exciting programme that includes both plenaries and thematic symposia, as well as a large number of contributed sessions. Currently scheduled symposia include:

- Next Generation Systematics - Studying Evolution and Diversity in an Era of Ubiquitous Genomics - Arthropod Systematics: are Morphology, Palaeontology and Molecules Coming Together? - Algal Systematics: Where Next? - Advances in Using Museum Specimens and Ancient DNA in Systematics Research

Symposia will include a mixture of talks from invited speakers and other contributions. The Biennial also presents excellent opportunities for contributed papers on any aspect of systematics and is a great forum for students and young researchers to present their work. For further details, please see <http://www.systass.org/-biennial2011/>. On behalf of the conference organisers, we hope to see you there!

Juliet Brodie, President James Cotton, Programme Officer Peter Olson, Treasurer Christine Maggs, Local Organiser

Sponsors: The Linnean Society of London, British Phycological Society, Cambridge University Press, Genetics Society, Queen's University Belfast

James Cotton Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge. CB10 1SA UK

james.cotton@sanger.ac.uk 01223 494864

james.cotton@sanger.ac.uk

Roscoff France Coevolution Sep3-7 DeadlineMay20

We would like to inform you that the deadline for the registration to the Jacques Monod Conference "Coevolutionary arms race between parasite virulence and host immune defense: Challenges from state of the art research" 3-7 September 2011 Roscoff (France), has been extended to May 20th.

A Jacques Monod Conference entitled "Coevolutionary arms race between parasite virulence and host immune defense: Challenges from state of the art research" will be held at the Marine Station CNRS at Roscoff (France) from 3rd to 7th September 2011.

The conference is organized by Gabriele Sorci (Dijon, France) and Manfred Milinski (Ploen, Germany).

Deadline for application: May 20 2011

Registration fee (including board and lodging)

400 euros for PhD students

600 euros for other participants

Application for registration

The total number of participants is limited to 115 and all participants are expected to attend for the whole duration of the conference. Selection is made on the basis of the affinity of potential participants with the topics of the conference. Scientists and PhD Students interested in the meeting should send:

their curriculum vitae the list of their main publications for the 3 last years the abstract of their presentation

to the*Chairperson of the conference* (Gabriele.sorci@u-bourgogne.fr) before the deadline. After it, the chairman will select the participants. Except in some particular cases approved by the Chairperson, it is recommended that all selected participants present their work during the conference, either in poster form or by a brief in-session talk. The organizers choose the form in which the presentations are made. No payment will be sent with application. Information on how and when to pay will be mailed in due time to those selected.

For further information please visit the following web site (<http://www.cnrs.fr/insb/cjm/2011/sorci.e.html>)

Gabriele Sorci (Gabriele.sorci@u-bourgogne.fr) and Manfred Milinski (milinski@mail.evolbio.mpg.de)

gabriele.sorci@u-bourgogne.fr

Shanghai LifeScienceModelling Sep25-30

Modelling in the Life Sciences, Shanghai 25-30 September 2011

Dear Colleagues,

On behalf of the programme committee, I am pleased to announce an International Conference on Modelling in the Life Sciences. This will be held at Fudan University, Shanghai, China, on 25th - 30th September 2011.

The conference will cover a broad range of subjects

that constitute or closely involve the Life Sciences, and will include topics where mathematical modelling has proven to be an indispensable way to gain understanding and knowledge of the science.

Registration and the call for abstracts is now open; see <http://math.fudan.edu.cn/ccsb/con11.htm> With regards,

David.

David Waxman dwxman.biology@gmail.com
www.dwaxman.com David Waxman
 <dwxman.biology@gmail.com>

Spain EvolutionEpigenetics Sep18-23

EPIGENETICS IN CONTEXT: FROM ECOLOGY TO EVOLUTION CONFERENCE

Senior and emerging researchers including evolutionary ecologists, population geneticists and molecular epigeneticists are invited to apply for the **Epigenetics in Context: From Ecology to Evolution Conference**. This conference is organised by the European Science Foundation (ESF) in partnership with the European Molecular Biology Organization. The conference will take place on **18 - 23 September 2011** in **Sant Feliu de Guixols, Spain**.

Submission Deadline: **14 June 2011** **Grants for Young and Early Stage Researchers** available. Further information can be found below and at: [www.esf.org/conferences/11357](<http://www.esf.org/index.php?id=7235>)

Epigenetics in Context: From Ecology to Evolution **18 - 23 September 2011**

Chaired by: **Dr. Vincent Colot**, Ecole Normale Supérieure Paris, FR **Dr. Oliver Bossdorf**, University of Bern, CH

We would very much appreciate it if you would circulate this announcement among your colleagues and contacts.

Programme

Ecological and Evolutionary Epigenetics is a new field of frontier research at the intersection between molecular genetics and evolutionary ecology. Research in this field is rapidly expanding because of the growing

realization that epigenetic processes, notably those involving DNA methylation, might be much more relevant for ecology and evolution than previously acknowledged. This conference would, to the best of our knowledge, be the first to bring together evolutionary ecologists, population geneticists and molecular epigeneticists, with the specific aim of setting ecological and evolutionary epigenetics on a strong theoretical and experimental footing. It will cover research on plants, animals and humans. **[[More]]**(<http://www.esf.org/-activities/esf-conferences/details/2011/confdetail357/-357-preliminary-programme.html>)

Invited speakers will include

Malika Ainouche, University of Rennes 1, FR
David Baulcombe, University of Cambridge, UK
Justin Borevitz, University of Chicago, US
Dorah Bourcâhis, Institut Curie Paris, FR
Vicki Chandler, University of Arizona, US
Caroline Dean, John Innes Center, UK
Regis Ferrière, Ecole Normale Supérieure Paris, FR
Ueli Grossniklaus, University of Zurich, CH
Carlos Herrera, Estación Biológica de Doñana CSIC, ES
Eva Jablonka, University of Tel-Aviv, IL
Frank Johannes, University of Groningen, NL
Claudine Junien, INRA Jouy-en-Josas, FR
Bill Kelly, Emory University, US
Rob Martienssen, Cold Spring Harbor Laboratory, US
Ortrun Mittelsten Scheid, Gregor Mendel Institute, AT
Jerzy Paszkowski, University of Geneva, CH
Stéphane Ronsseray, University of Paris 6, FR
Dirk Schübeler, Friedrich Miescher Institute, CH
Koen Verhoeven, Netherlands Institute of Ecology, NL
Jason Wolf, University of Bath, UK

How to Participate

Attendance is possible only after successful application. Full conference programme and application form accessible from [www.esf.org/conferences/11357](<http://www.esf.org/index.php?id=7235>).

A certain number of grants are available for students and early stage researchers to cover the conference fee and possibly part of the travel costs.

Closing date for applications: **14 June 2011**

European Science Foundation <conferences-info@esf.org>

Stockholm
EvolutionEnvironmentChange
Jun13

Dear EvoDir members,

We would like to invite you to a Symposium on Evolutionary Genetics and Environmental Change. The event will take place on Monday June 13th, 2011 between 9am-5pm at Störa Hörsalen, the Swedish Museum of Natural History in Stockholm.

Invited speakers: Juha Merila, University of Helsinki, Finland Ian Barnes, Royal Holloway University of London, UK Thomas Gilbert, University of Copenhagen, Denmark Nils Christian Stenseth, University of Oslo, Norway Mattias Jakobsson, Uppsala University, Sweden Per Palsboll, Stockholm University, Sweden Jakob Høglund, Uppsala University, Sweden

Please register by sending an email with name and title to: meetsymposium@gmail.com Registration deadline: June 8th. Registration is not mandatory for attendance but coffee/cake will be provided to those who register.

For more information and the detailed program please follow the link: http://www.zoologi.su.se/Symposium-Evolutionary_Genetics_and_Environmental_Change.pdf

The event is organized by the Molecular Ecology and Evolution forum (MEET).

Kind regards,

Eleftheria Palkopoulou, PhD student Molecular Systematics Laboratory Swedish Museum of Natural History Box 50007 SE-104 05 Stockholm SWEDEN Phone: +46 (0)8 5195 5162

Eleftheria.Palkopoulou@nrm.se

UCalifornia SanFrancisco Evolution
and Cancer Jun3-5

We need you! Because both the process of carcinogenesis and therapeutic resistance are evolutionary processes among somatic cells, evolutionary biology is fundamental to cancer biology. However, cancer research

has suffered from a lack of evolutionary biologists. We hope that you will join the field. A good way to start would be with the following conference:

We are excited to announce the First biannual international Evolution and Cancer Conference, June 3-5, 2011 at the University of California San Francisco (<http://cancer.ucsf.edu/evolution/conference-2011>). This conference is being hosted by the new Center for Evolution and Cancer at UCSF (<http://cancer.ucsf.edu/evolution>) and the Helen Diller Family Comprehensive Cancer Center. Speakers include Robert Gatenby (Moffitt Cancer Center), Carlo Maley (UCSF), Nicole King (Berkeley), Douglas Brash (Yale), Brian Reid (Fred Hutchinson Cancer Research Center), David Haig (Harvard), Steven Quake (Stanford), John Pepper (NCI), David Haussler (UCSC), Athena Aktipis (Arizona State), John Tooby (UCSB), Steven Neuberg (Arizona State), AJ Figueredo (U Arizona), Martie Haselton (UCLA) and Randolph Nesse (U Michigan).

Registration is required by May 25, but is free (<http://cancer.ucsf.edu/evolution/conference-2011>) and lunch will be provided for registered participants. Questions should be sent to ECC2011@evolutionandcancer.org.

Location and times: 9am-6pm, June 3, Mission Bay Conference Center, Fisher Hall, University of California, San Francisco

9am-6pm, June 4-5 Mission Bay, Byers Hall, University of California, San Francisco

Carlo C. Maley, Ph.D. Associate Professor Director, Center for Evolution and Cancer Helen Diller Family Comprehensive Cancer Center Department of Surgery University of California, San Francisco 2340 Sutter St. Box 1724 San Francisco, CA 94115

Carlo.Maley@ucsfmedctr.org

UCaliforniaSanFrancisco
EvolutionCancer Jun3-5

Evolution and Cancer Conference USCF June 3-5, 2011

First biannual international Evolution and Cancer Conference To inaugurate the world's first Center for Evolution and Cancer. Register by May 25th. No fee. 9am-6pm, June 3, Mission Bay Conference Center, Fisher Hall, UCSF 9am-6pm, June 4-5 Mission Bay, Byers Hall, UCSF Leading scientists in the evolutionary biology of cancer, theoretical biology and human evolution

will [...]

See <http://evmedreview.com/?p=695> –

Dr. B. Crespi, FRSC Professor of Evolutionary Biology Department of Biosciences Simon Fraser University, Burnaby BC V5A1S6 Canada 778 782 3533 phone 778 782 3496 fax <http://www.sfu.ca/biology/faculty/-crespi/> “crespi@sfu.ca” <crespi@sfu.ca>

USheffield EvolutionaryEcol Sep12-14

The abstract submission deadline for the 2011 meeting of the British Ecological Society is 22nd May 2011. Submit your abstract here:

http://www.britishecologicalsociety.org/meetings/-current_future_meetings/2011_annual_meeting/-index.php This year’s meeting (12-14th September) is at the University of Sheffield, UK.

An outstanding pair of keynote addresses and exciting thematic sessions are on offer, including sessions focused on evolutionary ecology:

Keynotes: BES Lecture: Prof. Jules Pretty Tansley
Lecture: Diana Wall

Thematic Topics: – Applying ecological research to address food security and sustainable production – Peatland Ecosystems – ‘Systems Ecology’ approaches to infectious disease – Parasites and Invasion – The role of soil ecological processes in ecosystem responses to global change – The ecological causes of evolution – Invasive Management

Don’t miss what is probably the largest meeting of ecologists in Europe!

a.beckerman@sheffield.ac.uk

UStAndrews Phylogeny Jun16

Dear Evoldir,

The first meeting of the Scottish Phylogeny Discussion Group will be at the University of St Andrews on 16th June 2011, 1 PM to 5:30 PM.

Professor Dannie Durand (Carnegie Mellon University) will talk on “Detecting incomplete lineage sorting and gene duplication in non-binary species trees”.

Her talk will be followed by several presentations by researchers based more locally.

Attendance is free, but please register in advance. For information and registration see:

<http://biology.st-andrews.ac.uk/cegg/spdg> Best wishes,

Daniel

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

db60@st-andrews.ac.uk

UStAndrews Phylogeny June16

Dear Evoldir,

Final reminder -

The first meeting of the Scottish Phylogeny Discussion Group will be at the University of St Andrews, UK, on 16th June 2011, 1 PM to 5:30 PM.

Professor Dannie Durand (Carnegie Mellon University) will talk on “Detecting incomplete lineage sorting and gene duplication in non-binary species trees”.

Her talk will be followed by several presentations by researchers based more locally.

Attendance is free, but please register in advance. For registration and further details, please see:

<http://biology.st-andrews.ac.uk/cegg/spdg> Thank you,

Daniel

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

db60@st-andrews.ac.uk

West Virginia Malaria Evolution Aug5-7

SECOND ANNOUNCEMENT

International Meeting on Malaria and Related Haemosporidian Parasites of Wildlife

Friday August 5th V Sunday August 7th, 2011

National Conservation Training Center, Shepherdstown, West Virginia

Sponsored by the NSF Research Coordination Network for Haemosporida of Terrestrial Vertebrates1

Organized by: Robert Fleischer and Ellen Martinsen, Smithsonian Institution Ravinder Sehgal, San Francisco State University

Dear Colleagues,

The NSF-sponsored Research Coordination Network for Haemosporida of Terrestrial Vertebrates invites you to participate in a three-day meeting on Malaria and Related Haemosporidian Parasites of Wildlife (<http://malariarcn.org/conference>). The meeting includes a Plenary address by Dr. Andrew Read, and invited Keynote talks by Drs. Jane Carlton, Sarah Knowles, Robert Ricklefs, and Gediminas Valkiunas. There will also be general paper and poster sessions, plus a taxonomy training session and roundtable discussions.

Topics for the meeting center around the Haemosporida of wildlife and include: haemosporidian systematics and genomics, species limits and definitions, generalist versus specialist parasites, evolution of virulence, geographic distribution of vectors and hosts, host shifts and emerging infectious diseases, parasite ecology, and vector-parasite relationships.

The meeting will commence on Friday morning, August 5th, with an optional half-day training session on haemosporidian classical taxonomy. Keynote talks and general paper and poster sessions will follow on Friday afternoon, Saturday, and Sunday morning. The meeting will end on Sunday afternoon, August 7th, with optional roundtable discussions on Limits in the Haemosporidians and Parasite Databases.

All food, lodging and meeting events will take place at the US Fish & Wildlife Services National Conservation Training Center in Shepherdstown, West Virginia, a site easily accessible through Washington, DC, area

airports.

Details, including conference logistics, an overview of events, the program of invited speakers, and the call for abstracts are available at <http://malariarcn.org/conference>. Further information can also be obtained from the meeting organizers (email: MalariaRCNMeeting@gmail.com).

The meeting will be preceded by a four-day workshop, suitable for beginning investigators, on the field, microscopic, molecular, and analytical methods to study haemosporidian parasites of wildlife. The workshop will begin early Monday morning, August 1st and continue through Thursday night, August 4th (email MalariaRCNWorkshop@gmail.com).

1 The Research Coordination Network for Haemosporida of Terrestrial Vertebrates (RCN), sponsored by the U. S. National Science Foundation and funded through 2015 at the University of Missouri-St. Louis, was established to promote communication among researchers working on the ecology and evolution of haemosporidian parasites of vertebrate wildlife populations (website: www.malariarcn.org).

“Fleischer, Robert” <FleischerR@si.edu>

Wuerzburg Germany GermanGeneticsSociety Sep14-16

Dear colleagues and friends,

we kindly would like to inform you about the upcoming abstract deadline for the Annual Conference of the German Genetics Society (GfG) from 14 to 16 September 2011 in Würzburg, Germany.

The conference traditionally is a meeting point for scientists and students from all fields of Genetics, including evolutionary and population genetics. Leading experts will present latest developments and research results in plenary and parallel sessions. A comprehensive poster exhibition will further promote the scientific exchange and discussions.

Detailed information, including preliminary program, conference venue and abstract submission details can be found following the link: <http://www.conventus.de/-index.php?id=genetics2011-home> The full list of conference topics include:

â Developmental genetics â Disease genetics â Epigenetics â Evolutionary genetics â Molecular genetics â

Neuro- and behavioral genetics à Population genetics and Genetic epidemiology

We welcome abstract submissions for one of these topics in English language online until 1 June 2011 (<http://www.conventus.de/index.php?id=genetics2011-registration>).

Please do not hesitate to contact us for further informa-

tion and questions. We are looking forward to welcome you in Würzburg in September!

Prof. Dr. Karl Schmid University of Hohenheim email: karl.schmid@uni-hohenheim.de

Dr. Bettina Harr Max-Planck Institute for Evolutionary Biology email: harr@evolbio.mpg.de

Bettina Harr <bettina.harr@mac.com>

GradStudentPositions

BangorU NGS biomonitoring	22	UExeter ViralEvolution	29
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BangorU NGS biomonitoring

PhD position: Enhancing freshwater ecosystem biomonitoring: defining and testing a next generation sequencing biodiversity identification framework.

Applications are invited for a fully-funded PhD studentship for full time study in the Molecular Ecology and Fisheries Genetics Laboratory (<http://mefgl.bangor.ac.uk>), School of Biological Sciences, supervised by Dr Simon Creer and Prof Gary Carvalho, to start no later than October 2011.

Summary of project: Biological indicators are used to estimate the state of the environment, in association with management thresholds for management action. The need for indicators is driven by global

initiatives in addition to European legislation. The UK Environment Agency (EA) mandatorily monitors the health of freshwater ecosystems throughout Wales. However, traditional monitoring approaches suffer from the identification bottleneck problem (e.g. lack of species-level resolution and the mismatch between ecosystem diversity and traditional morphological taxonomy). At the MEFGL we have recently developed a DNA-based biodiversity identification (metagenetic) approach that facilitates the identification of biodiversity on a massive scale using next generation sequencing (<http://www.nature.com/ncomms/journal/v1/n7/abs/ncomms1095.html>). Such approaches may be employed to enhance the field of biomonitoring, following the establishment of a DNA reference library. In this project, in collaboration with the Environment Agency (<http://www.environment-agency.gov.uk/>) we will populate a DNA reference library for up to 200 macroinvertebrate indicator species and test the metagenetic approach using controlled con-

ditions. Full funding and project details can be accessed here <http://www.higherskillswales.co.uk/kess/-vacancies.php.en> Summary of school: The successful applicant will join the large, thriving team in the MEFGL within the School of Biological Sciences Molecular Ecology and Evolution Group, one of the largest research areas within the University. Housed within the new Environment Centre Wales Building, the MEFGL benefits from fully equipped molecular labs, newly refurbished aquarium facilities and advanced bioinformatic analysis capability.

Bangor is located in North West Wales, situated in an area of outstanding natural beauty between Snowdonia National Park and the sea (<http://www.bangor.ac.uk/bangortv/bangorandthearea.php>). International links are facilitated easily via both Liverpool and Manchester airports.

The studentship includes a tax free maintenance grant of 14k per annum, with full-time fees paid and additional allowances. A requirement of the studentship is a minimum 30-day non-remunerated work placement per annum. More information on the studentship and application process can be found at www.higherskillswales.co.uk/kess The position has some fairly specific eligibility requirements (c.f. below). Informal enquiries regarding these and the project should be addressed to Dr. Simon Creer (s.creer@bangor.ac.uk; <http://mefgl.bangor.ac.uk/si.php>) in the first instance.

The closing date for formal applications will be 20th May 2011 and short-listed applicants will be required to attend an interview, initially scheduled to occur within the week of 6th-10th June, with an anticipated start date of no later than October 2011.

Eligibility To be eligible to participate in the KESS programme, prospective students must be resident in the Convergence Area (West Wales and the Valleys) on application, and be able to work in the Convergence Area upon completion of the scholarship.

Knowledge Economy Skills Scholarships (KESS) is a pan-Wales higher level skills initiative led by Bangor University on behalf of the HE sector in Wales. It is part funded by the Welsh Assembly Governments European Social Fund (ESF) convergence programme for West Wales and the Valleys.

– Simon Creer Senior Research Fellow Molecular Ecology and Fisheries Genetics Lab Environment Centre Wales Building School of Biological Sciences Bangor University Bangor Gwynedd LL57 2UW UK

e-mail: s.creer@bangor.ac.uk Tel: +1248 382302
Fax: +1248 382569 Home Page: [http://](http://mefgl.bangor.ac.uk/si.php)

[/mefgl.bangor.ac.uk/si.php](http://mefgl.bangor.ac.uk/si.php)
<s.creer@bangor.ac.uk>

“Creer,Simon”

CEFEMontpellier Forestbiodiversity

Title: Forest biodiversity and ecosystem functioning

Objectives: With an unprecedented effort at the European level, the EU project FunDivEUROPE (Functional significance of forest biodiversity in Europe, <http://www.fundiveurope.eu>) funded within the FP7 ENVIRONMENT will examine the multifunctional role (e.g. productivity, carbon and nutrient cycling, water cycling, forest pest resistance) of tree diversity for forest ecosystem functioning. This will be done by incorporating existing tree diversity experiments where tree species have been experimentally planted at different diversity levels, and the establishment of experimental plots within naturally occurring tree diversity gradients in six different regions of Europe harboring distinct forest ecosystems types (boreal forest - Finland ; mixed broadleaved-coniferous forest - Bialowieza, Poland ; montane mixed broadleaved-coniferous forest - Romania ; temperate broadleaf forest - Germany ; sub-mediterranean deciduous forest - Italy ; mediterranean evergreen forest - Spain). The PhD thesis advertised here will focus on carbon and nutrient recycling during decomposition of aboveground plant litter across the different forest ecosystems. The two main questions asked in this PhD project are 1) how does tree diversity affect decomposition of organic matter as a major determinant of the ecosystem C cycle and nutrient fluxes, and 2) whether this biodiversity effect differs among major European forest ecosystems and to what extent these differences are related to climatic conditions. This PhD thesis contributes to an integrative view of the importance of tree diversity for the productivity and stability of European forest ecosystems under climate change. Please contact Stephan Hättenschwiler (stephan.hattenschwiler@cefe.cnrs.fr) for further details.

Funding/Supervisors: A 3-year PhD salary (starting in fall 2011) is available from the 4-year European research grant FunDivEUROPE. The PhD project is supervised by Stephan Hättenschwiler (Centre d'Ecologie Fonctionnelle et Evolutive, CEFÉ-CNRS Montpellier) http://www.cefe.cnrs.fr/-fe/staff/Stephan_Hattenschwiler.htm and Michael Scherer-Lorenzen (University of Freiburg, Germany)

<http://www.biologie.uni-freiburg.de/data/bio2/-geobotanik/Scherer-Lorenzen/index.html> . Applications: Applications including CV, letter of motivation and two letters of recommendation from supervisors of previous projects should be send to Stephan Hättenschwiler. The successful candidate should be trained in at least one of the scientific fields of plant ecology, functional ecology, biogeochemistry, or soil ecology. He/she should also be experienced in experimental approaches, should work easily in a team, take responsibility and contribute to a collaborative research effort. He/she should be willing to travel across Europe for field work, and should have an exceptional capacity to communicate in English. Experience in chemical analyses, and knowledge in the statistical analysis of complex data sets would be welcome.

Dr. Stephan Hättenschwiler Center of Functional Ecology and Evolution CEFE-CNRS 1919, route de Mende F-34293 Montpellier cedex 5

New phone and fax number! Tel. +33 (0)4 67 61 32 36 Fax +33 (0)4 67 61 33 36 email: stephan.hattenschwiler@cefe.cnrs.fr

http://www.cefe.cnrs.fr/fe/staff/-Stephan_Hattenschwiler.htm ESF EuroDIVERSITY project: <http://biocycle.cefe.cnrs.fr/> stephan.hattenschwiler@cefe.cnrs.fr

EAWAG Switzerland Evolutionary Adaptation

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is a Swiss-based and internationally networked aquatic research institute within the ETH domain (Swiss Federal Institute of Science and Technology). It is committed to the ecologically, economically and socially responsible management of water resources and aquatic ecosystems.

The Department of Aquatic Ecology seeks a Ph.D. student to study

Eco-evolutionary responses of stream insects to glacial retreat

Climate change induced glacial retreat is occurring rapidly and in a replicated fashion (i.e. over multiple catchments and continents), providing a natural experiment for studying organismal and species diversity responses to environmental change. The primary

objective of the project is to understand the determinants of alpine stream macroinvertebrate responses to climate change induced glacial recession. The study will be conducted in replicated glacial systems within Switzerland and focuses on intraspecific phenotypic and genetic variation using experimental and population genetics approaches, in combination with spatio-temporal patterns in species distribution in nature.

The Department of Aquatic Ecology is situated in Dübendorf (near Zürich) and offers an international and dynamic environment with broad expertise in ecology and evolution. The working language is English. The project is conducted in collaboration with Dr. Katja Räsänen and Dr. Irene Keller, Departement of Aquatic Ecology, Eawag, Switzerland. A diploma or M.Sc. (or equivalent) degree in biology or related area is mandatory. The ideal candidate has a strong interest in evolutionary ecology, previous experience in population genetics and/or experimental studies and is able to conduct field work under (occasionally) challenging conditions.

The target starting date for the position is September 2011. The application should include an application letter (with a statement of research interests and relevant experience), a CV and a list of publications (if any), copies of academic qualifications and the names and e-mail addresses of three referees. The deadline for applications is June 6, 2011.

Applications must be submitted with the online-application tool, using the following link: <http://internet1.refline.ch/673277/0048/++publications+/-1/index.html> For further information consult www.eawag.ch or contact PD Dr. Chris Robinson (robinson@eawag.ch).

“Rasanen, Katja” <Katja.Raesaenen@eawag.ch>

Frankfurt FungalMetagenomics

PhD: Frankfurt.Fungal metagenomic

TheSchmitt laboratory at the Biodiversity and Climate Research Centre (BiK-F), Frankfurt, Germany, offers the position of a PhD student “Fungal communities on-poplar” [Ref.#C44]. The successful candidate will have a Master of Science (MSc) or equivalent in evolutionary biology, molecular biology, molecular ecology or related fields, and a strong interest in plant-fungal interactions, mycology. Experience in molecular laboratory

techniques and DNA sequence analysis, next generation sequencing, bioinformatics and statistics are an advantage. Furthermore, good written and oral communication skills in English, teamwork skills, the willingness to write research-funding proposals and to learn some German are essential for awarding research. Working language will be English.

We are applying metagenomics techniques to questions of evolution, climate change and fungal community composition. The focus of this position will be on the environmental influences and evolutionary processes acting on the communities of leaf-associated fungi in balsam poplar. You will use standard molecular genetic techniques as well as next-generation sequencing technology. Within the Biodiversity and Climate Research Centre you will have ample opportunities to interact and collaborate with faculty, postdocs and PhD students specializing in a variety of topics, such as biogeography, phylogenetics, macroecology, genomics, modeling, and bioinformatics. Frankfurt am Main is an attractive city in beautiful surroundings, with a multicultural population, and many educational and recreational opportunities. The Research Centre BiK-F advocates gender equality. Women and other underrepresented groups are strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference. The contract shall start on August 15 2011 and will be limited to three years. The start date is somewhat flexible. Salary and benefits are according to a public service position in Germany (TV-H E 13, 50%). The employer is the Senckenberg Gesellschaft fuer Naturforschung, the place for work is Frankfurt am Main, Germany. Please send your application by e-mail attachment, mentioning the reference of this position (#C44) and including (1) a letter outlining your interest in this kind of research, and your suitability for the post, (2) a detailed CV, (3) contact details of 2 referees and (4) a copy of your thesis and other relevant exams: Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. E-mail to Service and Finances: recruiting@senckenberg.de. Review of applications will begin on July 1, 2011, and continue until a suitable candidate is identified.

Informal inquiries to Imke Schmitt (imke@senckenberg.de) before the application are welcome.

imke@senckenberg.de

Jena 8 Evolutionary Biol

8 PhD fellowships in Jena, Germany, available The International Max Planck Research School (IMPRS) "The Exploration of Ecological Interactions with Molecular and Chemical Techniques" in Jena, Germany, is offering 8 PhD fellowships beginning in January 2012. 15 different projects are available including 4 projects with a strong evolutionary focus. Students holding a Master's degree (or equivalent) in molecular biology, ecology, zoology, microbiology, chemistry, biochemistry and neuroethology, with a proven record of success in one of the disciplines and interest in examining ecological interactions, are eligible to conduct a doctoral project within the IMPRS. Deadline for applications is June 26, 2011. For detailed information on the IMPRS, projects offered and the application procedure please check our website <http://imprs.ice.mpg.de> Karin

Karin Groten <kgroten@ice.mpg.de>

McGillU 2 Chipmunk Evolution

We are seeking two highly motivated PhD students to join our multidisciplinary research team working on different aspects of eastern chipmunks (*Tamias striatus*) evolutionary ecology in Southern Quebec, Canada.

The candidates will work with researchers from McGill University (Murray Humphries), Univ. of Sherbrooke (Dany Garant and Fanie Pelletier) and UQAM (Denis Réale) on a research project investigating the factors maintaining phenotypic and genetic variation in the wild. More specifically, depending on the interests of the candidates, different projects are available integrating aspects of behaviour, ecophysiology, genetics and population dynamics of chipmunks.

The fieldwork will take place 3-4 months each summer in southern Quebec. Ideally, the candidate will have previous research and fieldwork skills (MSc in biology or equivalent), and experience in handling of small mammals would also be an advantage.

The positions are open and funded for three years as

soon as September 2011. Please apply by sending your CV, including the email addresses of two referees, and a letter of motivation by 15 August 2011 to manuelle.landry-cuerrier@mcgill.ca. Candidates that are eligible to apply for scholarships from NSERC (Canada), FQRNT (Quebec) or international sources will be given priority.

Dany Garant Associate Professor Department of Biology University of Sherbrooke Sherbrooke QC J1K 2R1 Canada

Tel: (819) 821-8000 ext.63198 Fax: (819) 821-8049
Courriel: Dany.Garant@USherbrooke.ca

<http://pages.usherbrooke.ca/dgarant/>
dany.garant@usherbrooke.ca

Montpellier MusSpeciation

PhD Research project Genomics of speciation in the house mouse

We invite applications for a PhD research project on the *genomics of speciation in the house mouse*, Montpellier, France.

The PhD project will be part of a French Research Council ANR-funded project which involves scientists from the UK, USA and France and which addresses the mechanisms of sexual isolation between the two European subspecies of the house mouse. The student will more specifically look at the genetic basis of adaptive sexual isolation by developing population genomics approaches which will make use of next generation sequencing and associated high throughput methods (see references below).

We seek for a highly-motivated student with a strong interest in evolutionary biology and evolutionary genetics, and curiosity for the field of speciation research. Experience in molecular lab techniques would be an advantage, and skills in or interest for bioinformatics/programming would be a plus. Through this topic highly tuned towards key questions in evolutionary biology and cutting edge genomic techniques, the PhD candidate will have a unique opportunity to acquire important skills and gain experience in this fast-evolving field of research.

Project key words: speciation, natural and sexual selection, population genomics, assortative mating, genomics of adaptation, genomics of complex behaviours,

Next Generation Sequencing, house mouse

The PhD candidate will be based at the Institute for Evolutionary Biology - CNRS, Montpellier and will be supervised by Dr. Carole Smadja and Dr. Pierre Boursot. The Institute for Evolutionary Biology is a world-leading centre for excellence in evolutionary biology and is part of dynamic network of research departments which participate to the outstanding scientific environment in biodiversity research in Montpellier.

Criteria of eligibility : candidates must be citizen of a country member of the European Union or must have been awarded a Master degree or equivalent in a EU country or one of the following EU Partner countries : Andorra, Bulgaria, Croatia, Russia, Iceland, Norway, Roumania, Switzerland, Turkey and Vatican. Applicants must hold a Master degree or equivalent.

Application : To apply, please send a complete CV, letter of motivation, names of 2 referees as a single pdf file to carole.smadja@univ-montp2.fr or Pierre.boursot@univ-montp2.fr Deadline for application: **7 June 2011**. Candidates are strongly encouraged to make informal contact with Carole Smadja by email before this deadline in order to get important information about the application procedure. Short-listed candidates will be invited for an interview in Montpellier, France, 4 - 8 July 2011.

References from the research group related to the project: Boursot, P. et al., 1993. The Evolution of House Mice. Annual Review of Ecology and Systematics, 24(1), pp.119-152. Boursot, P. et al., 1996. Origin and radiation of the house mouse: mitochondrial DNA phylogeny. Journal of Evolutionary Biology, 9(4), pp.391-415. Smadja, C. & Ganem, G. 2002 Subspecies recognition in the house mouse: a study of two populations from the border of a hybrid zone. Behavioral Ecology 13, 312-320. Smadja, C., Catalan, J. & Ganem, G. 2004 Strong premating divergence in a unimodal hybrid zone between two subspecies of the house mouse. Journal of Evolutionary Biology 17, 165-176. Raufaste, N., Orth, A., Belkhir, K., Senet, D., Smadja, C., Baird, S. J. E., Bonhomme, F., Dod, B. & Boursot, P. 2005 Inference of selection and migration in the danish house mouse hybrid zone. Biological Journal of the Linnean Society 84, 593-616. Smadja, C. & Ganem, G. 2005 Asymmetrical reproductive character displacement in the house mouse. Journal of Evolutionary Biology 18, 1485-1493. Smadja, C. & Ganem, G. 2008 Divergence of odorant signals within and between the two European subspecies of the house mouse. Behavioral Ecology 19, 223-230. Stapley, J., Reger, J., Feulner, P. G., Smadja, C., Galindo, J., Ekblom, R., Bennison, C., Ball, A. D., Beckerman, A. P. & Slate, J. 2010 Adapta-

tion Genomics: the next generation. Trends in Ecology & Evolution.

– Dr. Carole Smadja CNRS researcher Chargée de recherche CNRS <http://www.carole-smadja.staff.shef.ac.uk/> – Institut des Sciences de l'Évolution cc065, Université Montpellier 2 34095 Montpellier France Phone: +33 (0)4 67 14 92 70 – carole.smadja@univ-montp2.fr

UAmsterdam Mycology Evolution Cooperation

PhD position: Mutualisms in a changing world

Vacancy number: 1.2011.00124

A PhD position is available at the Department of Ecological Science, Faculty of Earth and Life Sciences, Vrije Universiteit Amsterdam.

Mutualisms - cooperative interactions between species - are central to the survival and reproduction of most organisms on earth. Despite their ubiquity, explaining the evolutionary persistence of mutualisms remains one of the greatest challenges for evolutionary biology. This PhD position will utilize the arbuscular mycorrhizal mutualism to ask how ecological context modifies the evolutionary trajectory of plant and fungal partners.

Tasks Daily tasks will involve work in greenhouses, laboratories and with fungal culturing. Student must have an excellent knowledge of spoken/written English. No prior knowledge of Dutch is required. The project will be completed with papers in scientific journals and a PhD Thesis. Our group is a multidisciplinary, international team of ecologists, evolutionary biologists and plant physiologists. The student will be primarily housed in the Institute of Ecological Science, Vrije Universiteit. Funding will be provided for the student to travel to labs of other team members (France, Switzerland, USA, etc) to learn new techniques.

Requirements Candidates should have a Master's in biology, ecology & evolution, microbiology, or related fields. Experience in molecular biology, evolutionary game theory, isotope labeling, rhizosphere studies and/or plant physiology is a plus.

Further particulars The appointment will be initially for 1 year. After satisfactory evaluation of the initial appointment, it can be extended for a total duration of 4 years. You can find information about our excellent

fringe benefits of employment at www.workingatvu.nl Salary The salary will be in accordance with university regulations for academic personnel, and amounts euro 2.042,- gross per month in the first year up to euro 2.612,- in the fourth year (salary scale 8.5) based on a full-time employment.

Information For additional information please contact: prof. dr. Toby Kiers Phone number +31 (0)20 5987085 E-mail: toby.kiers@falw.vu.nl

Application Applicants are requested to write a letter in which they describe their abilities and motivation, accompanied by a curriculum vitae and one or two references.

It is possible to apply by e-mail. Send applications to: falw-vacatures@falw.vu.nl

Please cc: toby.kiers@vu.nl

Please mention the vacancy number in the e-mail header

toby.kiers@vu.nl

UBern Adaptive Radiations

PhD positions at the University of Bern - Population Genomics of Adaptive Radiation

Two PhD positions are available in the Institute of Ecology & Evolution, University of Bern, Switzerland.

The projects will investigate the population genomics of adaptation and speciation in adaptive radiations. We will investigate different stages in the progression of adaptive radiation, from invasion of a new adaptive zone to speciation and niche partitioning. We are using two of the best vertebrate systems available today for this purpose: East African cichlids and Three-spined stickleback. High-throughput next-generation sequencing, specifically RAD tag sequencing, on an Illumina HiSeq platform, will be used to study the signatures of selection, gene flow, reproductive isolation and hybridization, as well as the genomic architectures of adaptation and speciation. Our approach combines comparative population genomics with natural variation in the process of adaptation and speciation in replicate adaptive radiations.

We are looking for strongly motivated candidates eager to address cutting-edge questions in evolutionary biology, to analyse NGS data and develop and apply bioin-

formatics in an evolutionary genetics context. Candidates have a Masters degree in Biology or Bioinformatics and should possess an aptitude to work with very large data sets, strong desire to develop new analytical methods, and ability to work in team. Ideal candidates will have either a strong grounding in evolutionary biology with experience in programming and genetic data processing, or a strong grounding in bioinformatics or computer science with interest in evolution.

Both students will be supervised by Ole Seehausen, Arjun Sivasundar (Aquatic Ecology Division) and Laurent Excoffier (Population Genetics Division). Aquatic Ecology has its labs in Bern and at the Center for Ecology, Evolution & Biogeochemistry of Eawag in Kastanienbaum. Population Genetics has its labs in Bern. For details see our homepages at http://www.iee.unibe.ch/content/index_eng.html and http://www.eawag.ch/forschung/cc/ceeb/index_EN. The students will also enroll in our new SNSF doctoral program in Population Genomics (<http://www.unil.ch/pg>) and benefit from its activities.

Both positions are available to start immediately. Salary will be according to SNSF guidelines. Application deadline is May 13th, but applications will be considered until the positions are filled. Please send an application letter, CV and contact information of two references to Susanne Maurer (Susanne.maurer@iee.unibe.ch)

For inquiries please write to either Ole Seehausen (ole.seehausen@eawag.ch) Laurent Excoffier (laurent.excoffier@iee.unibe.ch)

Ole.Seehausen@eawag.ch

UCapeTown AvianSexualSelection

Could you please post the advert below. Many thanks

*MSc research at the Percy FitzPatrick Institute of African Ornithology, Department of Zoology, University of Cape Town***

Project: Dominance, sexual selection and conflict resolution in a cooperative species, the sociable weaver

We invite applications for the above full-time study opportunity at the FitzPatrick Institute, a world-renowned, national Centre of Excellence (CoE) in ornithological research with a strong emphasis on postgraduate studies.

The MSc student will integrate an international group of researchers investigating cooperation in sociable weavers /*Philetairus socius*/ near Kimberley, South Africa.

Sociable weaver individuals cooperate to build a massive communal nest structure and to raise young. How is this cooperation achieved and how do individuals decide whether to cooperate or to defect? One explanation for cooperation is kin selection, but this unlikely explains the maintenance of 'public goods' that concern a whole group rather than just kin.

This study will investigate the role of dominance and sexual selection in cooperation and conflict resolution in the sociable weaver. We will examine two behaviours: cooperative nest building and cooperative breeding. The study will involve extensive behavioural observations to establish dominance hierarchies and whether there is social segregation or competition for access to specific communal tasks (such as helping at the nest or nest-building activities). In addition, we will investigate the role of melanin-based plumage signals in both males and females.

The successful applicant will have a BSc Honours or equivalent, relevant ornithological field experience and a demonstrated ability to work independently. The student should have a strong interest in pursuing theoretical questions in behavioural ecology and motivation for conducting demanding fieldwork. Experience in handling birds and behavioural observations are important advantages.

Funding is secured for an annual R75 000 CoE bursary for two years and for project running costs.

To apply, please send a CV (including your academic record & names and contact details of three referees) and a short motivation for why you wish to undertake this research to Hilary Buchanan at hilary.buchanan@uct.ac.za. For more information on the FitzPatrick Institute visit www.fitzpatrick.uct.ac.za. For more information on the project, please contact: Dr Rita Covas (rita.covas@mail.icav.up.pt) or Dr René van Dijk (R.van.Dijk@sheffield.ac.uk)

/Closing date: 1 July 2011/

UCT is committed to the pursuit of excellence, diversity and redress. Students granted an award to study at UCT are required to comply with the UCT official and approved policies on postgraduate funding.

Rita Covas <rita.covas@gmail.com>

UExeter SexualSelection

A PhD position to work on genotype by environment interactions at the University of Exeter is being advertised. Successful applicants will work with Professor David Hosken and Associate Professor John Hunt using *Drosophila simulans* as a model. The position is only open to UK residents. For more details see:

<http://www.exeter.ac.uk/studying/funding/award/-index.php?id=781> And feel free to contact us for more information. Best David

Prof DJ Hosken Chair in Evolutionary Biology Director, Centre for Ecology & Conservation Biosciences, College of Life & Environmental Sciences University of Exeter, Cornwall Campus Tremough, Penryn, TR10 9EZ UK

d.j.hosken@exeter.ac.uk 01326 371843 http://-biosciences.exeter.ac.uk/staff/index.php?web_id=-david_hosken DJ Hosken <D.J.Hosken@exeter.ac.uk>

UExeter ViralEvolution

Fully funded PhD position: Modelling viruses in the marine ecosystem. University of Exeter.

A PhD position is available with Dr Hywel Williams in Biosciences, College of Life and Environmental Sciences at the University of Exeter (Streatham Campus, Exeter) to commence October 2011. The studentship will cover UK/EU tuition fees for three years, plus an annual stipend of £13,590pa for three years.

Viruses are the most abundant replicating entities on the planet, with an estimated 10^{31} viruses in the oceans alone. Marine viruses have a number of interesting roles in marine ecosystems, including as a significant agent of plankton mortality, as carriers of genes between microbial hosts, and as drivers of evolutionary change. However, viruses are not currently well represented (or often not represented at all) in marine ecosystem models, so it is hard to quantify the impacts of viruses on ecosystem function. This has significant implications for predictions of the marine carbon cycle and its response to global change.

This fully funded project will develop theoretical models of viruses in the marine ecosystem, in order to better understand their role in ecology, evolution and ecosystem function. The student will join a research team that is seeking to understand marine microbial ecology and evolution through the use of sophisticated computer simulations. A key goal of this work is to understand the response of marine ecosystems to global change.

This project offers the opportunity to work in the important and fast-developing area of marine ecosystem research. The student will develop generic skills in computational modelling of complex systems, as well as domain-specific knowledge of the marine microbial ecosystem. The ideal candidate will have a strong background in mathematics, physics, computer science or another quantitative discipline, as well as a keen interest in biology and environmental science. Within the broad remit described above there is some flexibility for the student to direct their own research and we welcome relevant project proposals.

<http://www.exeter.ac.uk/studying/funding/award/-index.php?id=774> Contact: Hywel Williams (h.williams@uea.ac.uk)
H.Williams@uea.ac.uk

UHull BiologicalInvasions

Fully funded NERC PhD studentship Predicting biological invasions: a phylogenetic approach

Department of Biological Sciences University of Hull

Supervisor: Dr. Isabella Capellini Co-Supervisors: Dr. Chris Venditti, Dr Darren Evans

We are inviting applications for this NERC-funded PhD studentship to commence in October 2011.

Aim of the project Non-native 'invasive' species are one of the major causes of the loss of native biodiversity, can alter ecosystem dynamics, and lead to considerable economic impacts. The strategies to cope with invasive species are often planned after the invader is well established and has colonized large areas; as a result the costs of eradication are high and often impractical. Preventing invasion is therefore the best strategy to avoid longterm environmental damage and economic costs. However, predicting potential invaders before they colonize habitats is at present a poorly resolved

task. This project will systematically test what biological characteristics known invaders share across a range of phylogenetic lineages, from plants to vertebrates and invertebrates, using cutting-edge phylogenetic comparative methods. The project will provide (i) comprehensive answers to the key question of what biological traits successful invaders share and identify potential differences across lineages and ecosystems; (ii) a much needed screening tool for predicting the potential for successful invasion of species introduced in the UK; and (iii) fundamental information for assessing the invasive potential of species under different scenarios of climate change.

Working at the cutting edge of ecology and evolutionary biology within the Department of Biological Sciences, the student will acquire cutting edge statistical methods, fundamental theoretical knowledge and critical thinking skills within a highly stimulating and lively research environment. The project will also address a key problem in conservation biology with potential applications for policy-makers and land managers.

How to apply Entry requirement. A first degree (at least an Upper Second Class Honours or equivalent) in biology, ecology, conservation biology or related discipline. A Masters degree in a relevant discipline will be an advantage.

Eligibility. Please refer to the NERC eligibility criteria <http://www.nerc.ac.uk/funding/available/postgrad/eligibility.asp> Application procedure. To apply a CV, covering letter and names of 2 referees should be sent to Sarah Richards (S.Richards@hull.ac.uk) by 6th June 2011.

To apply a CV, covering letter and names of 2 referees should be sent to Sarah Richards (S.Richards@hull.ac.uk) by 6th June 2011.

Informal enquiries to: Isabella Capellini (I.Capellini@qub.ac.uk).

- - Isabella Capellini, PhD Lecturer in Ecology

*** NOTE CHANGE OF ADDRESS FROM 1st AUGUST 2011 ***

Department of Biological Sciences University of Hull Cottingham Road, Kingston-upon-Hull HU6 7RX, UK

- Present address

School of Biological Sciences Queen's University Belfast 97 Lisburn Road, Belfast BT9 7BL (U. K.)

Phone: +44 (0)28 9097 2181

Personal website: <http://www.qub.ac.uk/bb/People/DrICapellini/> Evolutionary Architecture of Reproduction website & database: <http://www.dur.ac.uk/>

reproductionproject/ Phylogeny of Sleep Database
<http://www.bu.edu/phylogeny/> Isabella Capellini
<i.capellini@qub.ac.uk>

ULaval BacterialAdaptation

PhD: Québec. Lacustrine bacterial metagenomic and metatranscriptomic. The Derome laboratory at the Institut de Biologie Intégrative et des Systems (IBIS), Laval University, Québec, Canada, offers the position of a PhD student "Rapid adaptive strategies of Lacustrine bacterial communities". The successful candidate will have a Master of Science (MSc) or equivalent in evolutionary biology, molecular biology, molecular ecology or related fields, and a strong interest in network of functional interactions in bacterial communities. Experience in molecular laboratory techniques and DNA sequence analysis, next generation sequencing, bioinformatics and statistics are an advantage. Furthermore, good written and oral communication skills in English, team work skills, the willingness to write research-funding proposals and to learn some French are essential for a rewarding research. Working language will be French or English.

We are applying metatranscriptomic and metagenomics techniques to questions of evolution, climate change and bacterial communities functional capabilities. The focus of this position will be on the environmental influences and evolutionary processes acting on the communities of lacustrine bacterial communities. You will use standard molecular genetic techniques as well as next-generation sequencing technology (Roche 454). Within the Institut de Biologie Intégrative et des Systems (IBIS) you will have ample opportunities to interact and collaborate with faculty, postdocs and PhD students specializing in a variety of topics, such as molecular evolution, functional genomics, host/pathogen interactions, phylogeography, phylogenetics, ecology, modeling, and bioinformatics. Québec is an attractive city in beautiful surroundings, with many educational and recreational opportunities (Hiking, cross-country and downhill skiing, mountain biking, rafting, kayaking, whale watchingS).

The Laval University advocates gender equality. The contract shall start on September 2011 and will be limited to three years. The start date is somewhat flexible. Salary and benefits are according to a public service position in Canada (NSERC). The place for work is

Québec-City, QC, Canada.

Please send your application by e-mail attachment, mentioning the reference of this position and including (1) a letter outlining your interest in this kind of research, and your suitability for the post, (2) a detailed CV, (3) contact details of 2 referees and (4) a copy of your thesis and other relevant exams: nicolas[dot]derome[at]bio[dot]ulaval[dot]ca. Review of applications will begin on June 15, 2011, and continue until a suitable candidate is identified. Informal inquiries by e-mail before the application are welcome.

Nicolas Derome, Professeur adjoint Département de Biologie Chaire de recherche du Canada en Génomique et Conservation des Ressources Aquatiques

Institut de Biologie Intégrative et des Systèmes (IBIS) Pavillon Charles-Eugène Marchand, bureau 1255 1030, avenue de la Médecine Université Laval, Québec QC G1V 0A6 Canada

Téléphone : 1 (418) 656-7726 Télécopie : 1 (418) 656-2043

Courriel : nicolas.derome@bio.ulaval.ca

Internet : http://www.bio.ulaval.ca/no_cache/-departement/professeurs/fiche_des_professeurs/professeur/11/240/ <http://www2.bio.ulaval.ca/-louisbernatchez/laboderome.fr.htm>

Nicolas.Derome@bio.ulaval.ca

Umea PlantPopGenomics

PhD position in population genomics of local adaptation in European aspen (*Populus tremula*) Umeå Plant Science Centre, Umeå University, Sweden (www.upsc.se)

We are looking for a PhD student for a project aimed at investigating the genetic basis of naturally occurring variation in phenology in European aspen (*Populus tremula*) and association with. The project is based on data from whole-genome re-sequencing of a reference population consisting of approximately 120 individuals. The work will primarily involve bioinformatic and statistical analyses, but there are also possibilities for doing field work, greenhouse and lab experiments. The project is run in collaboration with a number of research groups at Umeå Plant Science Centre. The position is available from September 2011 although another starting date can be negotiated.

The PhD student will be supervised by professor Pär Ingvarsson (UPSC, Department of Ecology and Environmental Science, <http://www.emg.umu.se/-english/about-the-department/staff/view-person/?uid=pain0001&guise=anst2>) and co-supervised by Dr. Nathaniel Street (UPSC, Department of Plant Physiology, www.plantphys.umu.se/-english/about-the-department/staff/view-person/?uid=rona0006&guise=anst2). The candidate should have a solid background in biology. Working knowledge of computational biology (bioinformatics/statistics) is highly desirable. Excellent proficiency in English is required, as English is the working language in the research group and at the department. For inquiries about the position, please contact Professor Pär Ingvarsson, +46-(0)90-786 7414, email: par.ingvarsson@emg.umu.se

The application should include a short description of your research interests and why you are interested in the position, CV, certificates from higher education, copies of Bachelors/Masters thesis, and contact information for 3 reference persons. Please note that applications should be sent electronically (in PDF format) to jobb@umu.se. Mark your application with reference number 313-426-11. The deadline for application is May 31, 2011.

– Pär K. Ingvarsson Professor, Evolutionary Genetics Umeå Plant Science Centre Department of Ecology and Environmental Science Linneaus väg 6 Umeå University, SE-901 87 Umeå, Sweden tel. +46-(0)90-786-7414, fax. +46-(0)90-786-6705

par.ingvarsson@emg.umu.se

UPortsmouth EvolutionPlantSignals

PhD Studentship at University of Portsmouth, UK. (Sorry, only UK and European (EU/EEA) candidates)

The Ecology of Honesty: Evolution of Plant-Insect Signalling in *Dalechampia* vines.

Applications are invited for competition-funded PhD Studentship in the School of Biological Sciences at the University of Portsmouth. Portsmouth, UK, commencing on the 1st October 2011. (Stipend ca. 13,000 pounds per year, 3 years)

The evolution of signalling systems that determine the ecology and evolution of plant-animal relationships is poorly understood, yet these systems play important

roles in the origin and maintenance of biodiversity. Plants signal the availability of rewards to mutualists, while at the same time attempting to \pm minimise attraction of enemies. Stabilising selection may often result from the net effect of these two conflicting selective pressure, although this has only rarely been documented. Floral signalling systems include bright colours and fragrances to attract pollinators. Fully honest advertisements signal accurately the presence of pollinator rewards (e.g. nectar, pollen, or floral resin for nest construction), whereas dishonest advertisements allow plants to attract and exploit pollinators without providing rewards. There is a continuum between these extremes, however, as measured by the correlation between advertisement intensity \pm and amount of reward available. With few exceptions, the honesty of signalling systems is poorly understood, even though it not only affects the nature of the trophic relationships, but also potentially controls the evolutionary dynamics of plant-animal relationships. The pollinator-signal systems employed by plants fall into two main groups: visual (colour, shape) and olfactory (fragrances), and both vary dramatically across the study system we are investigating.

The purpose of this study is to understand the evolutionary dynamic of signal diversity in *Dalechampia* vines (Euphorbiaceae), assessing evolutionary trends in floral bract and resin pigmentation and fragrance production, in the context of bee-vision physiology, insect learning, and overall honesty/dishonesty of signalling to both pollinators and herbivores, in relation to rewards and defences. This study is one of the first to elucidate the evolution of signalling systems by assessing the effects of signal type on both reproductive fitness in the field and, using molecular-phylogenetic relationships in the genus, on diversification rates and trait-transition rates. The PhD student collaborating on this project will work with Prof Scott Armbruster and be involved in fieldwork in the tropics and greenhouse and lab work at the University of Portsmouth and the Norwegian University of Science and Technology (Trondheim). Additional expertise and training will come from project collaborators in insect-vision neurophysiology, bee behaviour, comparative methods and evolutionary theory, based at other universities in the UK, Norway, and the US.

Informal inquiries can be directed to scott.armbruster@port.ac.uk or +44 (0)23 9284 2081.

Application deadline 30th June 2011.

You can apply online, by email or by post to: Faculty of Science, Faculty Admissions Centre, St. Michael's

Building, White Swan Road, Portsmouth, Hampshire, PO1 2DT. Tel: +44 (0)23 9284 5550 Email : sci-pgrad@port.ac.uk

References: Armbruster, W. S. 2002. Can indirect selection and genetic context contribute to trait diversification? A transition-probability study of blossom-color evolution in two genera. *Journal of Evolutionary Biology* 15: 468-486. Armbruster, W. S., L. Antonson, and C. Plabon. 2005. Phenotypic selection on *Dalechampia* blossoms: honest signaling affects pollination success. *Ecology* 86: 3323-3333. Bolstad G.H., W.S. Armbruster, C. Pelabon, R. Perez-Barrales, T.F. Hansen. 2010. Direct selection at the blossom level on floral reward by pollinators in a natural population of *Dalechampia schottii*: Full-disclosure honesty? *New Phytologist* 188: 370-384.

– W Scott Armbruster University of Portsmouth, UK & University of Alaska, USA

W Scott Armbruster <wsarmbruster@alaska.edu>

URennes Evolutionary Biol

Call for application2011: PhD Studentship in Evolutionary Biology at the University of Rennes 1

Title: Modeling demo-genetic interaction in socially structured populations

Contact: Nelly Ménard (Nelly.menard@univ-rennes1.fr) or Pascaline Le Gouar (pascaline.legouar@univ-rennes1.fr), UMR 6553 EcoBio, University of Rennes 1 , France

Application to VAS doctoral school before the 10th of June (<http://www.vas.univ-rennes1.fr/en/home/-competitive-admission-process/>)

Scientific context:

On the one hand, several studies have shown the impact of the social structure of animal populations on their genetic structure and dispersal. On the other hand social interactions are known to affect survival and reproduction of individuals. Only an explicit integration of demographic and genetic mechanisms may help understand their interactions and to discriminate their respective impact on the functioning of populations, but it is rarely performed. Understanding these interactions in species with complex social structure and their influence on the response of populations to environmental perturbations is crucial for understanding the evolution

of sociality.

Topic / mains steps/ methodological approaches:

The thesis will focus on two main issues:

-How does social structure influence the interactions between genetic and demographic processes in small populations?

-What is the role of social structure in population responses to anthropogenic disturbances such as fragmentation of the landscape or population crashes?

The main hypothesis of this thesis is that the social structure of a population influences the life history traits and fitness of individuals through demo-genetic interactions, the intensity would vary with the size of the population, temporal and spatial scales and intensity of environmental selection pressures.

The project will be structured around the development of demo-genetic models mimicking the dynamics of populations with different degrees of social structures. Based on this model, different scenarios on possible interactions between genetic and demographic processes will be first considered according to published case of studies or species studied in UMR Ecobio (primate populations, for example). Secondly, the effects of population size, environmental selection pressure will be studied. The models will then be implemented into spatially explicit version to examine if any conflicts between demo-genetic processes occur among spatial scales.

The approach will be the development of stochastic models of population dynamics that explicitly link demography, genetics and social structure. The models can be validated using data from long-term monitoring of two primate species with contrasting social structures (Western lowland gorilla and Barbary macaque), both species experience anthropogenic threats.

Scientific and technical skills require by the candidate:

The candidate must have a solid background in evolutionary ecology and have experiences in modeling biological processes.

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Pascaline Le Gouar MC Université Rennes 1 UMR 6553 ECOBIO Station Biologique Salle 112 35380 Paimpont France

tel: +33(0) 2 99 61 81 73 mail: pascaline.legouar@univ-rennes1.fr

<http://www.sbp.univ-rennes1.fr> <http://ecobio.univ-rennes1.fr/> Pascaline Le Gouar

<pascaline.legouar@univ-rennes1.fr>

USherbrooke AvianEvolution

I am seeking a motivated PhD student to join my research group in the Department of Biology at the University of Sherbrooke (<http://pages.usherbrooke.ca/dgarant/>). The Department has an outstanding group of researchers in ecology and evolution and provides a dynamic and stimulating environment for graduate students.

The proposed project will investigate phenotypic and genetic correlations between reproductive traits and fitness in a long term studied population of tree swallows (*Tachycineta bicolor*) in southern Québec, Canada. The project will benefit from a genetic pedigree gathered over 8 years, which includes data collected over 10 000 individuals, to unravel the possible genetic constraints on population' evolutionary potential, and to assess links among traits and fitness in contrasted environments.

The fieldwork in southern Quebec will take place 2-3 months each summer. Ideally, the candidate will have previous research and fieldwork experiences and skills in handling birds would also be an advantage. A good background in evolutionary ecology and/or quantitative genetics is also desirable.

The position is open and funded for three years, starting as soon as September 2011. Please apply by sending your CV, including the email addresses of two referees, and a letter of motivation by 5 August 2011 to Dany.Garant@Usherbrooke.ca

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Je recherche un étudiant au PhD pour se joindre à mon groupe de recherche au département de biologie de l'Université de Sherbrooke (< <http://pages.usherbrooke.ca/dgarant/> > <http://pages.usherbrooke.ca/dgarant/>). Le département possède un groupe de recherche de haut niveau en écologie et évolution et procure un environnement stimulant pour les études gradués.

Le projet proposé portera sur l'analyse des corrélations phénotypiques et génotypiques entre traits reproducteurs et fitness dans un système d'étude à long terme de l'Hirondelle bicolore (*Tachycineta bicolor*) dans le Sud du Québec, Canada. Le projet bénéficiera d'un pedigree génétique couvrant une période de 8 ans et

de données récoltées sur plus de 10 000 individus, pour établir le potentiel évolutif de la population, les contraintes génétiques possibles et les liens entre traits et fitness sous des conditions environnementales variables.

Les travaux de terrain se dérouleront pendant 2-3 mois à chaque été. Idéalement, le candidat aura de l'expérience avec les travaux de terrain, avec la manipulation d'oiseaux et de bonnes connaissances en écologie évolutive et/ou génétique quantitative.

Le poste est financé pour 3 ans à compter de septembre 2011 au plus tôt. Veuillez envoyer un CV, une lettre de motivation et les coordonnées de deux références avant le 5 août 2011 à Dany.Garant@USherbrooke.ca

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Dany Garant Associate Professor Department of Biology University of Sherbrooke Sherbrooke QC J1K 2R1 Canada

Tel: (819) 821-8000 ext.63198 Fax: (819) 821-8049
Courriel: Dany.Garant@USherbrooke.ca

<http://pages.usherbrooke.ca/dgarant/>

UUppsala SexualDimorphismAgeing

PhD position in the evolution of sex differences in ageing is available at the Department of Animal Ecology, Uppsala University, Sweden in Alexei Maklakov's lab. The position is funded by an ERC Starting Grant 2010.

The project will focus on two main questions : i) how sex-specific selection produces sexual dimorphism and ii) how the shared genetic machinery constrains the sexes from reaching their sex-specific optima. The main study species is the dioecious nematode worm *Caenorhabditis remanei*, although classic model organisms such as seed beetles and fruitflies are readily available. The project will combine the experimental evolution and behavioural ecology approach with molecular methods. There is a possibility to develop and apply an RNAi knockdown technique in collaboration with Dr. Andrea Hinas from Biomedical Centre and to study the interactions between sex, learning, memory and ageing in collaboration with Dr. Niclas Kolm from our department. The main objective is to understand the evolution of sex differences in lifespan, and in reproductive and cognitive ageing.

Applicants should have a MSc (or equivalent) in biology/ecology and a strong interest in evolutionary bi-

ology. Special interest in the evolution of life-histories and/or sexual selection is a plus. The project is supervised by Alexei Maklakov (http://www.ebc.uu.se/-Research/IEG/zoeko/People/Alexei_Maklakov/) and the candidate will receive her/his postgraduate training within the postgraduate school at the Evolutionary Biology Centre (EBC) (see http://www.ebc.uu.se/-index_eng.php). The candidate will join an interprogram Ageing Research Group (<http://www.ebc.uu.se/-Research/groups/ageing/?languageId=3>), which will open many opportunities for collaborative projects with other group members. The working atmosphere is international with English as working language. EBC constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, with research programs including ecology, systematics, genetics, genomics, and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 40 minutes by train from Stockholm. Students gave Uppsala University the highest rating of all universities in Europe in biology in 2010.

This position is financed for four full years, and the successful candidate will receive a postgraduate fellowship the first year (15.500 SEK/month) and a postgraduate position year 2-4 (22.400 - 25.100 SEK/month).

Important points: The position is open until filled. To start in October, 2011, but this is flexible.

Applications should include: 1) short letter of interest / background (2 pages max); 2) complete CV; 3) a description of undergraduate training; 4) a copy of undergraduate degree and 5) the names and e-mail addresses of 2-3 referees. Applications should be sent by e-mail to Alexei.Maklakov@ebc.uu.se. Alternatively, send hardcopies to the following address: Alexei Maklakov, Animal Ecology, EBC, Norbyvägen 18D, Uppsala University, SE-752 36 Uppsala, Sweden. Please feel free to contact me via e-mail for more information.

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Dr Alexei A. Maklakov Department of Animal Ecology Evolutionary Biology Centre Uppsala University Norbyvägen 18D Uppsala, SE-752 36 Sweden

Tel: +46 18 471 2702 Fax: +46 18 471 6484

Home page: http://www.ebc.uu.se/Research/IEG/-zoeko/People/Alexei_Maklakov/ Ageing Research Group page: <http://www.ebc.uu.se/Research/groups/-ageing/> Alexei.Maklakov@ebc.uu.se

UWyoming SageGrouseEvolution

Graduate Assistantship: Sage Grouse Connectivity and Energy Development University of Wyoming

I have a newly funded project to determine how energy-related management activities (oil/gas development and subsequent reclamation) influence distribution and functional connectivity of Sage Grouse in Wyoming. Isolated populations of Sage Grouse are unlikely to continue to persist over time. Evaluating reclamation and conservation priorities in relation to distribution and functional connectivity of Sage Grouse is a vital need. To address this need, the project will integrate models of Sage Grouse distribution and functional connectivity, then use this information create tools that help managers prioritize reclamation and conservation activities. This project will rely on both innovative niche models (distribution) and landscape genetic approaches (functional connectivity). The goals of this project are to provide science-based management tools and technology-transfer to support Sage Grouse mitigation actions (avoiding impacts and focusing reclamation efforts on high-value sites).

I am recruiting a PhD student for this project starting in August 2011. The project includes a highly competitive 12-month stipend, tuition, fees, health insurance, and research funds. The selected student will be in the interdepartmental Program in Ecology (PiE; www.uwyo.edu/pie). Prospective students with a background in ecology, natural resources, conservation biology, landscape ecology and/or population genetics are encouraged to apply. Evidence of robust quantitative/analytical skills (including spatial modeling), strong work ethic, passion for investigating scientific questions, ability to work under harsh field conditions and collaborative skills will all be vital for the success of potential candidates.

Applications should be submitted by June 10th (early application is strongly encouraged as review of applications will begin immediately). Applicants should meet the following minimum requirements: MS degree or other evidence of independent research, total GRE of 1100, and undergraduate GPA of 3.3 (or MS degree). Applications should include: cover letter with statement of research interests, CV, transcripts, GRE scores, and contact information for three references. Please be sure to include any evidence GIS, statistical modeling

and/or population genetic analysis skills. The packet can be sent as a pdf attachment to Dr. Melanie Murphy (melanie.murphy@uwyo.edu). Please contact me if you have any questions.

University of Wyoming (www.uwyo.edu) is ideally located in Laramie, Wyoming with easy access to excellent outdoor recreation opportunities and beautiful field sites. In addition, the campus is only 1 hour from Fort Collins and 2 hours from Denver, CO.

“Melanie A. Murphy” <mmurph23@uwyo.edu>

WWU Munster PlantCoevolution

PhD position, WWU Münster.

The co-evolution of immunity and development in plants

For effective crop improvement, breeders must be able to select on relevant phenotypic traits without compromising yield. This project proposes to investigate the evolutionary consequences of flowering time modifications on a second trait of major importance for plant breeding: immunity. This will have implications both for understanding cross-talks between flowering time and defense network and for developing efficient breeding strategies.

There is clear evidence that plant maturity influences levels and effectiveness of defense. Theoretical models actually predict that changes in life-history can modulate the balance between costs and benefits of immunity. Simultaneously, actors of the immune system have often been observed to alter flowering time.

Two alternative and possibly complementary hypotheses can explain this link: genetic constraints due to the pleiotropic action of players in either systems, or co-evolution, if flowering-time changes modulate the cost-benefit balance of immunity. We will conduct field assays in *Arabidopsis thaliana*, to differentiate the action of the two explanatory hypotheses. Using transcriptome analyses, we will identify defense genes associating with flowering time modification (f-t-a defense genes). We will quantify their expression along the assay and test whether it varies with both flowering time and fitness. We will further test whether flowering time and immunity interact to determine yield in tomato and potato.

The IEB in Münster is unique in Germany (<http://->

ieb.uni-muenster.de/). Its marked focus on Evolution places it at the forefront of education and research in diverse sectors of evolutionary biology, from evolutionary ecology to phylogenetics, population genetics and evolutionary bioinformatics. This interdisciplinary environment, the diversity of model organisms as well as close proximity to world class research at the nearby Institute of Botany provides a unique setting that is about to be even further reinforced by a Graduate School of Evolution.

*Münster is a multi-faceted city. It is a city of science and learning. Westphalia's longstanding regional capital is a young city; one of 7 of its inhabitants is either studying or employed by university and half of its inhabitants are below 30 years of age. Compared to other German cities, Münster is a forerunner in the field of environment and climate protection. It is Germany's bicycle metropolis with more bikes than inhabitants, more than 250 kilometres of bicycle paths and an underground bicycle parking area in front of the main train station. High-tech and traditional trade coexist in this city, as well as baroque noble residences and

modern architecture, or a historic city centre and progressive urban development. This is how Münster can guarantee you the highest quality of life. *

**

*We are looking for a candidate with a strong background in either plant physiology, evolutionary biology or statistical genetics, documented by a master degree, and with a strong motivation for the assessment of plant performance in the field. A background in agricultural sciences is also welcome. The project is part of SPP1530 on Flowering time control. Funding is guaranteed for three years.** Applicants should send a detailed CV and the contact information of three referees to Prof. Juliette de Meaux (juliette.de.meaux@uni-muenster.de). Review of applications will begin immediately and until position is filled. The position is available from July 1st, but a later starting date can be negotiated. Fluency in German is NOT a pre-requisite for joining the lab. *

–

Juliette de Meaux <jmeau_01@uni-muenster.de>

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Dijon EvolutionaryBiology 2

Evolution, Morphology, Evolutionary Biology, Paleontology

The Ecole Pratique des Hautes Etudes (EPHE) opens a « Maître de conférences » position (permanent posi-

tion of Assistant Professor) at the « Paléobiodiversité & Evolution » lab, part of Biogéosciences unit (UMR CNRS) in Dijon (Burgundy, France).

Candidates are expected to develop a research program on the study of mechanisms leading to the emergence of particular phenotypes by favoring multi-scale approaches from the microevolutionary level (function, adaptation) up to the macroevolutionary level (historic contingency). The understanding of complex biological systems can be now approached through the concept of shape modularity and integration providing a relevant link between developmental processes and evolution.

The position concerns either a paleontologist or an evolutionary biologist (ecology, population biology) considering his(her) project at the interface between micro- and macro-evolutionary researches. Solid knowledge in morphometry and statistics are expected.

Teaching program will include Evolution, Morphometry, Paleontology courses, in particular in the Master BSE (Biologie Santé Ecologie) of the Ecole Pratique des Hautes Etudes and in the lectures given in Paléobiodiversité & Evolution lab in Dijon.

The review process will be held in Late Spring 2011, and the position will begin end of 2011 (pending final decision of French Academy of Sciences). The official announcement and the list of requested items for formal application is now posted on at the EPHE web site (<http://www.ephe.sorbonne.fr/> or <http://www.ephe.sorbonne.fr/actualites/recrutement-enseignants-chercheurs-2011.html>). Please follow the recommendations and send all the requested files to the following address: svt@ephe.sorbonne.fr

For any scientific or teaching questions, please contact : Dr. S. Montuire (head of the Paléobiodiversité & Evolution » lab or Dr. M. Veuille (head of the Life and Earth Sciences Section of EPHE).

Sophie.Montuire@u-bourgogne.fr Tél : +33 (0)3.80.39.63.47 <http://www.u-bourgogne.fr/BIOGEOSCIENCE/> <http://www.ephe.sorbonne.fr> veuille@ephe.sorbonne.fr @mnhn.fr Tél : +33 (0)1.53.63.61.65/66

Dr. Sophie Montuire EPHE & UMR CNRS 5561 Biogéosciences Université de Bourgogne 6 Bld Gabriel 21000 Dijon Tél.: 33. (0)3.80.39.63.47 Fax : 33. (0)3.80.39.63.87 Sophie.Montuire@u-bourgogne.fr <http://www.u-bourgogne.fr/BIOGEOSCIENCE/> <http://www.ephe.sorbonne.fr> Paleontological database <http://transtyfipal.u-bourgogne.fr/> Sophie Montuire <Sophie.Montuire@u-bourgogne.fr>

Helsinki ComputationalBiology

Open positions in computational sequence analysis at the Institute of Biotechnology, Helsinki, Finland

Dr. Ari Löytynoja will start as a group leader at the Institute of Biotechnology, University of Helsinki, from 1 September, 2011. He has open positions for Ph.D. students and a postdoc researcher.

The group's research interests are in evolutionary sequence analysis, both the development of advanced analysis methods and their application to biological questions of special importance. Current topics include e.g. phylogenetic sequence alignment and homology inference for evolutionary analyses, and the development of methods for comparative analysis of next-generation, high-throughput sequencing data.

An ideal candidate would be experienced with Linux/Unix systems and working with the command-line interface, and would master a scripting language such as Perl or Python. Some projects require experience on a low-level programming language such as C, C++ or Java (the current codebase is in C++). The work does not require background in biology, nor a formal training in programming or bioinformatics. The starting date is 1 September, 2011 or later.

Potential research projects are: (i) development/analysis of phylogenetic alignment methods efficiently using current computer hardware and strategies for their use on large datasets; (ii) development/analysis of phylogenetic alignment methods to account for uncertainties in the homology inference; (iii) development of methods for comparative analyses of next-generation sequencing data; (iv) evolutionary analyses of non-model organisms using next-generation sequencing data. A candidate's own project matching group's other interests can also be considered.

Information of the past work and research interests can be found from the following publications:

Löytynoja& Goldman. Science (2009), 324:1528.
Löytynoja& Goldman. Science (2008), 320:1632
Löytynoja& Goldman. Phil Trans Royal Soc B (2008), 363:3913
Löytynoja& Goldman. Proc Nat Acad Sciences USA (2005), 102:10557

and from the group's homepage at <http://www.biocenter.helsinki.fi/bi/loytynoja> . To apply

for a position, please send your CV and contact details of two referees to ari.loytynoja@helsinki.fi or to the address (valid until 31 July, 2011):

Ari Löytynoja EMBL-European Bioinformatics Institute Wellcome Trust Genome Campus Hinxton, CB10 1SD United Kingdom

– Ari Löytynoja tel:+44-(0)1223-494695 EMBL-European Bioinformatics Institute fax:+44-(0)1223-494468 Wellcome Trust Genome Campus, Hinxton, CB10 1SD, UK

ari@ebi.ac.uk

LundU SystematicBiology

Lund University (Sweden) announces an opening:

Professor in Systematic Biology

Lund University is Scandinavia's largest institution for education and research in a broad range of disciplines, such as engineering, natural sciences, law, social science, economics, medicine, theology and the arts. The University has over 40 000 students and approximately 6 000 employees located in Lund, Malmö and Helsingborg. We have a comprehensive global network and a growing co-operation within the Åresund University framework of Southern Sweden and Eastern Denmark.

The Department of Biology was founded on January 2010 by a fusion of the Departments of Ecology, Cell and Organism Biology (COB), Undergraduate Studies in Biology and the Biological Museums. At the same time, the building of the new Biology Centre has been completed within the North Campus, and all biology research and teaching at Lund University is now gathered together within a single site for the first time – providing unique opportunities for high quality research and innovative education within biology. The Department of Biology has ca. 300 employees, out of which ca. 80 are PhD candidates. The Biological Museums together represent one of the world's largest university collections (c. 12 million specimens) including, in particular, large collections of insects and vascular plants from the Nordic countries. Research at the Department is organized around research groups working within many areas of biology. We offer a range of bachelor and master teaching programmes in Biology and Molecular Biology to both Swedish and international students. Further information about the Department of Biology can be found at: <http://www.lu.se/biology> Basic facts

regarding the position

Reference no: 2184 Closing date for applications: September 15, 2011 Date of appointment: As soon as possible Placement: Department of Biology Trades unions at Lund University: OFR, SACO and SEKO Information about the position: Christer Löfstedt, Head of Department: +46-46-222 9338, christer.lofstedt@biol.lu.se; Information about conditions of employment and the application process: Faculty Personnel Manager Gunilla Thylander, +46 -46 222 40 32, gunilla.thylander@kanslin.lu.se

Description of responsibilities The main emphasis of the position is research within systematic biology with a focus on studies of evolutionary relationships at the level of species, and/or higher taxa.

The successful candidate will be expected to play a key role in establishing a competitive world-class research programme in systematics at the Department of Biology. The candidate should take responsibility for leading a research group, and be active in the development of the collections at the Biological Museums. He/she should actively seek external funding from national research councils and other research funds in order to cover part of the salaries and operational costs for the research group. The candidate is also expected to develop collaborations with other research groups within the Department that are active in related research areas, such as evolutionary biology, molecular ecology and biodiversity research.

In addition, the successful candidate is expected to be actively engaged in teaching and development of courses (at both basic and advanced levels) within systematics, evolution and biodiversity, and in the supervision of Bachelor and Master projects, as well as PhD students.

Qualifications According to Chapter 4, Section 3 of the Higher Education Ordinance (SFS 2010:1064) a person who has demonstrated both research and teaching expertise shall be qualified for employment as a professor except in disciplines in the fine, applied or performing arts.

The successful candidate is expected to have a distinguished record of achievements in the area of systematic biology with a focus on studies of evolutionary relationships at the level of species, and/or higher taxa. Scientific qualifications will be evaluated mainly on the basis of the quality and number of scientific publications at the highest international level. Demonstrated academic leadership skills, experience of supervising undergraduate and graduate students, collaborative skills, and an ability to compete successfully for external funding are

of central importance. Demonstrated ability to develop and teach undergraduate and graduate courses in systematic biology are also important merits. A demonstrated ability to establish intra- and interdisciplinary research collaborations is important for the position, and the ways in which the candidate's background and expertise may strengthen the research profile in evolutionary biology and biodiversity research at the new Department of Biology will be taken into consideration. Experience of curating of museum collections is regarded as a merit.

The assessment criteria for appointment as a professor, according to

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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>

MaxPlanckInst Leipzig ImagingHumanEvolution

Research Position in 3D Imaging and Human Evolution

The Department of Human Evolution of the Max Planck Institute for Evolutionary Anthropology, Leipzig (Germany) invites applications for a junior research position. This is a research-only post with no teaching obligations. We expect the successful candidate to work closely with Professor Fred Spoor, exploring the bony labyrinth of hominin fossils, using high-resolution CT and advanced morphometric methods. There will be time available for independent research as well. The department will provide substantial support in a highly stimulating environment.

The selected candidate will have a PhD, a strong track record of research, and appropriate experience in using 3D imaging software. Good knowledge of Avizo (Amira) would be a distinct advantage. The initial length of the appointment is two years but the contract is extensible.

Please send queries and applications (cover letter and cv in PDF format) to Professor Fred Spoor (f.spoor@eva.mpg.de).

The appointment will commence in July or August, and the application deadline is 4 June 2011.

– Alyson Reid Research Assistant to Prof. Jean-

Jacques Hublin/Dept. of Human Evolution Max-Planck-Institute for Evolutionary Anthropology Deutscher Platz 6, D-04013 Leipzig, Germany

Phone: 49-341-3550-368 Fax: 49-341-3550-399 E-mail: alyson_reid@eva.mpg.de Office: U2.15

Alyson Reid <alyson_reid@eva.mpg.de>

Moorea CoralReefs

Dear Listers,

This is the second announcement for a permanent position of Assistant Professor at EPHE (Ecole Pratique des Hautes Etudes), at the Centre for Island Research and Observatory of the Environment (CRIOBE). CRIOBE is an institution based in Moorea (French Polynesia) and Perpignan (France), part of both EPHE and the National Centre for Scientific Research (CNRS - France), whose research unit (UMS 3278 CNRS-EPHE) is known nationally and internationally for its scientific work on coral reef ecosystems. The successful candidate will develop his research project on the topic of coral reefs, in an ecological and environmental context. The scientific thematics of the project are wide: 'Macro-ecology in coral reefs, from genes to ecosystems (biotic interactions, resilience - disturbances, climate change - ecological evolution)'. The scientific excellence of the candidate will be rewarded. The successful candidate will be asked to implement a team within his own scientific field of expertise and in the context of the research unit. The application may be written in English or French. The launching of the position is forecast for May 5th. Please note the following agenda: - May 5th: launching of the position - June 3rd: deadline for sending application - June 10th: pre-selection of candidates for an audition in Paris - July 13th: audition in Paris.

The description of the application to be submitted can be downloaded at the following address: <http://www.ephe.sorbonne.fr/actualites/recrutement-enseignants-chercheurs-2011.html> If more information is needed, please contact Dr Serge Planes (planes@univ-perp.fr, veuille@mnhn.fr) or Pr Michel Veuille (veuille@mnhn.fr).

Please feel free to forward this message to your colleagues, other lists, etc.

– Dr Serge PLANES (Dir) USR 3278 CNRS - EPHE Centre de Recherche Insulaire et Observatoire de l'Environnement (CRIOBE) BP 1013 - 98 729, Pa-

petoai, Moorea, Polynésie française Tel : (689) 56 13 45, Fax : (689) 56 28 15 e-mail : serge.planes@criobe.pf

Centre de Biologie et d'Ecologie Tropicale et Méditerranéenne Université de Perpignan, 52 Av. Paul Alduy - 66860 Perpignan cedex, France Tel : (33) (0)4 68 66 17 11, Fax : (33) (0)4 68 50 36 86 e-mail : planes@univ-perp.fr

sarah.lemer@univ-perp.fr

NewMexicoStateU LabCoordinator GenomeSequencing

Job: Laboratory Coordinator, Genome Sequencing Laboratory

New Mexico State University, Department of Biology

Qualifications: BS in Biology, Molecular Biology or related field, plus one year of experience; MS in Biology preferred. Strong background in molecular biology techniques including Roche 454 shotgun, amplicon, and transcriptome pyrosequencing, qPCR, construction of normalized cDNA libraries, Sanger sequencing and capillary electrophoresis are preferred. Ability to communicate clearly, both verbally and in writing, with researchers, clientele, and students regarding molecular biology protocols and experimental design relating to ecology and evolution; previous scholarly products (e.g., papers, presentations) and teaching or academic supervisory experience is preferred.

Examples of Duties: Preparation, management, and expansion of NMSU's core Genome Sequencing Laboratory. Daily operation and routine maintenance of a Roche 454 GS FLX emPCR pyrosequencer (training is not available). Successful operation of the instrument requires meticulous adherence to protocols. Additional laboratory duties include the preparation of a wide variety of samples for genomic sequencing, and training/supervising graduate student laboratory assistants. Other duties include project management, record-keeping, accounting, and purchasing reagents/expendables. Must keep abreast of technical advances in genomics in order to advise research clientele in experimental design and seek new applications of genomics technology. Must work collaboratively with team of faculty researchers, bioinformatics specialists, graduate students, and facilities staff.

Benefits Offered: Group medical and hospital insurance, group life insurance, long-term disability insur-

ance, state educational retirement, worker's compensation, sick leave, annual leave and unemployment compensation. Opportunity for educational advancement.

Conditions: Offer of employment is contingent on funding.

All offers of employment, oral and written, are contingent on the University's verification of credentials and other information required by Federal Law, State Law, and NMSU policies/procedures, and may include the completion of a criminal history check.

Reply to/Deadline for Applications: Submit a formal letter of interest, current resume, and three professional references with names, titles, addresses, daytime phone numbers, and email addresses preferably as email and attachments to:

phoude@nmsu.edu

or hard copy by snail mail to:

Peter Houde New Mexico State University Box 30001
MSC 3AF Las Cruces NM 88003

Review of applications will begin April 19 2011 and applications received after this date may be considered. Incomplete application packets will not be considered.

phoude@nmsu.edu

NewZealand ComputEvolutionaryBiol

Computational Evolutionary Biology

The New Zealand Institute for Advanced Study seeks to appoint a new faculty member at the Professorial level.

The position is open to candidates who have a distinguished track record in computational evolutionary biology or computational biochemistry. Preference will be given to applicants willing and able to cross disciplinary boundaries and whose research interests complement existing NZIAS activities.

The overriding requirement for appointment is truly distinguished performance in research and a strong and successful record in attracting grant support. The successful candidate must contribute to an emerging and vibrant research environment with a strong commitment to post graduate training.

Further information can be found here: <http://->

jobs.massey.ac.nz/PositionDetail.aspx?p=6913

Paul B Rainey <paulbrainey@gmail.com>

NHM Paris BacterialGenomics

Assistant-Professor position in Bacterial genomics and metagenomics, EPHE/Natural History Museum, Paris

A tenure-track position as an assistant professor in bacterial genomics, metagenomics and statistical genetics is available at the EPHE /Integrative Population Biology /research group (Veuille Lab) in the Natural History Museum in Paris. The lab combines large empirical datasets and computational approaches to studying microbial population genetics (see <http://www.thierrywirth-lab.com/>). Current work in the lab focuses on a range of topics including (i) bacterial biodiversity and connectivity in Pacific Archipelagos, (ii) the interplay of sex and virulence in bacteria (/Escherichia coli/), (iii) the evolutionary history, demography and spread of major diseases using next-generation sequencing data. Our lab benefits from an excellent background in theoretical and modern population genetics (bioinformatics, modelisation, ABC, demogenetics) as well as an interdisciplinary research environment based on national and international collaborations (Institut Pasteur, Max-Planck Institute).

The successful candidate should have a postdoctoral experience, a strong background in computer science and statistics, and a deep interest in evolutionary genetics. A strong experience in genomewide and massive parallel sequencing datasets analyses is required. Programming skills and proficiency in unix-based computational environments are essential; finally a good publication record is required. She/he will also be involved in teaching activities in the /Biology, Health and Ecology/ Master

Remark: The position concerns evolutionary genomics, therefore a background in bacteria genetics and genomics is not mandatory.

Position link: <http://www.ephe.sorbonne.fr/-actualites/recrutement-enseignants-chercheurs-2011.html> Application deadline is the 2nd of June 2011.

Informal inquiries as well as applications (including a CV, copies of relevant publications and contact information for at least two references) should be emailed to both Thierry Wirth (wirth@mnhn.fr) and Michel Veuille (veuille@mnhn.fr). The starting date can be

as early as October 2011.

Prof. Thierry Wirth

Muséum National d'Histoire Naturelle - EPHE Department of Systematics and Evolution UMR-CNRS 7205 16, rue Buffon, 75231 Paris cedex 05 France tel. +33 (0) 1 4079 8036; gsm. +33 (0) 648155320 email: wirth@mnhn.fr url: <http://www.thierrywirth-lab.com>

OceanGenomeLegacy BioCollectionsDataSpecialist

Biological Collections Data Specialist (Job Code: OGL-ICBG-ED, posted 04/30/11)

The Ocean Genome Legacy Laboratory for Marine Genomic Research (www.oglf.org) seeks a Biological Collections Data Specialist to participate in data management associated with its Philippine Mollusk Symbiont-International Cooperative Biodiversity Group (PMS-ICBG) and to participate in operation of the Ocean Genome Resource DNA and Tissue Repository (OGR). The position will be part-time initially (20-30 hours per week), but may lead to a full-time position in the future.

We are seeking an employee with exceptional organizational and communication skills, a strong background in molecular biology, and 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 organizational development, competitive compensation, and the potential for advancement within an academically oriented non-profit research institution.

Brief Description- The successful applicant will have primary responsibility for managing, developing, maintaining, curating, and updating metadata and bioinformatic data associated with our PMS-ICBG project (<http://www.pms-icbg.org/>). There is a real opportunity for creativity with this position as key aspects include an interest and ability to develop a bioinformatics component for the project (e.g. analyzing and tracking genome sequence data); and an opportunity to work with a large, diverse group of project participants to ensure a complete and up-to-date dataset that is useful for project participants and for bi-annual project reporting. Fieldwork in the Philippines (1-2 trips per year) and occasional domestic travel for meetings are possible, as well as occasional travel to obtain

additional specimens for the Ocean Genome Resource (OGR) public biorepository. Currently, OGL is planning trips to Australia (1-3 weeks) and Florida (1 week) to subsample extensive museum collections. The timeline for these trips is very flexible.

Applicant Requirements- Applicants should meet the following basic requirements: - BS, MS or PhD in Biology, Microbiology, Marine Biology or related field - Coursework in molecular biology and taxonomy - Laboratory experience including genomic material handling and storage - Demonstrated expertise in database design and management; FileMaker Pro a plus. - Field collection experience and/or collections management experience

Apply for the Position- Applicants should submit a cover letter, CV/resume (including publications, if applicable), and contact information for at least three references by email to info@oglf.org (referencing job code OGL-ICBG-ED 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. OGL encourages its research staff to pursue their own research ideas, to publish their results, and to seek extramural support for their research.

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

deboer@oglf.org

PennStateU MultiMedia

Penn State evolutionary biologist Blair Hedges is seeking a multimedia designer for a full-time position in his lab on Penn State's main campus. Job includes video editing, photo editing, web design, and creating illustrations, graphs, maps, and other graphics for evolution and conservation research and outreach. A Bachelor's degree in graphic design or a related field (or equivalent) is required. Proficiency in Adobe After Effects, Photoshop, Illustrator, and InDesign is required. Individual

must have strong organizational skills. Familiarity with Google Earth and HTML/PHP is a plus, but not required. An interest in biology is also a plus, but it is not required. Application materials including a cover letter, resume and contact information for three references should be submitted via email (see www.hedgeslab.org for contact info). Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

sbh1@psu.edu

QueenMaryU Bioinformatics

Queen Mary University of London

Bioinformatics/Phylogenetics (details: <http://www.sbcs.qmul.ac.uk/>)

Lecturer/Senior Lecturer/Reader (= tenure track Assistant Professor / Associate Professor / Professor in US terms)

The deadline for this post has been extended to 13th May 2011 at 4.00pm BST (due to a problem with the advert in Nature). Interviews will be held on the 1st July 2011

richard.alan.nichols@googlemail.com

StanfordU FieldLabAssist SticklebackEvolution

Field and Laboratory Life Science Research Assistant in Stickleback Evolution

The Kingsley Lab at Stanford is seeking an enthusiastic field and lab research assistant to participate in a project on the evolutionary ecology and genomics of stickleback adaptation. Threespine sticklebacks are small marine and freshwater fish that have undergone a recent adaptive radiation across the northern hemisphere. They occupy a diverse range of habitats (lakes, streams, rivers, bogs, estuaries, ocean), and display a remarkable degree of morphological, physiological and behavioural diversity. We have developed a combination of genetic and genomic tools for the organism, making it possible to combine ecological, population,

developmental, and genomic studies of the molecular mechanisms that control evolutionary change in natural populations.

The successful candidate will sample sticklebacks from diverse environments during the summer field season, and catalog ecological, population, and individual-level data. Field-work will involve wading, water sampling, and hiking through rough terrain to access sample sites. International travel will be involved, and the applicant must be willing to work in long hours in remote locations. Laboratory-based work at Stanford will include logistics, data collection, digitizing images, making detailed morphological measurements, and preparing DNA for whole genome sequencing of multiple populations. This position is perfect for a highly motivated individual seeking both field-and lab based experience in evolutionary ecology and genetic/genomic analysis.

Requirements include:

1) bachelor's level or higher degree in biology, ecology, genetics or related field 2) drivers license and passport suitable for international travel 3) accurate, detail-oriented record keeping

Previous field and laboratory experience highly desirable. Salary and travel costs provided. The position will begin in May 2011.

If you wish to apply, please send a CV with a cover letter and contact details of two references (with e-mail addresses), to:

Professor David Kingsley email: kingsley@stanford.edu
Dept. of Developmental Biology Stanford University
California 94305-5329 USA

jones.floss@gmail.com

Depending on experience, teaching will cover topics such as anatomical or physiological zoology, parasitology, behavioural ecology or biodiversity.

The ideal candidate will be interdisciplinary and interactive, and will develop a dynamic, internationally renowned research programme in the broad area of comparative physiology and/or evolution. The appointee's research will provide opportunities for cross-disciplinary research both within the School of Natural Sciences and between Schools (such as furthering on-going collaborations with bioengineering). The appointee will support the College's Strategic Plan 2009-2014, by strengthening the physiological and evolutionary aspects of the central unifying theme of College's research strategy - the Sustainable Society.

The School of Natural Sciences comprises 38 academic staff working under the single overarching theme - Biodiversity and the Environment' underpinned by four subthemes: Ecology and Evolution, Earth and Environmental Science, Society, Space and Environment and Molecular and Comparative Physiology. The appointee will contribute to, and ideally promote synergy among some of these sub-themes. They will be expected to enhance research-led teaching in the School, increasing opportunities for graduate research.

Further details can be found here <https://jobs.tcd.ie/-pls/corehrrecruit/docs/0000019788.pdf>

Applications will only be accepted via E-Recruitment <http://www.tcd.ie/vacancies/> Dr Andrew Jackson Lecturer School of Natural Sciences Zoology Building, Trinity College Dublin, Dublin 2, Ireland Tel. + 353 1 896 2728, Fax. + 353 1 677 8094, Email. a.jackson@tcd.ie <http://www.tcd.ie/Zoology/-research/research/theoretical/AndrewJackson.php>
jackson.andrew.lloyd@gmail.com

TrinityCollege Dublin Evolution

Lectureship in Zoology, School of Natural Sciences, Faculty of Engineering, Mathematics and Science, Trinity College Dublin.

The Discipline of Zoology seeks to appoint an outstanding scientist to a five-year lectureship in Comparative Physiology and Evolution. The successful candidate will contribute to teaching on a variety of courses especially on the general undergraduate Freshman course in Natural Sciences, the degree courses in Zoology and Functional Biology and to Masters level teaching in Biodiversity and Conservation and Environmental Science.

UBristol UK Statistics

Two short term fellowships are available in the Department of Statistics, School of Mathematical Sciences, University of Bristol. UK. Details can be found at <http://www.sustain.bris.ac.uk/jobs.html> The posts are for all areas of Statistics, including Statistical Genetics and Population Genetics. Interested applicants are required to formulate their own projects as part of the application procedure. Specific enquiries not covered by the further particulars at the above URL may be made to Professor Peter Green

(p.j.green@bristol.ac.uk).
m.beaumont@bristol.ac.uk

/plantpathology.ucr.edu <http://genomics.ucr.edu>
<jason.stajich[AT]ucr.edu>

UCalifornia Riverside FungiDB programmer

The FungiDB project (<http://fungidb.org>) in the Stajich lab at University of California, Riverside, is searching for a programmer to support data loading and software development. FungiDB supports data mining of comparative and functional genomics of fungi. The duties include performing data loading into relational database system, development and improvement of scripts for data importing & downloading, and website development.

An ideal candidate will be a computer programmer with bioinformatics experience or a biologist accomplished in computer programming, however a demonstrated strong background with scripting languages such as Perl and experience with SQL is most important. The FungiDB project requires interfacing with scientists working on fungal pathogens of plants, animals, and model systems; perform research to acquire genomics datasets; integrate data into a relational database (www.gusdb.org) with existing scripts; and develop and run workflows to load the data.

The project is collaborative with team at UC Riverside and developers of EuPathDB (<http://eupathdb.org>) at the University of Pennsylvania & University of Georgia to load data, assess the quality of data loading & presentation to the user community. Participation in the preparation of scientific papers and technical documentation and attendance at scientific meetings are encouraged.

Applications should be made at the UCR HR site for job #11-04-010 (<http://bit.ly/dNDe3D>) <http://hrapps.ucr.edu/jobs/-JobsBrowse.aspx?@strJobNumber=3D11-04-010>
Informal inquiries about the project is encouraged, contact Jason Stajich <jason.stajich[AT]ucr.edu>

Jason – Jason E Stajich, PhD Assistant Professor Dept of Plant Pathology & Microbiology University of California, Riverside 951.827.2363
<http://lab.stajich.org> <http://fungialgenomes.org>
<http://fungidb.org> twitter @stajichlab @hyphaltip @fungialgenomes @fungidb <http://plantpathology.ucr.edu> <http://genomics.ucr.edu> [---

UChicago Programmer](http://-</p>
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Programmer position, University of Chicago

A programmer position is available in Molly Przeworski's lab in the Human Genetics department at the University of Chicago. Current work in the group focuses on a wide range of topics in primate evolution and population genetics, combining modeling and data analysis; for more information, see <http://-przeworski.uchicago.edu/>. The group shares space and weekly lab meetings with those of Jonathan Pritchard and Matthew Stephens and enjoys close ties with other members of the Human Genetics and Ecology & Evolution departments. Moreover, it benefits from the large and outstanding community of researchers in population genetics, statistics and genomics at the University of Chicago.

Applicants for the position must have training in computer science or bioinformatics, some background in biology (ideally in genetics or population genetics) and experience with scientific programming. More details about the position can be found at jobopportunities.uchicago.edu/applicants/Central?quickFind!0839. Applications must be submitted in response to the posting (rather than directly) by May 31 2011. The starting date is flexible, but could be as early as summer 2011.

Molly Przeworski Howard Hughes Medical Institute Early Career Scientist Dept. of Ecology & Evolution and Dept. of Human Genetics University of Chicago
molly.przew@gmail.com

UGlasgow 2 EvolutionaryBiol

TWO LECTURESHIPS IN ECOLOGY & EVOLUTION/ ORGANISMAL BIOLOGY AT THE UNIVERSITY OF GLASGOW

The Institute of Biodiversity, Animal Health and Comparative Medicine (BAHCM) is seeking to fill two lec-

tureships. The College of Medical, Veterinary and Life Sciences was created in 2010 from the fusion of the University's biologists, veterinary and medical scientists, and hosts a number of other research Institutes and Centres that offer excellent interdisciplinary collaborative opportunities. It has an annual research income of over £52M, with research activity concentrated in its research Institutes. BAHCM (<http://www.gla.ac.uk/researchinstitutes/bahcm/>) is a newly-formed multidisciplinary research institute that integrates expertise in animal biology and ecology with that in comparative and veterinary medicine. Unique in the UK, the range of our studies spans multiple biological levels: from research into molecules and cells, to research into individuals, populations and ecosystems. Given the threats posed by rapid environmental change and our increasing human population, there has never been a more pressing need for our holistic approach. Investigating key questions in environmental change, emerging diseases, and animal and ecosystem health requires an integration of empirical research at all biological levels with empirical data collection, rigorous quantitative analysis, appropriate theoretical frameworks and predictive modelling. Always striving to understand the interdependence of animal and human populations, ecosystems and the environment, our research is driven by the need to create multidisciplinary teams to address national and global research challenges.

The Institute prioritizes 4 research themes: evolutionary analysis, response to environmental change, animal health and food security, and infectious disease biology. Applicants whose research reaches across two or more of these research areas will be of particular interest.

The Institute currently has 17 academic staff, 32 associate academic staff, 20 management and support staff, 24 postdoctoral researchers (including Research Fellows) and 70 postgraduate researchers. The postgraduates are a mixture of PhD students and students undertaking one of the taught postgraduate (M.Res. courses) offered by the Institute (see <http://www.gla.ac.uk/researchinstitutes/bahcm/degrees/>).

The members of BAHCM are based in the Graham Kerr Building (on the University's main campus in Glasgow), at the veterinary sciences base on the Garscube estate and at the Scottish Centre for Ecology and the Natural Environment (SCENE, the University's field station on Loch Lomondside some 25 miles north of Glasgow; <http://www.gla.ac.uk/researchinstitutes/bahcm/researchcentres/scene/>). These locations house excellent facilities for research that would be available to the successful applicant. The Graham Kerr Building has 8 temperature-controlled aquarium rooms (with both seawater and freshwater supply) and 12 rooms for

holding other vertebrates, all Home Office-designated and maintained by dedicated animal husbandry staff. It also has a series of laboratories equipped for molecular, biochemical and physiological analyses, backed up by skilled technical staff (including electronic and mechanical workshops run by the College). SCENE also has Home Office-designated aquarium and animal rooms, including observation stream tanks, together with analytical labs, again maintained by permanent husbandry and lab technical staff. It also provides easy access to a diverse range of habitats including Loch Lomond itself, nearby rivers, lakes and streams, both coniferous and broadleaf woodland (which surrounds the field station and contains a study population of hole-nesting birds in c.400 nestboxes), agricultural pastures, moorland and mountain. SCENE also has en suite single bedrooms and suites that can be booked for short or long term research visits. The Institute also has excellent links with the University Marine Biological Station Millport (UMBSM, <http://www.gla.ac.uk/centres/marinestation/>), a marine station based on the island of Cumbrae in the Firth of Clyde (c.1.5h from Glasgow). It also has strong research links with many other research organisations both within Scotland (e.g. Marine Scotland, Scottish Natural Heritage, NERC Centre for Ecology & Hydrology, Macaulay Land Use Research Institute - now the James Hutton Institute) and further afield. (www.masts.ac.uk).

Undergraduate teaching within the College is organised through the Schools of Medicine, Veterinary Science and Life Science. The successful applicant

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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>

UIllinoisUC BiodiversityInformatics

BIOLOGICAL INFORMATICIAN ILLINOIS NATURAL HISTORY SURVEY, a division of the PRAIRIE RESEARCH INSTITUTE at the UNIVERSITY OF ILLINOIS

POSITION: The Illinois Natural History Survey, a division of the Prairie Research Institute, University of Illinois at Urbana-Champaign, is pleased to announce the position of Biological Informatician.

PROJECT DESCRIPTION: Cyber-technology in the Biological Sciences presents a nearly unbounded landscape for development and implementation of extensive and sustainable solutions in dissemination of scientific research data. World-renowned scientific research at the Illinois Natural History Survey, the nation's second oldest and largest biological survey, continues and with the application of cyber-technologies for integration and dissemination, will continue to have a major impact on society, science, and critical issues such as biodiversity and global climate change. We seek a highly motivated, innovative individual to contribute to a rapidly developing and transformative biodiversity informatics program at the Illinois Natural History Survey. The successful candidate will work with INHS scientists and IT staff to advise, develop, and implement sustainable and extensible database-driven web applications aimed at electronic dissemination of biological research results. Focal areas include biodiversity informatics (ecological and biotic community datasets), a developing extensible cybertaxonomy portal, and amalgamation and synthesis of the INHS natural history collections databases, which currently include more than 11 million objects. Half time will be devoted to informatics for collections-based research, while the other half will be devoted to the Species File program (<http://software.speciesfile.org>).

JOB DESCRIPTION: The successful candidate will be expected to coordinate INHS-wide efforts to develop and implement computer-based solutions for mobilization, use, and sustainability of biodiversity data; collaborate with INHS scientific staff to solicit and secure external funding to support new and ongoing projects related to biodiversity informatics; recruit, train and supervise hourly programmers and undergraduate computer science interns to support funded projects; train INHS scientific staff in the use of biodiversity informatics tools and participate in bioinformatics standards development; serve as liaison between INHS scientists and the INHS webmaster, network administrator, and other INHS/INRS IT support staff.

QUALIFICATIONS: This position requires a B.S. in Computer Science, Information Science, or Bio- (biodiversity) informatics. M.S. or Ph.D. degree desired. Emphasis in biological diversity informatics preferred. Individuals with a degree in a biodiversity-related field and relevant coursework and experience in scientific computing will also be considered. Experience with biological informatics support in a laboratory or organization setting is preferred. Experience with database-driven web application development with skills in database design and management, SQL, HTML, Visual Basic, CSS, CMS (e.g. Drupal),

and scripting languages (e.g. JavaScript, Python, Perl, Ruby, PHP). Demonstrated ability with programming languages and web application frameworks is required. Familiarity with Web 2.0 programming technologies is highly desirable.

SALARY RANGE: \$68,000 to \$75,000, commensurate with experience. This is a regular, academic professional, full-time, grant-supported, 9-month position/paid over 12-months (academic 9/12). Additional salary support for two summer months may be available through external funding obtained by the candidate through research grants or other funding opportunities. The estimated starting date is July 1, 2011.

BENEFITS: Generous sick leave. State Universities Retirement System. Group health, dental, vision and life insurance.

APPLICATION PROCESS: Applications must be received by May 27, 2011. To apply, all candidates must submit an online profile through <https://jobs.illinois.edu> by the close of the posting period. Qualified candidates must upload a cover letter which details qualifications noted above, curriculum vitae, working e-mail address, and the names, addresses, phone numbers, and e-mail addresses of three professional references. All requested information must be submitted for your application to be considered. Incomplete information will not be reviewed.

For further information please contact Erica Hanson, Human Resources, Illinois Natural History Survey, 217-333-6897, elhanson@inhs.illinois.edu. For technical questions, please contact: Dr. Andrew Miller, Search Committee Member, at amiller@inhs.illinois.edu.

The University of Illinois is an Affirmative Action/Equal Opportunity Employer. The administration, faculty, and staff embrace diversity and are committed to attracting qualified candidates who also

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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>

UMainz EvolutionaryBiology

University of Mainz *Assistant Professor (Akademischer Rat / A 13)* *Evolutionary Biology / Behavioral

Ecology * (non-tenure track, 6 years – with the possibility of further extension)* Closing date: *June 3rd 2011*

We invite applications for an *Assistant Professor (Akademischer Rat / A 13) *position in the newly established evolutionary biology group in the Institute of Zoology at Johannes-Gutenberg University of Mainz, Germany.

We are seeking a highly motivated young evolutionary or behavioral biologist with a strong background in genetics to establish a junior research group within Prof. Susanne Foitzik's research team. Candidates must hold a Ph.D. and postdoctoral experience is required. The successful candidate should address evolutionary or behavioral questions in social insects or other arthropods, and preferably use the latest genetic methods (e.g. next-gen sequencing, transcriptomics).

Our research focuses on behavioral and chemical ecology as well as on population genetics of ants (<http://www.bio.uni-mainz.de/zoo/evobio/>) and we are interested in collaborative projects. Excellent research conditions are available at the newly renovated and well-equipped genetic and chemical laboratories in Mainz. Furthermore, climate chambers are available for animal maintenance. For further information, please contact foitzik@uni-mainz.de.

The successful candidate should have an excellent publication record. Experience with grant acquisition and teaching is advantageous. The candidate should set-up an independent research lab and is encouraged to apply for grants in Germany or abroad (e.g., DFG, EU). The position comes with a teaching requirement of 4h per week during the semester. Some basic zoology classes have to be taught in German. Consequently, a willingness to learn German is required. The candidate has the option to acquire a "Habilitation". The working language of the lab is English.

The Johannes Gutenberg University of Mainz is interested in increasing the number of women in science. Applications from female scientists are strongly encouraged. Similarly qualified candidates with disabilities will be preferred. The University of Mainz hosts many excellent scientific institutions (<http://www.uni-mainz.de/eng/>) including the newly established Institute for Molecular biology (IMB, <http://www.imb-mainz.de/>). Mainz is a historic city located on the Rhine River with many students and a rich social and cultural life (<http://www.mainz.de/WGAPublisher/online/html/default/hpkr-5nkek8.en.html>).

Interested candidates should send an application (as a single e-mail attachment) containing a CV, a list of pub-

lications (including reprints of the three most important publications), research and teaching statements, and contact information for two potential referees to:

Prof. Dr. Susanne Foitzik Evolutionary Biology Institute of Zoology Johannes-v.- Müller-Weg 6 55099 Mainz

Germany foitzik@uni-mainz.de

*Closing date *for application is *June 3rd, 2011*

*Starting date*for the position *Oct. 1st 2011*, later starting dates are negotiable

Prof. Dr. Susanne Foitzik Evolutionsbiologie Institut für Zoologie Johannes Gutenberg Universität Mainz Johannes von Müller Weg 6 D-55099 Mainz Germany

Tel. +49 (0)6131 39 27 840 Fax. +49 (0)6131 39 27 850 email: foitzik@uni-mainz.de

Susanne Foitzik <foitzik@uni-mainz.de>

UPennsylvania LabTech Ant Evolutionary Genetics

A full-time Research Lab Technician position is available in the Linksvayer lab in the Department of Biology at the University of Pennsylvania. The research focus is on the evolution and genetic basis of complex social systems, using social insects as a model. A variety of approaches are used, including genomic, functional genomic, and evolutionary genetic approaches.

The position involves assisting with a range of experiments, including basic molecular genetics, measuring ant phenotypes, caring for ants in climate control rooms, as well as basic lab organization, maintenance, and administration.

The successful candidate will have a BA/BS in Biology or a related field, a strong work ethic, positive attitude, excellent communication and organizational skills, experience with basic molecular biology techniques such as DNA/RNA extraction, PCR, electrophoresis, sequencing, etc., and the desire to learn new skills. Experience working with insects is preferred but not required.

Applicants must apply directly through Penn's job posting website, <http://www.hr.upenn.edu/jobs/>. Search for the staff position with the reference number 110430423 and apply to the posting through the website.

Please contact me directly (tlinks@sas.upenn.edu) with any questions.

Timothy Linksvayer Assistant Professor Department of Biology University of Pennsylvania 225 Leidy Laboratories 433 South University Avenue Philadelphia PA 19104-6018 tlinks@sas.upenn.edu V +1 215 573 2657 F +1 215 898 8780 <http://www.bio.upenn.edu/faculty/linksvayer/> tlinksvayer@gmail.com

UppsalaU GroupLeader MolEvolBiol

A permanent position as Group leader in Molecular Evolutionary Biology, broadly defined, is available at the Dept of Ecology and Genetics (<http://www.ebc.uu.se/Research/IEG/>), the Evolutionary Biology Centre of Uppsala University

The position is connected to the sub-department Dept of Evolutionary Biology (<http://www.ebc.uu.se/Research/IEG/evbiol/>). Here, the research focus is in the interface of evolutionary biology and genomics. Examples of questions being addressed are the genetics of speciation, the genetic background to fitness-related traits and local adaptation (e.g., QTL and association mapping), bioinformatics, and general aspects of molecular, transcriptome and genome evolution. Please see our list of publications for further indications of on-going research (<http://www.ebc.uu.se/Research/IEG/evbiol/publications/>). There are no other specifications

of the position than that the candidate's research is expected to complement on-going research in the sub-department, with a clear goal to contribute to an already strong research environment by establishing collaborative links with other research groups.

Department of Evolutionary Biology, headed by Prof Hans Ellegren, currently includes 8 research groups with a total of about 50 persons, the majority of which are internationally recruited PhD students and post-docs. The location with the Evolutionary Biology Centre offers a most stimulating scientific and social environment with numerous seminars, journal clubs and possibilities for contacts and collaborations. A graduate school in 'The Genomics of Phenotypic Diversity in Natural Populations' (<http://www.ebc.uu.se/education/postgrad/gradschool/>) provides a framework for courses and other activities for PhD students. Local platforms for next-generation sequencing and high-performance computational analyses ensures immediate access to state-of-the-art technology.

The position comes with a start-up package including support for a PhD student. The successful candidate is expected to be highly competitive on an international level, including an ability to attract own funding. She or he most likely has a well documented record of independent research combining genetic/genomic approaches /data for addressing key evolutionary questions.

For informal inquiries and information on how to apply, please contact Hans Ellegren at Hans.Ellegren@ebc.uu.se

Hans.Ellegren@ebc.uu.se

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Bayesian tree convergence

Dear colleagues,

I am trying to use MrBayes to estimate a Bayesian tree of 10 mammal species. There are 3,873,035 sites in the alignment. I cannot determine whether convergence is reached. Below is the parameter setting.

```
set autoclose=yes nowarn=no; execute mammal.nex;
prset aamodelpr=fixed(wag); lset rates=gamma
Ngammacat=4 covarion=yes; mcmc nruns=1 ngen000
printfreqP0 samplefreq nchains=4; sumt burnin%0;
```

I have several output files, including mammal.nex.p mammal.nex.t mammal.nex.parts mammal.nex.con mammal.nex.trprobs mammal.nex.mcmc

Is there anyone who can help me find out the convergence information? Thanks!

Haiwei Luo Postdoctoral Associate University of Georgia

hluo2006@gmail.com

Biocluster

Hi all,

I want to run MCMC simulation in MIGRATE for my dataset, earlier have used Cornell Biocluster, that's closed now, so can anyone suggest other Bioclusters for faster computation; that would be of immense help!

Thanks in advance

AVIK RAY

– Visiting Fellow National Center for Biological Sciences Tata Institute of Fundamental Research GKVK Campus Bellary Road Bangalore-65 India 080-23666340

avik.ray.kol@gmail.com

Biogeography teaching exercises

Dear Evoldir,

I am designing a new course in biogeography, aimed at upper-division undergraduates. As part of the course I would like to include some simple exercises in GIS, phylogeny reconstruction, and/or phylogeography. If anybody has already developed exercises in these area and would be willing to share them with me, I would greatly appreciate it.

I am happy to post a summary of any replies I receive.

- Sarah Gilman

Sarah Gilman, Ph.D.

Joint Science Department Keck Science Center The Claremont Colleges 925 N. Mills Avenue Claremont, CA 91711

<http://faculty.jsd.claremont.edu/sgilman>

sgilman@jsd.claremont.edu 909-607-0715

SGilman@jsd.claremont.edu

Cabbage looper eggs needed

I'm looking for eggs of *Trichoplusia ni* for a series of experiments on resistance and tolerance to herbivory using *Arabidopsis*. My usual supplier from Ag Canada in London, Ontario is having some problems with his colonies, so I am looking for an alternative source for eggs. If you have a colony of this species and could send me some eggs please let me know. (Sources within Canada preferred due to customs restrictions) Thank you.

Dr. Germán Avila Sakar Assistant Professor Depart-

ment of Biology University of Winnipeg
(204)-786-9326
German Avila Sakar <gasakar@gmail.com>

Discount registration for Evolution2011

\$150 graduate student registration available for the Evolution conference in Norman, Oklahoma, USA, June 17-21. Normal grad student price is \$235. If interested, please contact amango[AT]life.bio.sunysb.edu.

I registered for the Evolution conference but am now unable to attend, two days after the deadline for refunds passed. However, registration is transferable, hence my discount offer.

amango@gmail.com

Discount registration for Evolution2011 2

\$170 graduate student registration available for the Evolution conference in Norman, Oklahoma, USA, June 17-21. Normal graduate student registration is \$235. If interested, please contact mniemill[AT]utk.edu

I registered for the meeting but am now unable to attend, as my father is having surgery. However, registration is transferable. mniemill@utk.edu

Matthew Niemiller <mniemill@utk.edu>

Diversification statistics question

Dear colleagues,

I'm analysing the diversification pattern of a group of organisms and I have a question concerning what appears to me to be an incongruent result. I have a negative gamma-statistic value, although the mcr test indicates that it is not significant (empirical g-value of -2.35

and mcrtest critical value -3.50, $p = 0.50$). Thus, I interpret this result as there not been a clear signal for a decrease in the rate of speciation. However, when I fit the rate-constant and rate-variable models to my data I can reject the constancy significantly, but the best model is the RV exponential density-dependent (DDX), which I would interpret as a signature of a decrease in the rate with time. This result to me is in contradiction to the gamma-statistic and I would like to know how can it be explained. However, I have to add that the second best model identified by the BDL approach is the yule2rate model, and the dAIC is pretty small (in one case is 0.05 and in other case 1.5).

I would appreciate your comments. Thanks.

Ramiro

—

Dr. Ramiro Morales-Hojas Molecular Evolution Lab
Instituto de Biologia Molecular e Celular (IBMC) Uni-
versity of Porto Rua do Campo Alegre 823 4150-180
Porto Portugal

e-mail: rmhojas@ibmc.up.pt tel.: +351226 074 900 ext
1612

rmhojas@ibmc.up.pt

Easy-IPD Teaching evolution cooperation

Greetings to all of you, especially those who teach about Robert Axelrod's iterated prisoner's dilemma (IPD) tournaments of the 1980's (the ones that led to the publication of his seminal book *The Evolution of Cooperation*).

I am proud to announce that I have produced (along with Jean Ho Chu, a graduate digital arts student) a new teaching and learning tool that will allow your students to experiment directly with IPD tournaments. The tool is a free, flash-based interface called "Easy-IPD", and you can learn more about it here:

<http://www.christopherxjensen.com/research/projects/online-cooperative-resource/easy-iterated-prisoners-dilemma/>

If you have any questions or suggestions we would be excited to hear them. If you decide to use this tool in your classroom, please let me know!

-Chris

Christopher X J. Jensen, PhD Pratt Institute Department of Math and Science 200 Willoughby Avenue - ARC LL G49 Brooklyn, NY 11205 Office: 718-636-3572 Department: 718-636-3764 FAX: 718-399-4482 <http://www.christopherxjensen.com/> Chris Jensen <cjensen@pratt.edu>

EvolDirNESCent EvolutionVideoContest 2

REMINDER:

Call for entries: NESCent announces Evolution Video Contest Application deadline: Friday June 10, 2011

Submit your best evolution-themed video for screening at this years Evolution meeting! The National Evolutionary Synthesis Center (NESCent) invites scientists of all stripes X graduate students, postdoctoral fellows and faculty X to enter the first-ever evolution video competition.

To enter, submit a video that explains a fun fact, key concept, compelling question, or exciting area of research in evolution in less than three minutes. Entries may be related or unrelated to your own research, and should be suitable for use in a classroom at any level (K-12, undergraduate, graduate...your choice). Videos should be both informative and entertaining. (In other words, no taped lectures or narrated Powerpoint presentations!) Animations, music videos, and mini-documentaries are all fair game.

Selecting the winners A panel of reviewers from both NESCent and the science video community will select the semi-finalists, who will be notified by e-mail. The top finalists will then be screened at a film festival at the 2011 Evolution meeting in Norman, OK, from 6:30 to 7:30 PM on Monday June 20th. After screening the videos, the audience will vote for their favorites. Prizes will be awarded for the top entries.

Eligibility

You dont need to attend the conference to submit an entry. All videos submitted by Friday June 10th (5:00 p.m. ET) are eligible to win. For more information and full contest rules, please see <http://evolutionvideo.wordpress.com/> or contact Dr. Jory Weintraub at jory@nescent.org, or Dr. Robin Smith at rsmith@nescent.org.

Jory Weintraub <jory@nescent.org>

IonTorrent outsourcing

Third-generation sequencing

Does anyone have any suggestions/recommendations for low cost high-throughput sequencing? I was considering an Ion Torrent, but I can not seem to locate any core facilities that offer this as an outsourced service.

Thank You! Mersee Madison-Villar

mersee@uta.edu

Mersee Madison-Villar PhD Candidate, UT Arlington Lab/Office B01 Genomics, Speciation, and Evolutionary Biology

“If evolution is outlawed, only outlaws will evolve”- Jello Biafra

“Madison-Villar, Mercedita J” <mersee@uta.edu>

Mismatches between markers

Dear evoldir members,

I would very thank you if somebody could help me in the next topic.

What can we concluded when diferent molecular markers (microsatellite, ITS, rcbL) provide diferent result about the taxonomic status of two putative species.? That is, the genetic analysis of two putatives species through 8 microsatellites loci in one hundred individuals, reveals that genetic diferentiation detected between two populations of the same species are higher than those recorded between populations of the two putative species. In addition, analysis of ITS1 and ITS2 sequence of both species only show one doubtful position in the nucleotide sequence. However, the analysis of rbcL sequence of two individuals of each species reveals differences in the nucleotide sequence. What can we concluded with these results? Are both taxa shared the same genetic pool (and they are probably the same taxa), or both species are independent taxa?

Thank in advance,

Miguel Angel

Miguel Angel González Pérez Universidad de Las Palmas de Gran Canaria Canary Islands, Spain mgonzalez@proyinves.ulpgc.es

canariensis750@hotmail.com

Mutadatabase

Movie dubbing

Dear evoldir community,

I am looking for help for recording German and French voices for a short movie about the evolution of lactase tolerance.

Since a few years we have been making short movies & other media about evolution. All material is freely available in English, French and German, from our webpage: <http://www.evolution-of-life.com/en/home.html>

We just finished the last movie of the project. It is a 6 min documentary about lactase tolerance in humans starring Joachim Burger and Sarah Tishkoff. We have (or soon will have) German and French translations for these movies, but we currently lack the necessary equipment and funding to hire actors & studios and technicians to make professional recordings of the German and French voices. I am hoping that someone in the evoldir community could help. Maybe you are an actor and German or French speaker with access to equipment?

Best wishes, Pleuni Pennings

<http://scholar.harvard.edu/pennings/home> Pleuni Pennings <pennings@fas.harvard.edu>

Multilocus coalescent

Dear all,

I am looking for a multilocus coalescent simulation which is able to take into account recombination and balancing selection. As far as I am aware Mlcoalsim only has the option for positive selection. Any recommendations would be greatly appreciated.

Thanks,

Jackie Lighten Dalhousie University

Jackie Lighten <jc807177@dal.ca>

Dear Colleague,

Many DNA variants implicated in genetic disease are not made public in papers or public databases, and therefore remain unclassified variants (VUS), which is a challenge for genetic counseling.

We therefore developed MutaDATABASE and MutaREPORTER.

MutaDATABASE (www.mutadatabase.org) is a human gene variation database which is centralized, standardized, open access and freely available to everybody. The centralised MutaDATABASE hosts all gene databases on a single standardised platform, and has a genome browser to visualize all variants and genes

MutaREPORTER is software available through a licence from MutaBASE (www.mutabase.com) to:

define, characterize and archive DNA variants retrieve molecular and clinical information from and submit into a central MutaDATABASE circulate info concerning a specific gene in community groups (MutaCIRCLES) An example of a locus-specific database (L1CAM gene) is shown by clicking on the following link: <http://www.mutareporter.org/-mutareporter/mutareporter.html?showgene=L1CAM>

If you want to contribute to the MutaDATABASE project as a curator supervising a gene, as a lab submitting molecular information or as a clinician submitting clinical info, or if you want to obtain MutaREPORTER, please let us know.

You can also find us at boot 284 at the upcoming European Society of Human Genetics meeting in Amsterdam. Also GENDIA will be at the same stand.

Thanks for your help

With kind regards,

Patrick Willems, MD, PhD MutaDATABASE

Emiel Vloorsstraat 9 2020 Antwerp, Belgium
 Email: info@mutadatabase.org Website: <http://www.mutadatabase.org> GENDIA <mailing@gendia.net>

Oikos blog

Dear Evodir subscribers,

The journal Oikos and the Nordic Society have a blog. <http://oikosjournal.wordpress.com/> We are working hard to make the blog a useful spot to comment on ecology and evolution papers, discuss relevant topics, connect with the editorial board, and provide a general forum to discuss synthesis in our discipline.

Oikos wants to promote novel synthetic ideas in ecology and evolution both in the the journal and online - in a timely manner. The mean turnaround time to first decision is now 50 days, and we are shooting for a lot less. We hope the blog can also serve as a place for discussion, and the editorial staff are reading it with an eye for hot topics for future Forum papers.

We hope you enjoy it.

cheers, chris lortie. Senior Editor

christopher lortie <lortie@yorku.ca>

PhenotypeRCN opportunities

We are pleased to announce two new opportunities for professional development through the Phenotype Research Coordination Network (<http://phenotypercn.org/>):

1) Have a strong desire to engage your peers at scientific meetings and to present on phenotype ontologies? The Phenotype RCN has the means to support participants' (two per year) travel to a national or international meeting to present ontology-based work. Funding priority will be to those researchers presenting to the broadest audience and/or who are students or postdocs. The goal is to broadly disseminate information to the larger scientific community regarding phenotype ontologies and their utility and involve new participants in the RCN. See below to apply for these funds.

2) The Phenotype RCN has the means to facilitate collaborations among network participants (2 per year @ \$1500 each). Students, postdocs, faculty, and/or small working groups can apply for travel funds to support

collaborations related to one or more of the RCN aims: a) Develop anatomical reference ontologies. b) Align and synchronize anatomy ontologies using homology and other similarity. c) Define anatomy ontology development best practices and standards. d) Reach out to ancillary phenotype groups to share with them common concepts and practices. e) Educate the community about the methods for developing ontologies and their importance and utility in research. Have a great idea for a research exchange? Consider submitting an application.

The application forms are available through our website: http://www.phenotypercn.org/?page_idV If you have questions about these opportunities please feel free to email us!

Sincerely, Paula Mabee (Vertebrate working group; Paula.Mabee@usd.edu) Eva Huala (Plants working group; huala@acoma.stanford.edu) Andy Deans (Arthropod working group; andy_deans@ncsu.edu) Suzi Lewis (Informatics working group; se-lewis@lbl.gov)

- Andrew R. Deans Department of Entomology North Carolina State University Campus Box 7613 2301 Gardner Hall Raleigh, NC USA 27695-7613

phone: +1 (919) 515-2833 fax: +1 (919) 515-7746 skype: ardeans <http://deanslab.org/> ardeans@ncsu.edu

Phyloseminar AdamSiepel May24 11amPST

Free online seminar next week:

Adam Siepel speaks Tuesday, May 24th at 11am PST on "Bayesian inference of ancient human demography from individual genome sequences"

Abstract: Besides their value for biomedicine, individual genome sequences represent a rich source of information about human evolution. I will describe an effort to estimate key evolutionary parameters from the genome sequences of six individuals from diverse human populations. We have used a Bayesian approach based on coalescent theory to extract information about ancestral population sizes, divergence times, and migration rates from inferred genealogies at many neutrally evolving loci from across the genome. We introduce new methods for accounting for gene flow between populations and integrating over possible phasings of

diploid genotypes. I will also describe a custom pipeline for genotype inference to mitigate possible biases from heterogeneous sequencing technologies, coverage levels, and read lengths. Our analysis indicates that the San of Southern Africa diverged from other human populations 108–157 thousand years ago (kya), that Eurasian populations diverged 38–64 kya, and that the effective population size of the ancestors of all modern humans was ~9,000.

Japan 03:00 (03:00 AM) on Wednesday, May 25
 Zealand 06:00 (06:00 AM) on Wednesday, May 25
 West Coast USA 11:00 (11:00 AM) on Tuesday, May 24
 East Coast USA 14:00 (02:00 PM) on Tuesday, May 24
 England 19:00 (07:00 PM) on Tuesday, May 24
 France 20:00 (08:00 PM) on Tuesday, May 24

For more details, please visit <http://phyloseminar.org>
 ematsen@gmail.com

Portuguese EvoBioSociety

[Full message in Portuguese below] Apologies for cross-postings!

Dear All,

During the last Portuguese Meeting of Evolutionary Biologists held in December, the group of people present decided to take the necessary legal steps in order to having a formal Evo Bio Society. The first steps for its constitution have been taken and we are now asking for people's input, in particular regarding the Mission Statements of the Society. To do that, we have created a poll (link below) where people can vote whether they agree/disagree with a society with these mission statements. Specific comments can be sent by email to any of us. The Society (and the poll) is directed to evolutionary biologists of all nationalities, who would be interested in joining. Please participate until May 31st.

Best regards, Hugo Gante hfgante@fc.ul.pt

>>>>>

Caros colegas,

No final do último Encontro Nacional de Biologia Evolutiva foi discutida a necessidade de nos organizarmos no sentido de formar a Sociedade Portuguesa de Biologia Evolutiva. O grupo de pessoas que estava presente acolheu bem a ideia. Felizmente este ano houve um grupo de 8 pessoas que se voluntariou para que tal seja

uma realidade muito em breve. Neste momento, este grupo encontra-se a trabalhar na elaboração dos estatutos, sendo que para tal é necessário definir as suas principais missões. A intenção desta comissão instaladora é que nos estatutos apenas sejam definidas missões gerais (ver em baixo), dando assim espaço para que as direcções eleitas possam delinear objectivos específicos para cada mandato, sempre no âmbito das missões principais que constituirão os estatutos. Para tal, definimos as seguintes missões: a) promover o conhecimento e divulgação de conhecimentos na Área da Biologia Evolutiva; b) fomentar o intercâmbio nacional e internacional no domínio da investigação e ensino na Biologia Evolutiva; c) colaborar com quaisquer entidades, oficiais ou privadas, nacionais, estrangeiras ou internacionais, no campo das suas competências técnicas e científicas. Nesta fase achamos importante divulgar as missões definidas por este grupo de modo a colocá-las à consideração de todos os potenciais futuros membros da Sociedade. O objectivo é auscultar a opinião geral sobre as missões, mas também de confirmar o interesse geral na constituição da sociedade, antes de avançar com os procedimentos finais para a sua oficialização. De modo a simplificar a consulta, resolvemos colocar uma pergunta simples: concorda com a forma de uma Sociedade com estas missões? POR FAVOR: siga este link [<http://doodle.com/us4dyhusrpbwtwr2>] e responda SIM ou NÃO, até ao dia *31 de Maio de 2011*. Independentemente da resposta é importante que participem, pois só assim sentiremos que há um interesse generalizado para a forma da Sociedade. Lembramos que: o ESEB meeting - maior encontro europeu de Biologia Evolutiva - vai ser realizado em Portugal em 2013; a ESEB está interessada em apoiar sociedades de biologia evolutiva; e que o ensino da Biologia e Medicina em Portugal muito provavelmente devia contemplar mais esta Área. Por favor divulguem esta mensagem pelos vossos colegas e instituições.

A comissão instaladora,

Alexandra Sá Pinto André Levy Hugo Gante Isabel Gordo Rita Campos Rui Castanhinha Rui Faria Sara Branco

hfgante@fc.ul.pt

Rap Guide to Evolution video launch

In partnership with The Wellcome Trust...

BABA BRINKMAN TO LAUNCH RAP VIDEO SERIES ON 25 MAY AT THE PRINCE CHARLES CINEMA, LONDON Award-winning performer produces videos to aide teaching of evolution

Baba Brinkman - the award-winning Canadian-born performer - is to launch a campaign, supported by the UK's largest charity the Wellcome Trust, to aide the teaching of evolution in schools - using his acclaimed show The Rap Guide to Evolution and a resource-packed website to assist.

The first step in the campaign is the launch of The Rap Guide to Evolution website later this month (www.rapguidetoevolution.co.uk) which will host a series of 12 specially produced music videos based on the show, as well as supporting materials that will assist teachers in utilising the videos in their work.

The launch at The Prince Charles Cinema in London on the 25th May 2011 will include previews of the videos, as well as performances by Baba and an introduction to the thinking behind the project.

Baba's aim is simple in principle but bold in practice - to combine the wit, poetry and charisma of an accomplished rapper with the accuracy, knowledge and expertise of an evolutionary scientist. Having performed The Rap Guide to Evolution at the Edinburgh Fringe in 2009, Baba was awarded a Scotsman Fringe First Award for Best New Theatre Writing as he combined original raps with remixes of well-known tracks - chronicling Natural Selection, Sexual Selection and Evolutionary Psychology.

The show owes its origins to Dr. Mark Pallen, author of The Rough Guide to Evolution, who had seen Brinkman's internationally acclaimed Rap Canterbury Tales and challenged Brinkman to "do for Darwin what he had done for Chaucer." In order to ensure scientific and historical accuracy, Brinkman consulted Pallen throughout the creative process, making The Rap Guide to Evolution the first peer-reviewed hip-hop show. Pallen has described Brinkman as having "swallowed the idea and turned it into a work of genius."

Baba has shared the stage with a number of high profile

science thinkers, from author Simon Singh to physicist Brian Cox to The God Delusion author Richard Dawkins, whilst he has also performed in Robin Ince's Nine Lessons and Carols for Godless People comedy series. The Rap Guide was described as "astonishing and brilliant" by the New York Times, with Science magazine writing that he "he marries the fast, complex, literate delivery of Eminem with the evolutionary expertise and confrontational manner of Dawkins."

Following on the show's success in Edinburgh, a host of science teachers contacted Baba to ask whether The Rap Guide to Evolution was available in DVD form for them to use in the classroom, and thus the seed was sown in Baba's mind to devise a way of taking the material into schools.

Baba partnered with SPL Productions - the company behind West End-hit Into The Hoods - and secured funding from the Wellcome Trust to help him with his campaign, as well as raising a further £12,000 directly from his fans through Crowdfunder.co.uk. With SPL Productions, Baba has split The Rap Guide to Evolution up into 12 parts, enlisting leading talent to produce and direct the videos with each video addressing a different area of the science behind evolution.

On the launch of the videos, Baba said: "The response to the show so far has been overwhelming, but these videos really take it to the next level. I hope educators all over the world find them helpful in overcoming the indifference and hostility that often impede the teaching of evolution, and science in general. Hip-hop music is all about rebellion, and no one's ideas are more revolutionary than Charles Darwin's."

The videos will be made available for free on www.rapguidetoevolution.co.uk, along with supporting educational resources and a host of bonus features and ongoing updates to facilitate their use by teachers in schools. Brinkman and SPL Productions are also creating a DVD with additional teaching materials that will be available to schools in the autumn.

Subsequent music videos in the series will be released over the coming months and made available for free online, and Baba will continue to promote their use throughout his live dates around the world, including an off-Broadway run that begins on June 17th.

TESTIMONIALS

"To hear the learning in the music makes things 10 times easier! Just wanna say thank you Baba for helping me realize how easy science could be! :) - Kadeidra, 15, Binghamton Public High School

"Baba made our students really think. They realized

that science really can be fascinating, challenging and genuinely stimulating - just as we've been trying to tell them for years... Great stuff!" - Simon Brookes, Professor of Human Physiology, Flinders University, Australia

LISTINGS

Video Premiere: The Rap Guide to Evolution

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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/evodir.html>

Software Announcing SequenceMatrix

Hi everybody,

My colleagues and I have released a Java-based sequence concatenation program called "SequenceMatrix". Files containing aligned gene sequences can be dropped straight into a spreadsheet-like window to combine them; the combined dataset can then be exported as a single Nexus or TNT file, with character sets and codon position data maintained intact. It has several other useful features, such as resplitting a combined dataset back into individual gene files, or exporting a table of the genes and species which make up a single dataset file. SequenceMatrix can also help identify some common forms of lab contamination [1]. You can get the program or its underlying source code from <http://code.google.com/p/sequencematrix/>. We've recently created a video which demonstrates SequenceMatrix combining multi-gene, multi-species datasets, available on YouTube at: <http://www.youtube.com/watch?v=Adwr-CZdNOM>. As first time screencasters, we'd really love your feedback on how well the video works and what we can improve for our next video.

Please let me know if you have any problems with either the program or the video!

cheers, Gaurav Vaidya <http://www.ggvaidya.com/>
[1] You can find out more about SequenceMatrix's contamination identification features in our paper: <http://dx.doi.org/10.1111/j.1096-0031.2010.00329.x>
ggvaidya@gmail.com

Software EggLib PythonModule

Dear colleagues,

We are pleased to announce the EggLib package.

EggLib is a C++/Python library and program package for evolutionary genetics and genomics allowing nucleotide sequence polymorphism analysis, coalescent simulations, Approximate Bayesian Computation, and more.

Most prominent feature is a Python module offering an intuitive and flexible interface to carry out a wide range of processing and analytical tasks. The Python module is supported by a computationally efficient (and independent) C++ library.

Several applications have been pre-implemented and are available as command line tools.

Full documentation, installation instruction and source code are available at the project home page:

<http://seqlib.sourceforge.net/> - Stéphane De Mita

Postdoctoral fellow IRD Montpellier 911 avenue Agropolis BP 64501 34394 MONTPELLIER cedex 5 France demita@gmail.com phone: +33 467416477 <http://sites.google.com/site/plantbiodiversityadaptation/> - Mathieu Sol

Postdoctoral fellow INRA Montpellier UMR Amélioration Génétique et Adaptation des Plantes Domaine de Melgueil 34130 Maugeio France phone: +33 4 67 29 29 90 email: Mathieu.Siol@supagro.inra.fr
demita@gmail.com

Teaching EvoDevo

Several people ask about the material I received by the list and I am sending again:

Dear friends,

Thanks to 30 people who wrote me indicating books and videos to use with undergrad classes about Evo Devo and these are the most cited material:

The most cited books:

Endless Forms Most Beautiful for Evo Devo. By Sean Carroll. http://www.amazon.co.uk/Endless-Forms-Most-Beautiful-Science/dp/1849160481/ref=sr_1_1?ie=UTF8&qid=01065731&sr=8-1 .It would be a good introduction to get students interested. Very accessible. From DNA To Diversity: Molecular Genetics and the Evolution of Animal Design, 2nd ed. Carroll, Grenier, Weatherbee. 2005. Blackwell Publishing. Wallace Arthur "Evolution. A developmental approach", which was just published by Wiley-Blackwell. Hall BK, Olson WM: Keywords and Concepts in Evolutionary Developmental Biology. 2003:476.

Other books: There is a very nice chapter on the topic written by John True in Futuyama's textbook, Evolution (2nd edition). "The Origin of Animal Body Plans" by Wallace Arthur The evolution of developmental pathways. Wilkins. Wray, G. A. 2010. Embryos and Evolution: 150 years of reciprocal illumination. In: Evolution Since Darwin: The First 150 Years, pp. 215-239, in M. A. Bell, D. J. Futuyama, W. F. Eanes, and M. A. Bell. Sinauer Associates, Sunderland. Developmental plasticity and evolution. West-Eberhard. (lots of overview material) Ontogeny and Phylogeny. Gould. (not exactly up to date, it's from 1977) Evolution - The Extended Synthesis IT Press, 2010 <http://mitpress.mit.edu/catalog/item/default.asp?tttype=2&tid=173> Evolution, Development, and the Predictable Genome. David L. Stern (Author) http://www.amazon.com/Evolution-Development-Predictable-Genome-David/dp/1936221012/ref=sr_1_6?s=books&ie=UTF8&qid=01078243&sr=1-6 Gilbert & Epel's "Ecological Developmental Biology: Integrating Epigenetics, Medicine, and Evolution The shape of life. Raff

VIDEOS: "Ghost in Your Genes" (http://www.amazon.com/Ghost-Your-Genes-Nova/-dp/B000XBPDYY/ref=sr_1_1?ie=UTF8&s=dvd&qid=01077278&sr=8-1) "What Darwin Never Knew" both produced by the television show NOVA. PBS video: <http://www.pbs.org/wgbh/nova/body/epigenetics.html> <http://www.pbs.org/wgbh/nova/body/rnai-explained.html> <http://www.pbs.org/wgbh/nova/body/rnai.html> http://www.hhmi.org/biointeractive/rna/rna_interference/01.html <http://www.nature.com/focus/rnai/animations/index.html> <http://learn.genetics.utah.edu/content/epigenetics/rats/> Website: On ENSI site, there is a very nice Threespine Stickleback lesson that introduces elements of evo-devo: <http://www.indiana.edu/~ensiweb/lessons/stickleback.html> Thanks for all of you and..... we need a website to organize references, links of videos and also a library of slides. We are always discussing about research but we need a place to centralize all

material for education!

VOLTOLINI <jcvoltol@uol.com.br>

Transposon copy number quantification

Dear Evoldir friends,

I would like to estimate the copy number of a transposon isolated from a sturgeon species. Sturgeons are known to have different levels of ploidy: they may be diploid, tetraploid or octoploid. What kind of method do you suggest for this estimation? I first would like to try with a qRT-PCR. For an accurate quantification with qRT-PCR, it is important to have a calibrator gene. As far as know, there are no reference genes for sturgeon with a known copy number. Nevertheless, there are genotyped microsatellite loci with defined allelic number. Can I use sturgeon microsatellites, or, alternatively, a gene standard isolated in an other species? In particular in my opinion it is not important the species origin of the internal calibrator, but the starting calibrator DNA concentration which should be the same of the template DNA. Moreover, what is the best bp length of the amplified product for a good qRT-PCR efficiency? and should the two pcr products (calibrator and transposon) have the same bp length? Do you suggest alternative methods?

thank you very much for your help Federica Barbisan

federica.barbisan@unipd.it

UMelbourne Avian Behaviour

We are looking for volunteer field assistants to help monitor a colour-banded population of superb fairywrens near Melbourne, Australia for a study on animal personalities. Start date: August 2011. Time period: approx 6 months. Duties include regular censusing of colour-banded birds, searching for and monitoring nests, mist-netting, behavioural observations, and data entry. Working days are long, with early starts six days a week. Enthusiasm and a strong work ethic are a must! The study is based at Serendip Sanctuary, a small reserve on the outskirts of Mel-

bourne. Qualifications: experience monitoring colour-banded birds, nest-searching, and mist-netting. Must also be early riser, physically fit and able to work in extreme weather conditions, and enjoy basic shared living conditions. Onsite accommodation in a shared dorm-style room is provided, but assistants cover travel to the site and their own food costs. The project will contribute AUD\$500/mo towards receipted food and travel expenses. For more information contact:

Michelle Hall (hall.m@unimelb.edu.au) and Raoul Mulder (r.mulder@unimelb.edu.au). To apply, please email a letter outlining previous field research experience, and a resume including names and contact information for 3 referees.

Dr Michelle L Hall Research Fellow Department of Zoology, University of Melbourne Melbourne, VIC, 3010, Australia

hall.m@unimelb.edu.au

PostDocs

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ATHCairnsAustralia BarcodingOrchids

Postdoc position at Australian Tropical Herbarium

We are currently inviting applications for a new post doc position (DNA barcoding and molecular systematics of Australian orchids) at the Australian Tropical Herbarium in Cairns. This is a 2.5 year position funded by an ABRS grant. Job description and further details below and at http://www-public.jcu.edu.au/jobs/-research/JCU_080011 Closing date: 17 June 2011

With kind regards, Katharina Schulte and Darren

Crayn —

POSTDOCTORAL FELLOW: Australian Tropical Herbarium Job Level(s): Academic A Employment Type: Appointment will be full-time for a fixed-term (specific project) to 30 November 2013 subject to a probationary period. Salary: \$65,902 - \$73,082 per annum. Commencing salary will be in accordance with qualifications and experience. Benefits include generous employer superannuation contribution and attractive options for salary packaging. Location: Cairns Closing Date: 17 June 2011 Reference No: 11123

Position Statement The Australian Tropical Herbarium (ATH) seeks an outstanding and highly motivated post-doctoral researcher with expertise in plant molecular systematics to join our dynamic research team. You will develop molecular identification tools (DNA-barcodes) for Australian Orchidaceae, generate and analyse multi-locus DNA data employing a variety of established and innovative approaches, and contribute to understanding the phylogeny, evolution and biogeographic history of Australian orchids. Your expertise in the collection and analysis of molecular and morphological data will lead to high impact research outcomes. The ATH offers an unrivalled specimen collection (herbarium, spirit and DNA) of Australian tropical rainforest plants, full taxonomic research and field facilities including a comprehensively equipped molecular biology laboratory, and is situated adjacent to a range of tropical biomes including the World Heritage listed Queensland Wet Tropics rainforests. Visit us at www.ath.org.au

Duties and Accountabilities The appointee will be required to:

- â Develop a molecular identification system for Australian Orchidaceae based on suitable plastid and nuclear DNA regions (i.e. DNA barcoding);
- â Generate and analyse multi-locus DNA barcode data employing a variety of established and where appropriate innovative approaches and methods;
- â Contribute to a collaborative research project that aims to re-evaluate current taxonomic concepts in Australian Orchidaceae based on multi-locus molecular evidence and to unravel the phylogeny, evolution and biogeographic history of Australian orchid groups;
- â Take responsibility for the curation of generated DNA barcode data and associated biological collections such as DNA, tissue, and databases at the Australian Tropical Herbarium, and for making the DNA barcode data publicly available through online portals;
- â Communicate the results of research and analyses orally and in written form to colleagues, industry, the scientific research community and other stakeholders.

Key Selection Criteria 1. PhD (conferred or pending) and documented research and publication history in plant molecular systematics; 2. Demonstrated ex-

pertise in relevant molecular biology lab techniques, such as primer design, sequencing of plastid and nuclear DNA markers, and cloning; 3. Evidence of high level of computing skills including phylogenetic analysis and multivariate analysis; 4. Demonstrated flexible and constructive approach to work design and work procedures, especially in the molecular lab; 5. Demonstrated knowledge of contemporary taxonomic concepts and processes, including the use of phenotypic and genotypic data; 6. Demonstrated ability to efficiently organize and conduct a research project including timely reporting on research milestones and outcomes, and maintaining a research budget; 7. Demonstrated ability and commitment to publish the results of scientific research in high quality scientific print and electronic media within agreed timeframes; evidence of high level written, oral and interpersonal communication skills to diverse audience; 8. Ability to work effectively as a member of a team, to interact and communicate effectively with staff, stakeholders and clients at all levels; 9. Ability to undertake field work in tropical ecosystems.

Desirable Selection Criteria 1. Expert knowledge in systematics and phylogeny of Orchidaceae; 2. Experience in DNA barcoding; 3. Competence and experience in the curation of biological research collections such as DNA or tissue banks, including databasing; 4. High level bioinformatics skills and experience.

Enquiries Name: Dr Katharina Schulte **Phone:** (07) 4059 5009 **E-mail:** katharina.schulte@jcu.edu.au

Method of Application Applicants must provide a full statement of qualifications and career,

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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>

Berlin FungalEvolution

We are currently looking for a postdoctoral researcher to work on the genetic basis of serpentine tolerance in the ectomycorrhizal fungus *Cenococcum geophilum*. The work will involve collecting samples in the field, maintaining cultures, phenotype testing and extensive genotyping using a variety of methods (AFLP, genotyping arrays, second-generation sequencing). A PhD degree in biology is required and experience in molecular

genetics and microbiology is highly desirable. Preference will be given to candidates with a good knowledge of population/quantitative genetics and statistics.

The position will be hosted at the Centre for Functional Ecology (<http://cfe.uc.pt/>) of the University of Coimbra (<http://en.wikipedia.org/wiki/Coimbra>) and the Institute for Biology (<http://www.biologie.fu-berlin.de/en/index.html>) of the Free University of Berlin (<http://en.wikipedia.org/wiki/Berlin>), under the supervision of Ludo Muller (ludo.muller@fu-berlin.de) and Susana Gonçalves (scgoncal@ci.uc.pt). The position is funded for a period of 12 months and the candidate will be assisted in obtaining further funding. Starting date is flexible but foreseen for the summer of 2011.

Please apply by sending a cover letter and CV, including a list of three references, to: ludo.muller@fu-berlin.de. Deadline for applying is May 31, 2011. Informal inquiries are welcome.

Dr. Ludo A.H. Muller Freie Universität Berlin Institut für Biologie - Botanik Altensteinstraße 6 14195 Berlin Germany Tel. +49 (0)30 838 56539 Fax +49 (0)30 838 55434

ludo.muller@fu-berlin.de

BrownU Phylogenomics

Postdoctoral Research Position Large Scale Phylogenetic Inference with Next-Generation Sequence Data

A postdoctoral position is available in Casey Dunn's lab (<http://www.brown.edu/Faculty/Dunn.Lab/>, casey_dunn@brown.edu) at Brown University in Providence, Rhode Island. The successful candidate will develop new methods and tools to address key challenges in constructing phylogenies with many genes and many taxa, and will use Illumina sequence data from a broad diversity of organisms to build species trees for several on-going projects. Research in related topics beyond these core goals will be strongly encouraged.

Applicants should hold a PhD in Evolutionary Biology or Computer Science. Qualifications should include a detailed understanding of phylogenetic inference methods and molecular evolution, experience building phylogenies, and programming experience (e.g., Python, R, SQL, and Unix).

Depending on the interests of the candidate, the post-

doc could also participate in fieldwork and sample preparation for sequencing.

Please apply by sending a cover letter, CV, and contact information for three references to Casey Dunn (casey_dunn@brown.edu). General inquiries are welcome. The position is available immediately.

– <http://www.brown.edu/Faculty/Dunn.Lab> <http://creaturecast.org> <http://practicalcomputing.org>
casey_dunn@brown.edu

CaliforniaAcademy AvianDiseaseDynamics

POSTDOC: Avian virus discovery and studies of disease dynamics

California Academy of Sciences San Francisco, California

We invite applications for a postdoctoral research fellowship to collaborate on studies of avian viruses and coevolution with hosts. Coevolutionary analyses will include microarray and next generation sequencing analyses of virus diversity, phylogeography and potential virus roles in declines or extinction of diverse avian host populations. The latter will involve comparison of avian and viral diversity and abundances in island and mainland habitats as well as in natural and environmentally-stressed habitats.

We are looking for an enthusiastic and motivated individual to join our research team. The ideal candidate will have experience in molecular techniques including DNA and RNA extraction, sequencing, gene profiling via microarrays, Illumina sequencing and analysis, as well background in phylogenetics, molecular evolutionary analyses and avian or virus evolution. The position will be based at the California Academy of Sciences (CAS) in the lab of Jack Dumbacher and will collaborate closely with David Mindell (CAS) and Joe DeRisi (Univ. of California at San Francisco).

CAS and UCSF have vibrant communities of researchers working on evolutionary and systematics topics involving both theory and practice, population dynamics, and infectious disease coevolution with hosts. Our groups have close ties with many other researchers in the Bay Area. CAS is situated in Golden Gate Park in San Francisco, within minutes of the ocean, biking and hiking trails, and the rich cultural and culinary offerings of the city.

The position is available as early as Summer 2011, and may last up to two years, pending appropriate progress and favorable annual reviews. Starting salary will be in the range of \$43,000 to \$50,000 per year, plus benefits, depending on experience.

To apply please send a CV, letter of interest and contact information for three references to Jack Dumbacher at jdumbacher@calacademy.org. Review of applications will begin on 20 May and will continue until the position is filled. The California Academy of Sciences is an Equal Opportunity Employer and welcomes applications from individuals who will contribute to its diversity.

John P. Dumbacher (Jack) Curator and Department Chair Department of Ornithology and Mammalogy Division of Research and Collections California Academy of Sciences p. 415.379.5377 f. 415.379.5738 jdumbacher@calacademy.org www.calacademy.org 55 Music Concourse Drive Golden Gate Park San Francisco, CA 94118

“Dumbacher, Jack” <JDumbacher@calacademy.org>

EmoryU GeneticsDrosophila ParasiteInteractions

Drosophila Genetics Postdoctoral Position Emory University, Atlanta, GA USA Laboratory of Dr. Todd Schlenke

We are looking for a highly motivated postdoctoral researcher to work on the genetics of *Drosophila* resistance against parasitic wasps. *Drosophila* are a model system for study of innate immunity, and wasps are one of the most common pathogens of fruitflies in nature. It is the interaction between the innate immune response of the flies and the venom of the wasps that determines the outcome of any infection. We currently have funding to use a combination of candidate gene approaches, QTL mapping, and association mapping to identify fly loci that control resistance. The resistance genes we identify will be functionally characterized using a variety of cell and molecular biology techniques, and any history of adaptive evolution at such loci will be determined with population genetic and molecular evolution analyses. Applicants will preferably have a background in some combination of *Drosophila* biology, host-pathogen interactions, population genetics, genetics, and molecular biology.

The Schlenke lab (<http://www.biology.emory.edu/-research/schlenke/>) is part of Emory's Biology Department (<http://www.biology.emory.edu/>) and is affiliated with the Genetics and Molecular Biology (GMB) and Population Biology, Ecology and Evolution (PBEE) graduate programs. These groups have a strong emphasis on host-pathogen interactions, *Drosophila* molecular genetics, and bioinformatics, and we regularly collaborate with multiple labs across campus. Atlanta is also a great place to live.

Interested candidates should send a CV, along with a brief statement of interests and experiences in the above-mentioned areas, to Todd Schlenke by June 25th, 2011. Candidates can start any time between now and January 2012.

Dr. Todd Schlenke Emory University Department of Biology tschlen@emory.edu

“Schlenke, Todd” <tschlen@emory.edu>

FloridaStateU EvolutionaryBiology

Postdoctoral Researcher in Evolutionary Biology and Behavioral Ecology: Florida State University

Dr. Emily Moriarty Lemmon

Department of Biological Science, Florida State University

Position Description: A postdoctoral position (up to three years) is available in the laboratory of Dr. Emily Moriarty Lemmon to collaborate on an NSF-funded project to study the effect of community interactions on evolution of male reproductive signals and female preferences in chorus frogs (*Pseudacris*) and the genetic consequences for speciation.

The postdoctoral scientist will lead a team of graduate students and field technicians to conduct fieldwork across the southeastern United States and perform behavioral experiments in a portable lab during the spring field seasons (approximately three months per year). Outside of the field season, the postdoctoral scholar will analyze behavioral data, genotype samples, and collect next-generation sequencing data. The ideal candidate will have field experience with frogs, experience conducting behavioral experiments, training in molecular biology, and computational experience. However, applicants with some combination of the above qualifications will also be considered. The start-date for this position

will be fall 2011 (exact date flexible), and salary will be competitive.

Minimum Qualifications:

- A Ph.D. in biology, molecular biology, or a related field with a focus on evolution - Previous research experience and a strong publication record - Extensive field experience, preferably with amphibians - Ability to communicate clearly, work efficiently and independently, interact collaboratively, and lead a field team

Additional Preferred Qualifications:

- Molecular biology and genetics training (e.g., phylogenetics, population genetics, phylogeography) - Computational experience - Experience with next-generation sequencing - Experience conducting behavioral studies

Application Deadline: 1 June 2011 (or until filled).
Start date Fall 2011 (exact date flexible).

To Apply: Application materials consisting of (1) a CV, (2) a statement of research interests and experience including how previous experience relates to the position description (2 page max), and (3) contact information for three references must be submitted to chorusfrog@bio.fsu.edu . Review of applications will begin June 1, 2011 and continue until the position is filled. Informal inquiries are welcome. General information about the lab can be found at <http://www.bio.fsu.edu/chorusfrog/index.html> .

About Florida State University: The successful applicant will be affiliated with the Department of Biological Science (<http://www.bio.fsu.edu/>) and will also interact with the Department of Scientific Computing (<http://www.sc.fsu.edu/>), and the College of Medicine (<http://med.fsu.edu/>). These groups collaborate extensively on evolutionary, behavioral, statistical, mathematical, genomic, and computational projects. The postdoctoral researcher will join this community of highly interactive research laboratories. Florida State University is located in capital city Tallahassee on the Florida Panhandle immediately adjacent to the Apalachicola National Forest, which is the largest national forest in Florida (nearly 900 sq. mi.). The forest borders the Apalachicola National Estuarine Research Reserve, which is one of the most productive estuarine systems in the Northern Hemisphere. The Apalachicola River basin contains the highest herpetofaunal diversity in the U.S. and Canada.

The researcher chosen will become part of the integrative laboratory groups of Emily Moriarty Lemmon and Alan Lemmon at Florida State University. More information is available at these websites:

<http://www.bio.fsu.edu/chorusfrog/index.html> <http://www.bio.fsu.edu/faculty-moriarty-lemmon.php>

<http://www.evotutor.org/LemmonLab/>

Dr. Emily Moriarty Lemmon Assistant Professor Department of Biological Science 319 Stadium Drive, P.O. Box 3064295 Tallahassee, FL 32306-4295 Phone: 850-645-9170 chorusfrog@bio.fsu.edu

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

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Frankfurt FungalAdaptation

PostDoc: Frankfurt.Fungal adaptation to climate change

TheSchmitt laboratory at the Biodiversity and Climate Research Centre (BiK-F),Frankfurt, Germany, offers the position of a postdoctoral researcher“Adaptation of fungi to climate change” [Ref. #C43]. The successful applicantwill investigate short term evolutionary processes in fungal communities,species or populations as a response to climatic factors. He or she has theopportunity to independently develop a project on the above theme preferablyusing mutualistic fungi, e.g. lichens, endophytes or mycorrhizae as studysystems. Experiments involving the use of terrestrial model ecosystems, genomicand metagenomic approaches including next generation sequencing are possible.The institute offers ample opportunities to interact with researchers focusingon modeling, statistics, genomics, or social sciences approaches to studyingthe relationships between biodiversity and climate.

The applicant should hold a Ph.D. in evolutionary biology, ecology or a related field, and have a strong backgroundin some of the following areas: mycology, evolutionary theory, molecularcommunity assessment, phylogenetics, population biology, and bioinformatics.Post-doc experience is preferable, but not necessary. A solid publicationrecord, good written and oral communication skills in English, the willingness to write research

papers and research proposals, work productively in a team, and to learn at least basic German are required.

We offer a competitive salary (TV-H E 13, a public service position in Germany), full benefits, and training opportunities at Goethe University Frankfurt and international/national laboratories. The position is available from August 15th 2011, but the start date is flexible. The initial contract will be for one year with the possibility of multiple year extensions for up to six years. Habilitation is possible. The Biodiversity and Climate Research Centre advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference.

Please send your application by e-mail attachment, mentioning the reference of this position (#C43) and including a letter outlining your suitability for the post, a detailed CV, contact details of 2-3 referees and a copy of your PhD thesis 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 Service and Finances: recruiting@senckenberg.de.

Review of applications will begin on July 1st, 2011, and continue until a suitable candidate is identified.

Informal inquiries to Imke Schmitt (imke@senckenberg.de) before the application are welcome.

imke@senckenberg.de

IndianaU Evolutionary Genomics

Postdoctoral associates and graduate students in environmental genomics

Indiana University has institutional goals to establish leadership in the area of environmental genomics to understand how gene function is influenced by environmental conditions, while accounting for variation that exists within and among natural populations. The Shaw lab in the School of Public and Environmental Affairs and the Center for Genomics and Bioinformatics at Indiana University is looking for talented, creative, and motivated post-doctoral associates and graduate students who want to make a positive impact on the world, while advancing their careers in this exciting new area of study. We have current openings to work on an NIEHS funded project that couples mu-

tation accumulation studies, population genome scans, and QTL experiments to explore the causes and phenotypic consequences of gene copy number variation as they relate to adaptation, disease, and susceptibility in the NIH model *Daphnia* (Science, 2011, 331: 555-561). Individuals with strong quantitative backgrounds in genomics, population genetics, computational biology or related fields are encouraged to apply. Knowledge of statistics, in particular high-throughput data analysis is also highly desired. Candidates must be effective working independently and confident leading projects, while also collaborating and assisting the group in its collective goals. Those applying for graduate studies should have prior research experience a Master's degree or equivalent is preferable, and meet the academic requirements of the School. Applicants for post-doctoral positions must have a strong record of productivity as evidenced by publications. All should possess exceptional written and oral communication skills. To apply, please send a cover letter that explains how this position fits with your experience and goals, CV, and references to joeshaw@indiana.edu or mail a hard copy to: Joseph Shaw, Ph.D., School of Public and Environmental Affairs, Indiana University, 1315 East 10th Street, Bloomington, IN 47405. For more information visit (<https://daphnia.cgb.indiana.edu/Projects#Projects-19>).

Indiana University is an Equal Opportunity/Affirmative Action Employer, Educator and Contractor, and is strongly committed to achieving excellence through cultural diversity. The university actively encourages applications and nominations of women, persons of color, applicants with disabilities and members of other underrepresented groups.

jcolbour@cgb.indiana.edu

IowaStateU TurtleChromosomeEvolution

Postdoctoral Position in Evolutionary Genomics V Turtle Chromosome Evolution

A postdoctoral position is available immediately to work in the laboratory of Dr. Nicole Valenzuela at Iowa State University on an NSF-funded project in collaboration with Dr. Scott Edwards from Harvard University.

The research focuses on evolutionary genomics to study the evolution of sex chromosomes and sex-linked genes in turtles, by the use of high resolution cytogenetic

techniques and existing genomic resources, and is expected to result in very high impact publications. We are exploring the origin and divergence of various sex chromosomes systems in turtles, the evolution of syntenic groups of sex-related and sex-linked genes, and the molecular divergence of such genes in turtles with genotypic and temperature-dependent sex determination.

The ideal candidate will have a PhD degree and strong background in molecular and classic cytogenetic techniques including chromosomal preparation, fluorescent in situ hybridization/chromosome painting, karyotyping, and the use of Cytovision or other chromosomal analysis platform. Other qualifications such as evolutionary biology background and experience with cell culture are a plus.

Interested candidates should email a cover letter describing their research interests and experience, CV, two letters of recommendation, and copies of up to two relevant publications to Dr. Nicole Valenzuela at nvalenzu@iastate.edu.

The department of Ecology, Evolution, and Organismal Biology at Iowa State University is comprised of over 40 faculty, whose active research programs span many areas of E&E from classic to modern -omic approaches, and interactions with faculty in other departments and programs are extensive.

Iowa State University does not discriminate on the basis of race, color, age, religion, national origin, sexual orientation, gender identity, genetic information, sex, marital status, disability, or status as a U.S. veteran.

Dr. Nicole Valenzuela Associate Professor Department of Ecology, Evolution, and Organismal Biology 253 Bessey Hall Iowa State University Ames, IA 50011, USA URL: <http://www.public.iastate.edu/~nvalenzu/> Nicole Valenzuela <nvalenzu@iastate.edu>

campus is one of the greenest in the country and is set in beautiful pastoral landscapes next to the city of Newcastle-under-Lyme.

The Research Associate will be responsible for managing targeted re-sequencing projects and contributing to the bioinformatics workflow of various collaborative projects. This position will thus offer ample opportunities for the candidate to develop their own ideas but it is paramount that she/he thrives to design simple bioinformatics tools that are tractable and accessible to all collaborative parties involved. We are looking for a team player with excellent communication skills and an international outlook.

The ideal candidate will have good quantitative skills and a strong background in bioinformatics. Candidates should be able to demonstrate their programming skills in C-related languages (R, python) during the interview. The Research Associate will be involved in experiments leading to the generation of DNA samples for genomic analyses, hence some background in molecular biology is important and experience in insect ecology/rearing would be a plus.

This full-time position is available for a 3-year duration and will start as soon as possible. Salary will be ~ £38k-42k/year.

For informal enquiries and information about the application process contact Dr. Frederic Tripet, f.tripet@biol.keele.ac.uk

Frederic Tripet, Ph.D Lecturer in Molecular Biology of Insect Disease Vectors Msc in Molecular Parasitology and Vector Biology, Program Director Center for Applied Entomology and Parasitology School of Life Sciences, Huxley Building Keele University Campus, Keele, Staffordshire ST5 5BG UK

Email: f.tripet@biol.keele.ac.uk Tel: ++44 1782 733873 Fax: ++44 1782 733516 Website: <http://www.keele.ac.uk/research/istm/tripet.html> f.tripet@biol.keele.ac.uk

KeeleU MosquitoSpeciation

A Postdoctoral position in Bioinformatics is available in Frederic Tripet's research group based at the Center for Applied Entomology and Parasitology at Keele University, in the West Midlands, UK. The successful applicant will work on UK and UK-African collaborative projects focusing on the genomics of speciation in the *Anopheles gambiae* mosquito complex and sponsored by the MRC and NERC. The Keele University

Lyon ComparativeBacterialGenomics

A 24 months post-doctoral position is available to work on the comparative genomics of piezophilic microorganisms, i.e. bacteria and archaea adapted to high pressure such as those living next to deep-sea hydrothermal vents, at the LBBE (Biometry and Evolutionary

Biology lab) of the university of Lyon, France (<http://lbbe.univ-lyon1.fr/?lang=en>).

The successful candidate will have a strong background in Bioinformatics, Molecular Evolution and Statistics and good programming skills. Some knowledge of structural biology would be a plus. He/she will have to interact with microbiologists and biochemists in the context of a larger project funded by the ANR (National Research Agency) in collaboration with labs in Lyon, Grenoble and Brest, France. The aim of this project is to understand the genetic basis of life at high pressure.

The work will be conducted by Vincent Daubin from the Bioinformatics and Evolutionary Genomics Group and Laurent Gueguen, from the Baobab group.

The BBE lab offers a highly stimulating scientific environment, and Lyon is a beautiful, history rich, lively city. Net salary is around 2000 per month.

Please send a CV, motivation letter and the names of two referees to Vincent Daubin (vincent.daubin@univ-lyon1.fr) and Laurent Gueguen (laurent.gueguen@univ-lyon1.fr).

Keywords: Phylogenetics, comparative genomics, models of sequence evolution, biochemistry

Vincent Daubin <vincent.daubin@univ-lyon1.fr>

Marseille GenomeEvolution

2 years post doc position, on the role of HGT (Horizontal gene transfert), is available at the EBM lab at marseille. A solid back ground in molecular evolution is necessary, programming skills will be a plus. more info: http://sites.univ-provence.fr/evol/index.php?option=com_content&view=category&layout=blog&id=139&Itemid=225&lang=en Pierre Antoine Pontarotti Equipe Evolution biologique et Modélisation UMR 6632 Université de Aix Marseille/CNRS . <http://sites.univ-provence.fr/evol/> Pierre PONTAROTTI <Pierre.Pontarotti@univ-provence.fr>

Montpellier ComputationalPhylogenetics

Postdoc position:

Fast algorithms for dating and phylogeography Montpellier, France (www.lirmm.fr/mab)

Our group is working on mathematical and computational phylogenetics. We are interested in theory (e.g. properties of distance methods [1]), models (e.g. amino-acid replacement processes [2]), algorithmics and software development (e.g. PhyML [3]), and biological applications, mostly to pathogens (e.g. malaria [4, 5]). We are ~25 people in the group, with nearly half permanent researchers and half PhDs and postdocs. Our group belongs to a large computer science laboratory, situated at Montpellier near the Mediterranean Sea. To know more on us, our research, publications and lab: www.lirmm.fr/mab We are looking for a postdoc to work on fast (typically distance- and parsimony-based) methods for dating and phylogeography, with applications to virus epidemiology and plant migrations. Interpreting phylogenies in terms of time and space become highly topical with the ever increasing amount of sequences, but standard ML and Bayesian methods are much to slow to deal with the data sets available today (typically several thousands taxa with HIV or FLU). The aim of this postdoc is to propose alternative, efficient methods, which will be statistically well-founded but faster by several orders of magnitude.

We have a one-year position available, starting in 2011 (ideally mid-September), with possibilities of extension. The successful candidate will have strong skills in algorithmics, statistical modelling and phylogenetics. To apply please send CV, motivation letter and references to me. All enquiries are welcome.

Olivier Gascuel www.lirmm.fr/gascuel gascuel@lirmm.fr

[1] Gascuel O., Steel M., Neighbor-Joining Revealed±, *Molecular Biology and Evolution*, 23(11), 1997-2000, 2006.

[2] Le S.Q., Gascuel O. Accounting for Solvent Accessibility and Secondary Structure in Protein Phylogenetics is Clearly Beneficial±, *Systematic Biology*, 59:277-87, 2010.

[3] Guindon S., Gascuel O., “A simple, fast and accurate algorithm to infer large phylogenies by maximum-likelihood±, *Systematic Biology* 52(5), 696-704, 2003.

[4] Blanquart S, Gascuel O., Mitochondrial genes support a common origin of rodent malaria parasites and *Plasmodium falciparum*'s relatives infecting great apes±, *BMC Evol Biol.* 2011 Mar 15;11:70.

[5] Brhlin L, Dufayard JF, Gascuel O., PlasmoDraft: a database of *Plasmodium falciparum* gene function pre-

dictions based on postgenomic data±, BMC Bioinformatics. 2008 Oct 16;9:440.

Olivier gascuel <gascuel@lirmm.fr>

NewYorkU PlantEvolutionaryGenomics

Post-doctoral Position in Plant Evolutionary Genomics at the New York University Center for Genomics and Systems Biology

A Post-doctoral position is available as part of the NSF Plant Genome Grant DBI -0922738 entitled: "Comparative Genomics of Seed Evolution". The successful applicant will have skills and experience in Genomics, Bioinformatics and Evolutionary Biology. The position will include experimental/informatic analysis on NextGen datasets (e.g. overseeing laboratory work, planning, leading and conducting analyses on RNASeq data). Skills in R, Perl, Python or other programming language are strongly preferred. This position also includes Project Manager duties, which involve coordinating scientific activities at four participating institutions; organizing group meetings, writing grant reports, and communicating our work in conferences and meetings.

This project involves the collaboration of systematists, molecular biologists, genome scientists and bioinformaticians from four research/ educational institutions. PI: Gloria Coruzzi (NYU Center for Genomics and Systems Biology); Co-PI(s): Robert DeSalle (AMNH); Dennis W Stevenson (NYBG); W. Richard McCombie (CSHL); Senior Personnel(s): Rob Martienssen (CSHL); Dennis Shasha (NYU). Project description: This project involves the construction and analysis of a phylogenomic view of the seed plants. In the previous cycle of funding, we generated BigPlant v1.0 a phylogenomic tree constructed from a matrix of 22,121 orthologs from 150 seed plant species (<http://nypg.bio.nyu.edu/bp/>). The main goal of our current funding cycle is to generate deep-transcriptomes to fill key gaps in taxa and genomic coverage in the seed plant phylogenetic tree, and to develop bioinformatic and phylogenomic resources that will enable a better understanding of the evolutionary history of plants. Overview of Aims 1-4: Aim 1: Select 35 species for transcriptome analysis of leaf, ovule and seed RNA (RNASeq) to fill in gaps in depth/breadth of taxa/ortholog coverage in BigPlant phylogenomic tree

and to provide expression data. Aim 2: Generate deep-transcriptome data used for unigene assembly, ortholog identification and expression data. Aim 3: Automate recurrent growth of our current phylogenomic matrix and integrate trait and expression data as characters. Develop phylogenomic and machine learning methods to make functional predictions for genes associated with clades and/or traits of economic interest. Aim 4: Perform functional validation of trait-to-gene predictions for seed traits in model (*Arabidopsis*) and crop (maize) species. Project website: <http://nypg.bio.nyu.edu/-main/>. Please send resume and 3 letters of reference to:

Dr. Gloria Coruzzi (gc2@nyu.edu) New York University Biology

Center for Genomics and Systems Biology

12 Waverly Place, 8th Floor

New York, NY 10003

acibrian@amnh.org

PennsylvaniaStateU HumanCranioEvolution

Post doctoral positions at The Pennsylvania State University

Department of Anthropology

Post-doctoral opportunities:

The complex genomic architecture of biological traits and their evolution, with application to craniofacial development and evolution

The Penn State Department of Anthropology involves a widely recognized research program in developmental and evolutionary genetics. We collaborate with local bioinformatics, computational biology, genomics, and neuroscience centers. We are searching for post-doctoral research scientists in three areas. The positions will integrate biological insight and analysis involving existing software and programming of new applications (Linux & MacOS):

1. Evolutionary simulation and analysis of complex genetic architecture. This project involves the use of a forward evolutionary simulation package (ForSim) that we have developed to simulate the genomic architecture and evolution of complex traits such as neurologic disease and the morphogenesis of craniometric traits. How

well can this architecture be inferred by current methods such as whole-genome sequence or marker-based GWAS or family data? Are there better criteria than statistical significance for understanding complex genomic causation? Script writing is essential, C++ programming desirable.

2. Simulation of quantitative developmental morphogenesis. We are developing morphometric simulations of the intercellular signaling interaction interactions among tissues in craniofacial development and its evolution. The goal is to generate ‘movies’ of simulated tissue interactions and their resulting overall shape, that can be compared to morphometric data from high-resolution MRI and CT imaging of normal and transgenic mouse models generated in our laboratories. This position involves programming (current modeling is in C++).

3. Bioinformatics/Genomic data analysis and modeling. We are doing genomewide mapping on normal craniofacial variation in mouse and baboon models. This project involves the dissection of implicated genome regions by integrating results from different species and other sources of externally derived information such as regulatory networks and genomic sequence conservation. We relate these results to our other work in neurologic and craniofacial dysgenesis (Down syndrome, craniosynostosis). Ability to use genome database and other bioinformatics resources is required.

These integrated research projects have existing NSF and NIH funding. We will be filling 1-year appointments, that can be extended to 2 or more years. Salary will be NIH/NSF post-doctoral levels based on experience, and starting date can be any time. Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce and our group is already an appealing and successful mixture of different but collaborative people of various genders and cultural backgrounds. Contact Ken Weiss (kenweiss@psu.edu) or Joan Richtsmeier (jta10@psu.edu) for information, or to apply submit CV and names of 3 potential persons we could contact as references.

Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

Faye L. Maring Administrative Support Coordinator
Department of Anthropology College of the Liberal Arts
The Pennsylvania State University 414 Carpenter Building
University Park, PA16802814-867-0006
(phone)814-863-1474 (fax)www.anthro.psu.edu “Faye L. Maring” <fmaring@la.psu.edu>

RutgersU ComputationalEvolutionaryGenomics

Postdoctoral positions in Computational Genomics at Rutgers University

Seeking qualified applicants for two post-doctoral positions with Andrew Kern in the Department of Genetics and the Human Genetics Institute of New Jersey at Rutgers University. There is no particular project associated with either of these positions, however recent work in the lab spans the intersection of machine learning, population genetics, comparative genomics, and evolutionary biology. Our lab is part of a newly formed Genome Variation and Evolution group within the department of Genetics that includes the labs of Jody Hey and Kevin Chen. More information about the department can be found here (<http://genetics.rutgers.edu/>). More information about the Kern lab can be found here (<http://northstar-www.dartmouth.edu/~adk/>)

The ideal candidate would hold a Ph.D. and have a record of research achievement in computational biology, population biology, computer science, statistics, or any quantitative field. A background in comparative/population/evolutionary genomics is highly desirable. In addition the candidate should have experience programming in C, a scripting language (Ruby, Python, or Perl is fine), and be comfortable with cluster computing environments.

Review of applications will begin immediately and continue until positions are filled. Interested candidates should submit an electronic version of their CV along with a cover letter describing their qualifications and relevant experience to andrew.d.kern@dartmouth.edu

SaudiArabia Dinoflagellate MolecularDiversity

Dear evoldir members,

a 2-year postdoc position is available in my lab. See below regarding further infos.

Many thanks, Chris

– Christian R. Woolstra Assistant Professor of Marine Science Coral Reef Ecological Genomics, Red Sea Research Center King Abdullah University of Science and Technology (KAUST) 23955-6900 Thuwal, Kingdom of Saudi Arabia Phone: +966 5 44 7000 87 E-mail: christian.woolstra@kaust.edu.sa Web: <http://faculty.kaust.edu.sa/sites/christianwoolstra/Pages/home.aspx> Description: A 2-year postdoc position in Christian Woolstra's lab (<http://faculty.kaust.edu.sa/sites/christianwoolstra/Pages/home.aspx>) is available as part of an ongoing project to look at the molecular diversity of Symbiodinium around the Arabian Peninsula. The project is an international collaboration and will involve phylogenomics, field trips, and stays in research labs in the UK and US.

The ideal candidate is expected to be an independent and motivated individual with excellent communication skills and a background in any of the following disciplines: Coral Reef Ecology, Coral Reef Genomics, Symbiodinium, Phylogenetics, Phylogenomics, Marine Biology, Bioinformatics. Familiarity with scientific diving operations and PADI certification are an advantage.

The position is available from June 2011 on. King Abdullah University of Science and Technology (KAUST) is a dynamic new university campus and campus community in Saudi Arabia that opened in September 2009. The campus is located directly at the Red Sea, near Jeddah. Postdoc package includes competitive salary, health insurance, free housing.

To apply: Please send cover letter summarizing your qualifications and interests, a curriculum vitae, published papers, and the names and contact information for three references to christian.woolstra@kaust.edu.sa. Applicants are encouraged to send a brief research proposal outlining their particular interests in this field.

chris.woolstra@googlemail.com

TexasAMU MolPopGenetics

POSTDOCTORAL RESEARCH SCIENTIST
- MOLECULAR POPULATION GENETICS/ECOLOGY

Department of Wildlife and Fisheries Sciences Texas A&M University College Station, Texas 77843-2258

Responsibilities: Position responsibilities involve devel-

opment and assay of nuclear-encoded microsatellites and of mitochondrial DNA sequences for projects involving population genetics and molecular ecology of marine fishes. Primary responsibilities include data acquisition and analysis, and preparation of reports and publications.

Qualifications: Dissertation or postdoctoral work in molecular population genetics and/or molecular ecology is required, as is experience with microsatellite and/or mtDNA data acquisition and analysis. Experience with major software programs (e.g., ARLEQUIN, GENEPOP, MIGRATE, LDNE, etc.) also is required.

Salary: Salary range is from \$32,000 - \$38,000/year and will depend on experience. Benefits include health care and retirement. Position is for 12-24 months.

Closing date: Position will remain open until filled.

Contact: Send curriculum vitae, description of research experience, and names, addresses, phone numbers, and e-mail of three references to: Dr. John R. Gold, Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, Texas 77843-2258. Electronic submissions are acceptable: goldfish@tamu.edu. International applicants will be considered if they hold the correct visa(s). Texas A&M University is an Equal Opportunity/Affirmative Action/Equal Access Employer.

John Gold <goldfish@tamu.edu>

Trentino Italy Biodiversity

The Department of Biodiversity and Molecular Ecology of the Research and Innovation Centre (CRI), Fondazione Edmund Mach, Trentino, Italy, is currently seeking to recruit an enthusiastic and highly motivated Post-doctoral Researcher to join the new Biodiversity and Environment Group.

This Group focuses or will focus on epidemiological and evolutionary aspects of interactions between pathogen and parasite communities and their animal vectors and hosts, including their microbiomes; however, the researcher's own interests will also be considered. Experience and interest in one or more relevant fields (molecular ecology, genetic epidemiology, virology, metagenomics and/or functional biodiversity) with relevant knowledge of laboratory and bioinformatics training is required.

Because this is a fairly senior position, applicants should have an internationally recognized track record. We are interested in having an experienced post-doc join this group who is particularly capable of drafting scientific papers and grant proposals (hence, fluent written English is essential); however, the candidate will also be expected to perform laboratory genetic, genomic and data analyses, learn new techniques and optimize them in our laboratory, take oral presentation of results to national and international conferences/workshops, supervise of young researchers (MSc and PhD students, technician), and spend some time in the field on sample collection. The Group is currently involved in projects on arthropod vectors, rodent-borne disease, speciation and conservation genetics.

Currently, CRI comprises over 250 staff, coordinates international PhD programmes and operates research programs fully integrated with state-of-the-art genetics, genomics, metabolomics and GIS platform technologies. Almost 20% of researchers are now non-Italian.

The Fondazione is a non-profit organization, with private legal status. Employment conditions are in line with prevailing European standards, including benefits and a highly competitive salary scheme. All openings are effective immediately (although starting date is flexible) and will be for three years initially, with a possibility of extension and/or transformation into permanent positions for exceptional candidates.

Set among the Dolomites, Trento is a particularly attractive province of Italy, offering a wide range of cultural and outdoor activities for all ages (please see www.ap.trento.it).

All candidates, with at least 2 years of Postdoctoral experience, proven ability to publish and attract funding, are invited to follow the application instructions at the link: http://www.fmach.eu/sperimentazione.context2.jsp?ID_LINK=-3D4051&area=3D6. See also Nature Jobs 28 April 2011.

Please also feel free to contact Heidi Hauffe (heidi.hauffe@iasma.it) for more information.

Closing date for applications: 31 May 2011.

– Heidi C. Hauffe Department of Biodiversity and Molecular Ecology, Research and Innovation Centre, Fondazione Edmund Mach, Via E. Mach 1, 38010 S. Michele all'Adige (TN), Italy tel.: 0461-615558 cell.: 348-7263653 e-mail : heidi.hauffe@iasma.it

heidi.c.hauffe@gmail.com

Trentino Italy ConservationGenetics

The Department of Biodiversity and Molecular Ecology of the Research and Innovation Centre (CRI), Fondazione Edmund Mach, Trentino, Italy, is currently seeking to recruit an enthusiastic and highly motivated Post-doctoral Researcher to join the Conservation Genetics group. The group's research lines aim at giving insight into patterns of distribution of genetic diversity and structure in mountain ecosystems. The group has a fully equipped molecular biology lab with dedicated facilities for aDNA and degraded DNA. We're actually working in conservation genetics, phylogeography and landscape genetics studies of several species ranging from reptiles to amphibians, birds, fishes and mammals. The ideal candidate should be able to analyse both neutral and adaptive markers, with a particular emphasis on the correlation between genetic and environmental data; however, the researcher's own interests will also be considered. The Conservation Genetics group (<http://congen.fem-environment.eu/>) is a partner of the European consortium ConGRESS (<http://www.congressgenetics.eu/default.aspx>) with several international collaborations. Experience and interest in one or more relevant fields (conservation genetics, molecular ecology, population genetics, evolutionary genetics, spatial ecology) with relevant bioinformatics training knowledge and basic laboratory knowledge is required. Because this is a fairly senior position, applicants should have an internationally recognized track record. We are interested in having an experienced post-doc join this group who is particularly capable of drafting scientific papers and grant proposals (hence, fluent written English is essential); however, the candidate will also be expected to perform genetic, genomic and ecological data analyses, take oral presentation of results to national and international conferences/workshops, supervise of young researchers (MSc and PhD students, technician). Currently, CRI comprises over 250 staff, coordinates international PhD programmes and operates research programs fully integrated with state-of-the-art genetics, genomics, metabolomics and GIS platform technologies. Almost 20% of researchers are now non-Italian. The Fondazione is a non-profit organization, with private legal status. Employment conditions are in line with prevailing European standards, including benefits and a highly competitive salary scheme (e.g. 75 % tax reduc-

tion for people coming from abroad). All openings are effective immediately (although starting date is flexible) and will be for three years initially, with a possibility of extension and/or transformation into permanent positions for exceptional candidates. Set among the Dolomites, Trento is a particularly attractive province of Italy, offering a wide range of cultural and outdoor activities for all ages (please see www.ap.trento.it). All candidates, with at least 2 years of Postdoctoral experience, proven ability to publish and attract funding, are invited to follow the application instructions at the link: http://www.fmach.eu/-sperimentazione.context2.jsp?ID_LINK=4051&area=6. Ref. Code CONGEN. Application deadline is May, 31st, 2011. See also Nature Jobs 28 April 2011.

For any further information, please contact Cristiano Vernesi: [vernesi\[at\]cealp.it](mailto:vernesi[at]cealp.it) Cristiano Vernesi

Cristiano Vernesi Dept. of Biodiversity and Molecular Ecology Research and Innovation Centre, Fondazione Edmund Mach address: Centro di Ecologia Alpina - Viote del Monte Bondone 38040 Trento - Italy tel + 39 0461 939523 fax + 39 0461 948190 skype name: cvernesi
Cristiano Vernesi <vernesi@cealp.it>

Trentino Italy Promoter Evolution

The Department of Biodiversity and Molecular Ecology of the Research and Innovation Centre (CRI), Edmund Mach Foundation, Trentino, Italy, is currently seeking to recruit an enthusiastic, highly motivated, focused Post-doctoral Researcher to join the Ecogenomics Group.

The project aims at dissecting the evolution of gene regulation at different taxonomic levels in plants. In particular, computational approaches based on comparative genomics and Next-Gen-Seq will be used to determine the relevance of regulatory vs coding regions in adaptive trait evolution. In the Ecogenomics Group there is solid hands-on expertise with Next Generation Sequencing data production and analysis (in-house Roche-454 GS FLX sequencer, robotic liquid handling stations, pipelines for data analysis, etc.).

Preference will be given to candidates with > 2 years of post-doctoral experience in promoter evolution/comparative genomics (animal or plant systems), with strong computational/programming skills. Proficiency in programming (preferred scripting languages:

Perl, Python) and both Unix/Windows operating systems are required. Candidates should be familiar with the most common DNA sequencing and editing software and evolution/population genetics programs; hands-on experience with software for the analyses of regulatory regions and next generation sequencing data will be evaluated extremely favorably. Proven ability to publish and attract funding to investigate regulatory variation in plants, strong commitment to group activity, ability to supervise MSc/PhD students or technicians, fluent English are absolutely required. Lab expertise is appreciated, but not strictly required.

Employment conditions are in line with prevailing European standards, including benefits and a highly competitive salary scheme. All openings are effective immediately (although starting date is flexible). Appointment will be for three years initially, with a possibility of extension and/or transformation into permanent positions based on appointee's performance during this period.

Edmund Mach Foundation is a non-profit organization, with private legal status. Currently, the Research and Innovation Centre of the Foundation comprises over 250 staff, coordinates international PhD programmes and operates research programs fully integrated with state-of-the-art genetics, genomics, metabolomics and GIS platform technologies. Almost 20% of researchers are non-Italian.

Set among the Dolomites, Trento is a particularly attractive province of Italy, offering a wide range of cultural and outdoor activities for all ages (please see www.ap.trento.it).

All candidates, with at least 2 years of Postdoctoral experience, proven ability to publish and attract funding, are invited to follow the application instructions at Nature Jobs, 28 April 2011: <http://www.nature.com/naturejobs/science/jobs/-194605-Postdoctoral-Research-Scientist-Evolutionary-Biologist-Geneticist> Please feel free to contact Claudio Varotto ([claudio.varotto\[at\]iasma.it](mailto:claudio.varotto[at]iasma.it)) for more information.

Closing date for applications: 31 May 2011.

Claudio Varotto, PhD EcoGenomics Group Department of Biodiversity and Molecular Ecology, Research and Innovation Centre, Edmund Mach Foundation Via E. Mach, 1 38010 San Michele all'Adige (TN), Italy Tel: (+39) 0461 615 108 Fax: (+39) 0461 650 956 [claudio.varotto\[at\]iasma.it](mailto:claudio.varotto[at]iasma.it)

[claudio.varotto\[at\]gmail.com](mailto:claudio.varotto[at]gmail.com)

UAlabama EvolutionaryBiology

Postdoctoral Position in Evolutionary Biology

Dr. Leslie J. Rissler

Department of Biological Sciences, University of Alabama

A 1-year (possibly 2-year) postdoctoral position is available in the laboratory of Leslie Rissler at the University of Alabama. The successful candidate will work on projects involving biogeography, conservation genetics, and the landscape ecology of amphibians and reptiles. The candidate will also help the P.I. mentor graduate students, teach evolutionary biology or conservation biology classes, and manage an active lab working on diverse grant-supported projects. The candidate will have the opportunity to develop collaborative research project(s) that are linked to an ongoing NSF-funded project that examines the impact of the environment on neuroendocrine responses and genetic diversity across a latitudinal gradient in natural populations of the wood frog.

MINIMUM QUALIFICATIONS:

- A Ph.D. in biology or related field with a focus on evolution, population genetics, biogeography, ecology, conservation, behavior, and/or systematics.
- Previous research experience and a strong publication record.
- Field experience and familiarity with IACUC procedures.
- Strong interpersonal skills and the ability to work as part of a team.

ADDITIONAL PREFERRED QUALIFICATION:

- Experience with GIS and modeling using Maxent or similar algorithms.
- Molecular biology experience (microsatellites, SNPs, sequencing, etc. with associated skills in the analysis of these types of data).
- Desire to teach undergraduate classes in evolution and conservation biology.

APPLICATION DEADLINE: 1 June 2011 (or until filled). Start date 1 August 2011.

To Apply: Apply online at the UA staff job application site: <http://jobs.ua.edu/> The specific job is Requisition # 0804834. Applicants must have been awarded a Ph.D. degree by August 2011. Interested individuals should send a cover letter, a CV, a 2-page (maximum) statement of interest including research and teaching background and goals, and contact details for three in-

dividuals who could provide a confidential letter of recommendation.

Info on the University of Alabama can be found here: <http://www.ua.edu/> Rissler's lab information can be found here: <http://web.mac.com/ljrissler/lab/> Dr. Leslie J. Rissler Associate Professor Department of Biological Sciences Box 870345 MHB Hall University of Alabama Tuscaloosa, AL 35487

205-348-4052 (office) 205-348-4039 (lab)
 rissler@as.ua.edu <http://web.mac.com/ljrissler/lab/>
 rissler@as.ua.edu

UBC SpatialEvolutionaryGenomics

Post-doctoral position in evolutionary genomics University of British Columbia Vancouver, BC, Canada

A post-doctoral fellowship is available to develop and apply methods to measure local adaptation using genomic data. This position is part of AdapTree, a larger project on adaptation to climate change in lodgepole pine and white spruce, which will genotype and analyze thousands of SNPs from several thousand individuals of each species, spread over their full geographic ranges. We seek to further develop methods to correlate local adaptation at specific loci with environmental measurements associated with climate change, accounting for spatial autocorrelation in both allele frequencies and environmental values, and apply these approaches to data from the AdapTree project.

The project needs an individual with interests in evolutionary biology and strong skills in statistics and computer programming. The position starts Jan. 1, 2012, with funding for up to 2.5 years.

If you are interested in this position, please send a CV and the names and e-mail addresses of potential references, to Michael Whitlock, Department of Zoology, University of British Columbia, at whitlock@zoology.ubc.ca. The job is open to all nationalities. Please contact me if you have any questions about the position.

- Michael Whitlock whitlock@zoology.ubc.ca

Department of Zoology - University of British Columbia
 6270 University Blvd, Vancouver, BC V6T 1Z4
 CANADA phone: (604) 822-2069 FAX: (604) 822-2416
whitlock@zoology.ubc.ca

UCaliforniaSanFrancisco EvolutionCancer

The Maley Lab is looking for a postdoctoral fellow to start in the fall of 2011 or later. The ideal candidate would have training in evolutionary biology and statistics/bioinformatics. Projects will include analysis of high-throughput sequencing and SNP arrays to study the evolution of therapeutic resistance in AML and neoplastic progression in Barrett's esophagus. Send a cover letter, CV, and contact information for 3 references to carlo.maley [at] ucsf.edu.

Carlo C. Maley, Ph.D. Associate Professor Director,
Center for Evolution and Cancer Helen Diller Family
Comprehensive Cancer Center Department of Surgery
University of California, San Francisco 2340 Sutter St.
Box 1724 San Francisco, CA 94115

office:415-476-9239 cell: 415-294-1793

carlo.maley@ucsf.edu

Carlo.Maley@ucsfmedctr.org

UCambridge FloralEvolution

Postdoctoral Research Associate In Floral Morphology
And Development, University of Cambridge

Funding for this post is available for 19 months. Our interests lie in understanding how structural colour is generated by plants, with particular reference to floral iridescence.

We are seeking a researcher with strong skills in comparative morphology and molecular genetics, to investigate the morphological and ultrastructural features that underlie structural colour and the genetic mechanisms controlling its development.

The successful applicant will undertake a molecular genetic study of the development of cuticular striations on the petal epidermis, and will therefore require standard DNA and RNA manipulation skills. They will also identify other structures generating iridescence, requiring the use of a range of light and electron microscopy techniques.

The research is funded by the Leverhulme Trust and is a collaboration between Dr Beverley Glover (Department of Plant Sciences, Cambridge University), Dr Paula Rudall (Royal Botanic Gardens, Kew), Professor Richard Bateman (Royal Botanic Gardens, Kew) and Professor Ulli Steiner (Department of Physics, Cambridge University).

<http://www.plantsci.cam.ac.uk/jobs/pd08164.pdf>
"B.J. Glover" <bjpg26@cam.ac.uk>

UCLondon EvolutionaryBiology

Dear all,

The Department of Genetics, Evolution and Environment (GEE) at University College London invites applications for independent fellowships.

UCL's Division of Biosciences has launched an internally funded fellowship scheme (see https://www.ucl.ac.uk/biosciences/research-departments/-independent_fellows for details). This scheme provides funding to support outstanding young scientists while they prepare applications for externally funded fellowships. Expressions of interest for this scheme, including CV, cover letter and a short outline of the proposed project, should be sent to Max Reuter (m.reuter@ucl.ac.uk) before Monday May 23rd. The Department will then select candidates who will be invited to submit a full application to the Division of Biosciences (final deadline June 17th).

GEE also invites expression of interest for externally funded fellowship applications to be held at the department. A number of fellowship schemes for early career scientists are available from UK and European funding agencies (see list below for the most important schemes) and GEE is keen to support applications from outstanding young researchers. If you are interested in joining GEE on a fellowship, please contact us (email CV, cover letter and project outline to m.reuter@ucl.ac.uk) before the end of June. The department will assist selected candidates with developing their applications, with final submission deadlines for most schemes during the autumn.

For more information or informal enquiries, do not hesitate to get in touch.

Best regards, Max

Natural Environment Research Council: Postdoctoral

and Advanced Fellowships <http://www.nerc.ac.uk/funding/available/fellowships/> Biotechnology and Biological Sciences Research Council: David Phillips Fellowship <http://www.bbsrc.ac.uk/funding/fellowships/david-phillips.aspx> Medical Research Council: Career Development Awards, CDA in biostatistics, training fellowships in biomedical informatics <http://www.mrc.ac.uk/Fundingopportunities/Fellowships/index.htm> Royal Society: University Research, Dorothy Hodgkin and Newton International Fellowships <http://royalsociety.org/grants/schemes/> European Science Foundation: Starting Independent Researcher Grant <http://erc.europa.eu/index.cfm?fuseaction=3Dpage.display&topicID=3D65>
Max Reuter

Research Department of Genetics, Evolution and Environment Faculty of Life Sciences University College London

NEW ADDRESS Darwin Building Gower Street London WC1E 6BT, UK

Phone: +44-20-76792201 (internal 32201)

Lab: <http://www.homepages.ucl.ac.uk/~ucbtmre/Labsite/> Department: <http://www.ucl.ac.uk/gee>
m.reuter@ucl.ac.uk

UCopenhagen Bioinformatics genomics

Postdoctoral Fellowships in Bioinformatics of high-throughput DNA sequencing

Three two-year postdoctoral fellowships are available at the Bioinformatics Centre, Department of Biology, University of Copenhagen. The positions will be available to commence August 1st, 2011. The positions are in the group of Professor Anders Krogh. The group is working in computational analysis of post-transcriptional regulation (focus on small RNAs), ancient genomics, and metagenomics. Common to all projects is the analysis of high-throughput sequencing data, mostly from Illumina sequencers. We are doing both software development and analysis of experimental data. We are collaborating closely with local experimental groups for instance in miRNA research, and is deeply involved in ancient DNA research at the Centre for Geogenetics.

Qualifications: The postdocs will be expected to participate both in the development of computational tools and in the experimental collaborations and data anal-

ysis. As a postdoc you are expected to be able to work fairly independently and to be able to co-supervise Ph.D. and Master's students.

For consideration, applicants must: - Have a PhD in bioinformatics, statistics or a similar field - Have demonstrated experience in the analysis of Next Generation DNA Sequencing data - Be experienced with programming in perl, Python, or similar and be familiar with linux/unix - Have published in high-quality international peer-reviewed journals

Skills of additional interest include: - Experience in statistics (including R) and probabilistic models/machine learning - Experience with small RNAs, ancient DNA, gene expression analysis and/or metagenomics - Ability to program in C or C++

The working language is English, thus excellent English speaking, reading and writing skills are required.

Deadline is May 30th

For full details, see <http://people.binf.ku.dk/~krogh/tmp/postdoctoralFellowshipsApr2011.pdf> Best wishes,

- Anders

- Anders Krogh Professor krogh@binf.ku.dk - The Bioinformatics Centre Dept of Biology, University of Copenhagen Ole Maaloes Vej 5, 2200 Copenhagen, Denmark Ph. +45 3532 1329 Dept +45 3532 3710
www.binf.ku.dk krogh@binf.ku.dk

UExeter HostVirusCoevolution

Postdoctoral position: Mathematical modelling of host-virus coevolution, University of Exeter

We are recruiting a Research Fellow to participate in an exciting interdisciplinary collaboration between a mathematical modelling group of Dr Ivana Gudelj, University of Exeter, UK and an experimental evolution group of Dr Samantha Forde, University of California at Santa Cruz, US. The position is available from 1st September 2011 for the period of 3 years and will employ a combination of mathematical modelling and experimental microbial evolution to answer the following question: Why do some viruses evolve to be specialists while others are generalists?

The successful applicant will be working on the development and analysis of mathematical models in Dr Gudeljs lab at the University of Exeter, in close collaboration with experimental colleagues at the University

of California at Santa Cruz. Applicants will possess a PhD in a quantitative discipline (mathematics, physics, engineering or computer science) and ideally be familiar with ordinary differential equations, their use in modelling, analysis (Dynamical Systems techniques) and simulation. The successful candidate should be able to communicate effectively with individuals from a wide range of disciplines.

More information about the project and how to apply can be found at: <http://people.exeter.ac.uk/ig232/Positions.html> Closing date is 27th May 2011

“Gudelj, Ivana” <I.Gudelj@exeter.ac.uk>

UFlorida HumanEvolutionaryGenetics

Postdoctoral position in Human Molecular Genetics

A postdoctoral position (two years at least) is available in Connie Mulligan’s lab at the University of Florida.

Two NSF/NIH/UF-funded projects are currently ongoing and the successful candidate can work on one or both: 1) Examination of DNA methylation patterns in mothers and newborns from the Democratic Republic of Congo (DRC) to test whether epigenetic alterations mediate the effects of maternal exposure to stressors on fetal development and neonatal health. Specifically, we are testing if epigenetic modifications may mediate changes in gene expression in infants that result from maternal trauma and material deprivation associated with the war in the DRC. More broadly, we are interested in the idea that behavior and complex phenotypes may be shaped by early life experiences that alter gene expression through epigenetic alterations. 2) Investigation of the genetic and cultural underpinnings of complex diseases that exhibit racial inequalities, using hypertension in African-Americans as a model phenotype. We are combining the analysis of genome-wide SNPs, genetic ancestry estimates, and epigenetic variation with sociocultural data including experience of discrimination and social network analysis. By combining genetic and socio-cultural data, our goal is a more comprehensive investigation of complex disease and racial disparities than is possible with only one type of data. See related study - <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0006821>

Qualifications: A PhD and a strong background in

generation of genetic data (DNA sequencing, SNP detection, microarray analysis, etc.) and data analysis (gene association analysis, regression analysis, genetic ancestry estimation, etc) are essential. Experience generating methylation data or additional computational experience (e.g. computer programming, simulation analysis, etc) is a plus. In addition to the projects listed above, there are excellent opportunities for the successful candidate to develop new lines of research as well as productive collaborations outside the lab.

The University of Florida is a leading research institution with a university-wide commitment to genetics research. The Department of Anthropology (www.anthro.ufl.edu) has 30 full-time faculty with diverse interests and a very strong biological subfield, with emphases on molecular, paleo, and forensic anthropology. The department is one of the top rated programs in the country (6th among public institutions, 11th overall). The University of Florida Genetics Institute (www.ufgi.ufl.edu) is an inter-college entity with a new research building to enhance opportunities for collaboration. Gainesville is located in north central Florida (away from the hurricanes!), with average temperatures ranging from 45F to 90F. Beaches on the gulf and Atlantic coast are ~ 2 hours away.

To apply: via email, send a CV, a statement of research interests, and the names and contact information (including email and phone) for three references. Applications and inquiries should be addressed to Connie Mulligan at cmulligan@ufl.edu.

Review of materials will begin June 1 and will continue until the position is filled. Start date is flexible and can start as early as Summer, 2011. Salary is commensurate with experience. Position may be extended for a total of three years. Informal inquiries prior to submitting a formal application are welcome. AA/EOE.

Connie J. Mulligan, PhD Professor, Department of Anthropology Associate Director, UF Genetics Institute 2033 Mowry Rd, PO Box 103610 University of Florida Gainesville, FL 32610-3610 Office: 409 Genetics Institute Telephone: 352-273-8092 Fax: 352-273-8284 Email: cmulligan@ufl.edu Website: <http://www.clas.ufl.edu/users/mulligan/Webpage/index.html> “Connie J. Mulligan” <cmulligan@ufl.edu>

ULausanne SocialEvolution

1 postdoctoral position: Evolutionary transi-

tion/cultural transmission/social evolution

A postdoctoral position for 1 to 3 years is available, for theoretical research at the Department of Ecology and Evolution of the University of Lausanne. It is funded by a project of the Swiss National Science Foundation aiming at investigating the role of cultural transmission (non-genetically transmitted actions and technologies) in the evolutionary transition from small-scale egalitarian groups to larger-scale stratified groups.

The project, which is at the interface of biology, anthropology, and economics, aims at studying the following type of questions. How did large-scale stratified human societies emergence from small-scale egalitarian societies? Did it happen through an increase in the technologies of production and exchange (e.g. invention of agriculture and trading) or in the technology of appropriation (intensification of warfare)? What are the selective pressures that could lead to within group stratification? Did trading co-evolve with the specialization of cultural trait accumulation within and between groups? Other topics of theoretical research on the evolution of social behaviors are also possible if they fit the research interests of our group:

http://www.unil.ch/dee/page84917_fr.html Applicants should have a Ph.D. in a relevant area (e.g. evolutionary biology, economics, anthropology, or mathematics), with strong mathematical and computing skills, and a vivid interest in fundamental research.

The Department of Ecology and Evolution is a well-funded and vibrant research institution, with excellent facilities:

<http://www.unil.ch/dee/> Inquiries and applications should be sent to: laurent.lehmann@unil.ch. Applications should be sent by June 10th, and should include a CV, a one-page statement of research interests, and names of 2-3 referees. Only applications with all these information will be considered.

Laurent Lehmann <laurent.lehmann@unil.ch>

UManitoba MicrobialBioinformatics

PDF or Research Associate in Bioinformatics Microbial Genomics for Biofuels and Co-products from Biorefineries Department of Plant Science, University of Manitoba Start date: 11 July, 2011 Closing date for applications: 20 June 2011, or until position is filled

Project Description: One position is available to conduct cutting-edge research employing the tools of bioinformatics in a multidisciplinary team including microbiologists, molecular biologists and biosystems engineers. This is an outstanding opportunity to contribute to research whose aim is to develop a sustainable energy source from cellulosic wastes. This collaborative project seeks to characterize both known and newly discovered cellulose-degrading microbes and their genomes, leading to metabolic engineering, and to the development of designer microbial consortia, to enhance synthesis of fuels and bioproducts. A range of organisms, approaches and biofuels will be investigated. A project summary can be viewed at <http://www.microbialrefinery.com>. This project is co-funded by Genome Canada and the Manitoba Ministry of Science, Technology Energy and Mines (STEM).

The successful applicant will join a team of bioinformaticists and information technologists who are mining and managing data from this project. This team carries out work in the following areas: de-novo annotation of newly-sequenced microbial genomes; development of high-throughput analytical pipelines; database design; software design; comparative genomics of cellulose degrading microorganisms; analysis and mining of microarray data; data mining and in-silico metabolic engineering. This project affords many opportunities for original contributions in both basic and applied research in bioinformatics, as they relate to the project.

Qualifications: Qualified applicants must: possess a Ph.D. in Microbiology or Bioinformatics from a recognized University; have knowledge of microbiology and biochemistry with strengths in data mining and programming; have extensive experience in object-oriented programming in Java or Python on a Unix platform; have a demonstrated record of independent as well as collaborative research and scholarly publications; and excellent oral and written communication skills.

The University and Community: The University of Manitoba is located in Winnipeg, the largest city in the province of Manitoba. The city has a rich cultural environment including symphony, opera, dance, theatre, sports, and ethnic festivals. The region provides ample opportunities for outdoor recreation in all seasons. Learn more about Winnipeg at <http://www.winnipeg.ca>.

Applications: Applications are invited at the level of Post Doctoral researcher or Research Associate. Funding for the project is available through September 30, 2013. The University of Manitoba exercises a Canadian-first policy; however, all those qualified are

encouraged to apply. The review of applications will continue until the position is filled. Application materials, including letters of reference, will be handled in accordance with the protection of privacy provisions of the Freedom of Information and Protection of Privacy Act (Manitoba). Please note that your curriculum vitae will be provided to participating members of the search process. Applications, including curriculum vitae, short statement of research interests and the names and addresses (including phone, fax and e-mail addresses) of three referees should be sent to:

Dr. Brian Fristensky Associate Professor Department of Plant Science University of Manitoba Winnipeg, MB CANADA R3T 2N2 Phone: 204-474-6085 FAX: 204-474-7528 Email:frist@cc.umanitoba.ca <http://home.cc.umanitoba.ca/~frist> Brian Fristensky <frist@cc.umanitoba.ca>

UMontreal PlantBioinformatics

Postdocs>UMontreal.PlantTranscriptomics

A postdoctoral position is available to study plant transcriptomics via deep RNA sequencing in a phytoremediation context. The objective of the project is to find candidate genes potentially involved in the degradation or accumulation of organic and inorganic pollutants. Our model plants are willows (*Salix* sp.) that have high phytoremediation potential because of their rapid growth, their high biomass production, and their ability to grow in highly contaminated soils. Experiments will take place in the greenhouse as well as in the field.

This position is part of a large genomic project that aims at increasing our understanding of phytoremediation. It is a highly multidisciplinary project that studies simultaneously soil chemistry, soil microorganisms, fungi, and plants. The work will be performed at the University of Montreal Biodiversity Centre (www.biodiversite.umontreal.ca/), which is part of the Plant Research Institute (www.irbv.umontreal.ca).

The successful candidate will be involved in the collection and processing of RNA samples. He will also be responsible for managing important amounts of deep RNA sequencing data, developing analytical tools and pipelines, and analyzing and interpreting the results. The successful candidate will also be involved in the redaction of research reports and scientific papers.

MINIMUM QUALIFICATIONS Ph.D. in tran-

scriptomics, bioinformatics, or other relevant field. Proven research experience and a strong publication record. Solid analytical, computing, and statistical skills. Candidates should be comfortable working in a UNIX environment, have a strong programming background, and be proficient in working with large datasets.

PREFERRED QUALIFICATIONS Strong abilities for team work Experience with biological experimental designs such as randomized block designs Candidates with a background in interdisciplinary research, spanning both biological sciences and applied mathematics/computer science, are especially encouraged to apply. Candidates will ideally be conversant in a compiled programming language (e.g., C or C++), a scripting language (e.g., Perl), and a statistical environment (e.g., R).

APPLICATION DEADLINE: 1st August 2011

Funding is available for three years. The position will remain open until filled. To apply formally, submit the following documents in PDF format: 1. A brief statement of research interests, qualifications and experience and why you feel you are a good candidate for this position. 2. Curriculum vitae, including a list of scientific publications. 3. The names and contact details of at least two references willing to provide a confidential letter of recommendation upon request.

CONTACT Enquiries may be sent to: Simon Joly, Ph.D. Email: simon.joly@umontreal.ca

Simon Joly <simon.joly@umontreal.ca>

UOregon Phylogenetics

Postdoctoral Research Associate Center for Ecology and Evolutionary Biology Posting: 11121 Location: Eugene Closes: Open Until Filled

Postdoctoral Position in Phylogenetic Ecology and Computational Genomics

Jessica Green (<http://biology.uoregon.edu/~people/green/>) and Brendan Bohannon (http://biology.uoregon.edu/ceeb/faculty_pages/Bohannon/)

are currently seeking a postdoctoral researcher to collaborate on projects combining approaches from phylogenetic ecology and computational genomics to explore fundamental questions in microbial ecology and evolution. Applicants should have a PhD with

extensive training in ecology and/or evolution, experience applying genome-based bioinformatics (e.g. comparative genomics, analysis of protein families, multiple sequence alignment, phylogenetic analyses) to understand the ecology and/or evolution of complex biological communities, and strong writing skills. The successful candidate will play a key role in the Biology and Built Environment (BioBE) Center (<http://biology.uoregon.edu/biobe/>). The BioBE Center is training a new generation of innovators and practitioners at the architecture-biology interface to understand the built environment microbiome - the diversity of indoor microbial life, their genetic elements and their interactions. The vision of this national research center, funded by the Alfred P. Sloan Foundation, is to integrate recent advances in microbial genomics and biological theory to develop hypothesis-driven, evidence-based approaches to sustainable building design.

The position is available for 1 year with the possibility for renewal depending on performance. The start date is flexible. Applications will be considered starting on May 31, 2011. Please email questions regarding the position to Jessica Green (jlgreen@uoregon.edu).

To apply

A complete application will consist of the following materials:

- (1) a brief cover letter explaining your background and career interests
- (2) CV (including publications),
- (3) names and contact information for three references.

Submit materials to ceebjobs@uoregon.edu, Subject: Posting 11121

To be assured full consideration, applications must be received by May 31, 2011 but position will remain open until filled.

Women and minorities encouraged to apply. We invite applications from qualified candidates who share our commitment to diversity. EO/AA/ADA institution committed to cultural diversity.

ceebjobs@uoregon.edu

UOslo Thermotogales Comparative Genomics

Postdoctoral Research Fellow in Comparative and Evolutionary genomics of Thermotogales bacteria

A three-year position as Postdoctoral Research Fellow is available in Comparative and Evolutionary genomics of Thermotogales bacteria in the laboratory of Camilla Nesb  at CEES at University of Oslo and Department of Biology, University of Alberta. The CEES is a centre of excellence for integrative biological research and is well-funded. It provides a stimulating research environment, situated at the Department of Biology, 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 Professor Nils Chr. Stenseth and currently employs 19 faculty members, 45 postdocs/researchers, 32 PhD students and 30 MSc students. Information about the centre can be found at: <http://www.cees.uio.no>. The candidate will be part of a project funded by The Norwegian Research Council. The successful candidate will perform research in the area of genomics and metagenomics, focusing on Thermotogales bacteria. The postdoctoral research fellow will be employed by the University of Oslo, but will spend time both at University of Oslo and University of Alberta. The successful candidate will work on a project - Biogeographic and population analyses of Thermotogales from hydrocarbon environments - funded by the Norwegian Research Council, and will also be involved in collaborative projects with Julia Foght at University of Alberta and with Nils Chr. Stenseth at University of Oslo.

Requirements: Ph.D. in bioinformatics, microbiology, biology or a related field; with strong background in molecular evolution or environmental microbiology; and evidence of successful teamwork abilities are required. Experience working with Thermotogales bacteria and/or their genomes, next-generation sequence data, Unix operating system, anaerobe microbiology, petroleum microbiology, are desirable. A good command of English is required. http://www.matnat.uio.no/english/research-education/proficiency_in_English.html The main purpose of post-doctoral research fellowships is to qualify researchers for work in top academic positions within their disciplines. No one can be appointed for more than one period at the same institution. Please also refer to the regulations pertaining to the conditions of employment for post-doctoral fellowship positions: <http://www.uio.no/admhb/reglhb/personal/-tilsettingvitenskapelig/regulationstermcondition.xml>
Salary:

Postdoctoral Research Fellow (SKO, 1352), pay grade:

57 - 64 (NOK 455 900 - 518 900 depending on qualifications and seniority).

The application must include an Application letter including a statement of interest, summarizing the applicant's scientific work and interests and describing how she/he fits the description of the person we seek an CV (summarizing education, positions, pedagogical experience, administrative experience and other qualifying activity), including a list of published and unpublished works an Copies of educational certificates, transcript of records, letters of recommendation an A complete list of publications and up to 5 academic work that applicant wishes to be considered by the evaluation committee an Names and contact details of 2-3 referees (name, relation to candidate, e-mail and telephone number).

Foreign applicants are advised to attach an explanation of their University's grading system. Please remember that all documents should be in English or a Scandinavian language.

Closing date for applications: 02.06.2011

To send application: <http://uio.easycruit.com/-vacancy/555458/64421?iso=no> Review of applications will begin June 1, 2011 and continue until the position is filled The University of Oslo has an agreement for all employees, aiming to secure rights to research results a.o. The University of Oslo has a goal of recruiting more women in academic positions. Women are encouraged to apply. In accordance with the University of Oslo's equal opportunities policy, we invite applications from all interested individuals regardless of gender or ethnicity.

Olaf Kristian Sund <o.k.sund@mn.uio.no>

UPennsylvania SociogenomicsEvolutionaryGenetics

Postdoctoral position in evolutionary genetics and sociogenomics

The Linksvayer lab in the Department of Biology at the University of Pennsylvania seeks a postdoctoral researcher. The lab studies the evolution and genetic basis of complex social systems using social insects as a study system. The postdoc will use a variety of approaches, including RNA sequencing, genomics, and quantitative genetics.

The ideal candidate will have a strong background in

molecular biology, genomics, transcriptomics, and/or bioinformatics along with an interest in social evolution.

Applications will be accepted until the position is filled and the start date is flexible.

To apply, send the following to tlinks@sas.upenn.edu: your CV, contact information for three references, up to three representative publications, and a brief cover letter explaining your research interests and experience. Please contact me (tlinks@sas.upenn.edu) with any questions.

Timothy Linksvayer Assistant Professor Department of Biology University of Pennsylvania 225 Leidy Laboratories 433 South University Avenue Philadelphia PA 19104-6018 tlinks@sas.upenn.edu V +1 215 573 2657 F +1 215 898 8780 <http://www.bio.upenn.edu/faculty/-linksvayer/> tlinksvayer@gmail.com

UppsalaU ComputationalGenetics

Post-doc position available: Development of methods, algorithms and tools for understanding complex trait genetics

We are looking for a Post-doc to join our young and growing group. We provide a supportive environment and strongly believe in an interdisciplinary approach, so we encourage applicants with a non-standard background to apply. We are based in Uppsala, Sweden at the Swedish University of Agricultural Sciences and also have links with Uppsala University.

Our group use a Computational Genetic approach to understand the mechanisms by which heritable genetic variation regulate phenotypic expression in individuals and populations. As input we use empirical data from experimental or natural populations that have been characterized phenotypically and genetically (e.g. genome resequencing and high-density genotyping). The focus of this post will be to develop methods, algorithms, tools and software for using modern genetics data to understand complex trait genetic inheritance. For this work you will need a strong background in informatics (one or several of the disciplines mathematics, statistics, computer science, programming or bioinformatics) as well as a thorough theoretical background in genetics.

Aside from work, you will have the chance to get to know Uppsala, which is a pretty university town, no-

table for its castle and cathedral. It is 40 minutes by train from Stockholm. We get some snow in winter and beautiful long summer days.

Qualifications A successful applicant should have relevant scientific education, have programming experience, be highly motivated for research and have an interest in molecular, quantitative and computational genetics. A strong mathematical/statistical background is advantageous.

Forms for funding or employment Employment as Post-doctoral researcher student for 1 year with possibility of extension 1+2 years.

If you have questions about us or our work, please contact Örjan Carlborg (Orjan.Carlborg@slu.se) or Ronnie Nelson (Ronnie.Nelson@slu.se). You can also find more information about our group at <http://www.computationalgenetics.se> We are looking forward to hearing from you!

Selected recent publications:

Carlborg, Ö. and Haley, C. Epistasis: too often neglected in complex traits studies? *Nature Reviews Genetics* 2004 5:618-625.

Carlborg, Ö., Jacobsson, L., Åhgren, P., Siegel, P., Andersson, L. Epistasis and the release of genetic variation during long-term selection. *Nature Genetics* 2006 38:418-20.

Le Rouzic, A., Siegel, P. and Carlborg, Ö. Phenotypic Evolution from Genetic Polymorphisms in Radial Network Architectures. *BMC Biology* 2007, 5:50.

Alvarez-Castro, J., le Rouzic, A. and Carlborg, Ö. How to perform meaningful estimates of genetic effects. *PLOS Genetics* 2008 May 2; 4(5):e1000062 Le Rouzic, A., Alvarez-Castro, J. and Carlborg, Ö. Dissection of the genetic architecture of body weight in chicken reveals the impact of epistasis on domestication traits. *Genetics* 2008 179:1591-1599.

Rubin CJ, Zody MC, Eriksson J, Meadows JR, Sherwood E, Webster MT, Jiang L, Ingman M, Sharpe T, Ka S, Hallböök F, Besnier F, Carlborg Ö, Bedhom B, Tixier-Boichard M, Jensen P, Siegel P, Lindblad-Toh K, Andersson L. Whole genome resequencing reveals loci under selection during chicken domestication. *Nature*. 2010 Mar 25;464(7288):587-91. Epub 2010 Mar 10.

Johansson AM, Pettersson ME, Siegel PB, Carlborg Ö (2010) Genome-Wide Effects of Long-Term Divergent Selection. *PLoS Genet* 6(11): e1001188. doi:10.1371/journal.pgen.1001188

Orjan.Carlborg@slu.se

UPretoria ForestGenomics

BACKGROUND The Forest Molecular Genetics (FMG) Programme is an industry (Sappi and Mondi), government (THRIP, NRF and DST) supported research programme in the Department of Genetics and Forestry and Agricultural Biotechnology Institute (FABI) at the University of Pretoria. It focuses on the genomics, molecular genetics and biotechnology of wood and fibre development in eucalypt tree species. This year, 2011, marks the completion of the Eucalyptus grandis Genome Project (www.eucagen.org), in which we are playing a leading role. The completed genome sequence is providing exciting opportunities for genomics, molecular genetics and biotechnology research in the most widely planted and commercially important hardwood fibre crop in the world.

Project Description: Transcriptome-wide and genome-wide resequencing of Eucalyptus tree species for SNP marker discovery, association genetics and marker-assisted breeding. The project will contribute to two large association genetics studies in Eucalyptus grandis and E. dunni populations, as well as provide support for an international initiative to develop a SNP genotyping platform for commercially important Eucalyptus species.

Requirements: Expertise in DNA sequence analysis, familiarity with Unix and some scripting languages. **Recommended:** Post-graduate training in Bioinformatics, and/or undergraduate and postgraduate training in molecular, population and quantitative genetics. Expertise in next-generation DNA sequence analysis is also highly recommended.

The FMG Programme offers competitive bursaries, as well as industry-funded bursary additions. We also strive to create opportunities for students to work for several weeks to months at a time in the laboratories of our international collaborators in the USA, Canada, Belgium and Australia. Interested persons are encouraged to contact the Project Manager, Mr Eshchar Mizrachi (eshchar.mizrachi@up.ac.za). Deadline for applications: 5 July 2011. Interviews will be scheduled on an ad hoc basis.

Thank you.

Kind regards Marja O'Neill

Research Administrator Forest and Molecular Genetics

Research Group Department of Genetics University of Pretoria Pretoria South Africa

Marja O'Neill <Marja.O'Neill@up.ac.za>

USheffield PlantGrowthDiversity

For anyone who is in the market for a postdoc and missed this one - the deadline for applications is coming up in a couple of days' time.

University of Sheffield, Department of Animal and Plant Sciences Postdoc

We seek a highly motivated and dynamic individual for a project investigating the diversity of growth traits among plant species. Its particular focus will be on the roles of C3 and C4 photosynthetic pathways, ecological adaptation, and evolutionary history in the grasses. The post-holder will carry out large-scale comparative experiments, sampling hundreds of species under a range of controlled environment conditions. Methodological development will be required to streamline high-throughput approaches to measuring growth, and to apply phylogenetic comparative approaches to growth analysis. The use of large species samples will allow us, for the first time, to unravel the interacting roles of multiple factors within a unified framework. This approach has been opened up through significant recent conceptual and methodological advances in a number of areas, and represents a major step in the fusion of the fields of ecological and evolutionary informatics.

The project will capitalize upon state-of-the-art plant growth and laboratory facilities, and newly available ecological informatics resources developed at the University of Sheffield. The successful candidate will work in a team with Colin Osborne, Mark Rees, Rob Freckleton and Ken Thompson.

The Department of Animal and Plant Sciences is one of the largest departments in the UK devoted to the study of whole organism biology, with over 45 academic staff, 50 support staff and 130 postgraduate and postdoctoral researchers. We are ranked joint 3rd in the UK for biology research and 70% of our research activity has been judged to be 'world-leading' or 'internationally excellent' (RAE 2008). We have a strong ethos of research-led teaching and a high standard of student recruitment. We enrol over 150 undergraduate students per year on to 8 degree programmes and are

ranked 4th in the UK for biological sciences teaching (The Complete University Guide, 2010).

The post is funded by NERC, and is fixed-term with a start date of 1 June 2011. We have funding for up to three years' work.

For informal enquiries contact Colin Osborne (c.p.osborne@sheffield.ac.uk).

Formal applications should be made by Friday 6th May via <http://www.sheffield.ac.uk/jobs>, quoting the reference UOS002525.

Colin Osborne Dept. Animal and Plant Sciences University of Sheffield

tel: +44-114-222-0146 lab pages: <http://web.me.com/-colin.osborne/lab/home.html> ecological informatics: www.grassportal.org c.p.osborne@sheffield.ac.uk

UToronto AirwayMicrobeEvolution

A postdoctoral/research associate position is available immediately to investigate the airway microbiome in cystic fibrosis. This research will be conducted as part of a collaborative, multidisciplinary team funded by the Canadian Institutes of Health Research and the National Sanitarium Association, and involves both culture-independent and culture-based approaches to characterizing the microbiome and its impact in adult and pediatric patients with cystic fibrosis. The successful applicant will be based at the Toronto General Hospital Research Institute of the University Health Network (UHN), a fully affiliated teaching hospital of the University of Toronto, with opportunities to collaborate with team members at other hospitals and at the University of Toronto.

Qualifications/Requirements:

Ph.D. or equivalent degree in microbiology or a related field, with strong proficiency in microbiological and molecular biologic techniques.

Experience in microbiome/metagenomic research, bioinformatics, or epidemiology is desirable.

Self-motivated, with strong organizational skills and ability to work independently.

Excellent interpersonal, analytical and communication skills (both written and verbal).

To apply, please send your curriculum vitae and 3 references to Dr. David Hwang (David.Hwang@uhn.on.ca),

Department of Pathology, Toronto General Hospital, 11th floor, 200 Elizabeth Street, Toronto, ON, Canada M5G 2C4.

David Guttman <david.guttman@utoronto.ca> David Guttman <david.guttman@utoronto.ca>

UZurich SeahorseGenomics

Postdoctoral position available in Comparative Functional Genomics in the Institute of Evolutionary Biology and Environmental Studies at the University of Zurich in Switzerland

The research group in Evolutionary Biology and Biodiversity led by Professor Tony Wilson in the Institute of Evolutionary Biology and Environmental Studies at the University of Zurich (<http://www.ieu.uzh.ch/-agwilson/>) is seeking a postdoctoral research associate for a position in comparative functional genomics. This position is funded for 1-2 years, beginning in July 2011, with a yearly salary of ca. 84,000 Swiss Francs (\$95,000US).

The postdoctoral associate will work on a project which is using next-generation sequencing and microarray 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 evolution of reproductive complexity in a comparative evolutionary framework.

The candidate will use a customized Agilent microarray recently developed for the seahorse 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 spatial and temporal changes in gene expression have contributed to the development of the morphological, physiological and hormonal traits that characterize the most complex forms of male pregnancy in this group. Microarray screening will be complemented by RT-PCR and in situ gene expression anal-

yses to elucidate the location and mode of action of key transcripts.

The ideal candidate will have experience in functional genomics methodologies and familiarity with gene expression analyses 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@ieu.uzh.ch) before June 15.

Tony Wilson Assistant Professor, Evolution and Biodiversity Institute of Evolutionary Biology and Environmental Studies Room Y44J55 Winterthurerstrasse 190 CH 8057 Zurich Switzerland Tel: 41 44 635 4790 Fax: 41 44 635 4780 <http://www.ieu.uzh.ch/agwilson> tony.wilson@ieu.uzh.ch

WestVirginiaU MicrobialComparativeGenomics

A postdoctoral position is available immediately in Dr. Olga Zhaxybayeva's lab in the Biology Department of West Virginia University in Morgantown, WV. The successful candidate will perform research in the area of computational genomics, focusing on deciphering processes governing microbial evolution through the analysis of patterns in genomic and metagenomic data sets. More information about the laboratory is available at <http://ecg.bio.wvu.edu>. Ph.D. in bioinformatics, biology, microbiology, computer science, statistics or a related field - with background and strong interest in molecular evolution - is required. Programming and scripting expertise, evidence of successful team-work abilities, experience working with next-generation sequence data and knowledge of Unix operating system are desirable.

The successful applicant will be expected to contribute to a variety of ongoing collaborative research projects with teams across the United States and Canada, as well as establish his/her own independent projects, and will be provided with training opportunities of grant writing and student supervision.

Review of applications will continue until the position is filled. The initial appointment is for one year with the possibility of renewal for up to two additional years contingent upon performance and funding. Salary will be offered commensurate with experience and skills. Com-

petitive benefits package is included.

Interested applicants should send a single PDF file containing CV, one-page statement of research interests and contact information of three references to ECGLab-Jobs@gmail.com.

West Virginia University is an Affirmative Action/Equal Opportunity Employer and the recipient of an NSF ADVANCE award for gender equity.

– Olga Zhaxybayeva, Ph.D. Assistant Professor Department of Biology West Virginia University PO Box 6057 Morgantown, WV 26506 USA

Office: (304) 293-5201 ext. 31531 Lab: (304) 293-5201 ext. 31331 Fax: (304) 293-6363 Email: olgagh@mail.wvu.edu Web: <http://ecg.bio.wvu.edu/> olgagh@mail.wvu.edu

WorkshopsCourses

Barcelona StatisticalGenetics Aug22-26	82	Messina MicrobialEvolution Jun7-10	90
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Barcelona StatisticalGenetics Aug22-26

Would you please post the following short course announcement? - Janet Sinsheimer

STATISTICAL GENETICS SHORT COURSE 22-26
August 2011

Barcelona, Spain Hosted by Centre Nacional d'Anàlisi Genòmica (CNAG)

<http://www.genetics.ucla.edu/courses/statgene> email: statgene@mednet.ucla.edu

We are offering a five full-day intensive workshop on

state-of-the-art statistical methods for detection of genetic loci for complex traits.

Each day will include hands-on computer exercises using statistical genetics computer programs, especially the Mendel software package, with its new graphical front-end.

We will cover the general theory behind the methods as well as emphasize the practical aspects needed to give the best chances of success. The Course is designed to assist people who will be performing statistical analyses to discover the genetic basis of complex traits. The methods covered are appropriate to both human and non-human populations. Topics will include:

* Statistical Reviews * Genetic Study Design * Quality Control and other data issues * Haplotyping * Analysis of Qualitative and Quantitative Traits including: -

Parametric and Non-Parametric Linkage (NPL) analysis - Methods for Large Pedigrees - Genome-Wide Association Studies (GWAS), or smaller scale, including: + Case/Control or Random Sample + Family-based Designs + Complex Pedigrees derived from Inbred Strains * Ethnic Admixture Analysis * Gene Co-Expression Network Analysis * Rare Variant Analysis Methods Applicable to SNP or Genome Sequence Data

Participants in the Course need no prior experience with these methods or programs. Participants will be required to bring a laptop computer to run the analysis exercises.

The Course features instructors from the Statistical Genetics Group of the UCLA Department of Human Genetics and other leading genetic researchers:

- Kenneth Lange - Simon Heath - Steve Horvath - Jeanette Papp - Janet Sinsheimer - Eric Sobel - Hua Zhou

The cost of the course, which includes lunch and snacks every day and a group dinner on Thursday, is:

900 EUR for students from non-profit institutions 1200 EUR for postdocs, staff, and faculty from non-profit institutions 1600 EUR for individuals from for-profit institutions

Transportation and lodging are not included.

The course will be held 22-26 August 2011 in Barcelona, Spain.

For more information, including the simple application process, please visit <http://www.genetics.ucla.edu/courses/statgene> Please email statgene@mednet.ucla.edu for more information or to submit the simple application material.

JanetS@mednet.ucla.edu

rence Hurst (Bath) Henrik Kaessmann (Lausanne) Fyodor Kondrashov (Barcelona) Michael Lynch (Bloomington) Duncan Odom (Cambridge) H. Allen Orr (Rochester) Dmitri Petrov (Stanford) Stephan Schuster (Philadelphia) Kenneth Wolfe (Dublin)

The scientific coordinators of the OWS are Martin Vingron, Peter Arndt and Brian Cusack at the Max Planck Institute for Molecular Genetics. The aim of this program is to bring together researchers and PhD students from different backgrounds (including molecular biology, bioinformatics, biological physics, mathematics) to discuss recent advances in evolutionary genomics in an interactive environment. The program focuses on high-level teaching and topical research seminars. Participants are expected to give poster presentations or contribute talks.

We invite applications from PhD students and a limited number of PostDocs. Please apply for attendance before June 12, 2011 via our website <http://ows.molgen.mpg.de/>.

The registration fee is 950 Euros. Costs for meals, accommodation and social events will be covered. Some travel subsidies are available. The programs (and video streams) of previous Summer Schools can also be found on the school's website.

For questions please contact Kirsten Kelleher (kelleher@molgen.mpg.de)

-

Kirsten Kelleher Max Planck Institute for Molecular Genetics Ihnestrasse 73 14195 Berlin

Tel: +49 30 8413-1154 Fax: +49 30 8413-1152 Email: kelleher@molgen.mpg.de <http://ows.molgen.mpg.de>

kelleher@molgen.mpg.de

Berlin Evolutionary Genomics Sep14-22

Dear colleagues,

this is the second call for applications to the Otto Warburg International Summer School and Research Symposium (OWS) on Evolutionary Genomics, to be held in Berlin from September 14th to 22nd, 2011.

<http://ows.molgen.mpg.de/> The following speakers have confirmed their attendance at the school: Hans Ellegren (Uppsala) Nicolas Galtier (Montpellier) Lau-

Bremerhaven Climate Adaptation Sep18-21

With the support of the network Thermal adaptation in ectotherms: Linking life history, physiology, behaviour and genetics (ThermAdapt) of the European Science Foundation, the Alfred Wegener Institute for Polar and Marine Research and with the Patronage of the Department of Evolutionary Biology of the University of Florence, we are pleased to announce the workshop:

The effects of climate change on vulnerable life traits of

aquatic ectotherms: towards an integrated approach.

Schedule and Venue: The course will be held at the Alfred Wegener Institute for Polar and Marine Research, in Bremerhaven, Northern Germany, the 18th-21st September, 2011.

Aims: - to provide PhD students and post-docs with challenging points of view and ideas on the effects of climate change on aquatic ectotherms species and communities; - to gather a multidisciplinary and heterogeneous cohort of scientists to merge the various approaches in an integrated discussion about future studies dealing with vulnerable life stages. - to build a new and integrated approach to the study of ecosystem responses and species resilience to climate change, seen from the point of view of the weakest traits of marine and freshwater ectotherms life cycles.

Focus: The workshop will focus on the effects of climate change on the overall life cycle of aquatic ectotherms, stressing the importance of their weakest links and phases. We think, in fact, that a new ontogenetic approach is needed to forecast the effects of climate change on aquatic communities. As consequence, we will put the emphasis on the specific pressure exerted on embryos, larvae and sub-adults as well as on reproducing and spawning individuals. Young researchers from a wide range of theoretical and experimental fields, from physiology to evolutionary ecology, from behavioral biology to ecological modeling, are called.

Specific Topics to be Covered: - Forecasting the effects of global change on reproduction of ectotherms; - Tolerance to change of embryos: implications for ectotherms ecology; - Tolerance to change of larvae: implications for ectotherms population connectivity; - Thermal tolerance of ectotherms; - Phenotypic responses to climate change in susceptible populations; - Physiological and ecological aspects of reproduction and development in aquatic ectotherms; - Acute vs. chronic stress on vulnerable life stages.

Keynote speakers: - Frank Melzner - Leibniz-Institute for Marine Science, Kiel University, DE - Hans-Otto Pörtner - Alfred-Wegener-Institute, Bremerhaven, DE - Enrique Queiroga - Centre for Environmental and Marine Studies, University of Aveiro, PT - Nia M. Whiteley - Bangor University, School of Biological Sciences, Bangor, UK - Gray A. Williams - Swire Institute of Marine Science, University of Hong Kong, CN

Registration: The workshop is open to up to 30 participants and the registration is free of charge. We will accept applications from PhD students as well as from Post Doctoral researchers received before June 30, 2011. With the support of ESF, we will cover accommoda-

tions and meals for all applicants, while a limited number of travel reimbursements (10-15) will be assigned on competitive basis.

Applicants are invited to download and fill the Application form (available at www.unifi.it/-climateandectotherms) and to send it back as PDFs to climateandectotherms@dbe.unifi.it

Deadlines: 30th June, 2011 - Application form and abstract submission 15th July, 2011 - Final approval of the participants list by the organizing committee.

For more information visit the web site www.unifi.it/-climateandectotherms or contact the organizing committee (specifying workshop infos as subject):

Stefano Cannicci - Firenze, IT stefano.cannicci@unifi.it
Folco Giomi - Bremerhaven, DE Folco.Giomi@awi.de
Felix Mark - Bremerhaven, DE Felix.Christopher.Mark@awi.de
Organising Committee, climateandectotherms@dbe.unifi.it

Folco.Giomi@awi.de

Budapest BeyondNextGenerationSequencing Jul20-23

Beyond Next Generation Sequencing workshop

The main aim of this workshop is to discuss the current scientific and technological challenges in the Next Generation Sequencing era. We will bring together scientists, SMEs and RTDs to share their opinion, introduce their cutting-edge results and highlight the current main barriers in research and technology. Above that, we are going to introduce the work of the CO-GANGS (Comparative Genomics and Next Generation Sequencing) consortium sponsored by EU FP7.

We wish to bring together researchers and companies to facilitate new collaborations. We encourage everybody working on novel sequencing techniques and/or modern genomics to participate in this workshop. There is no registration fee for this workshop, however, registration is necessary.

Confirmed invited speakers, participating companies:

CLC Bio BIOBASE Omixon BayGen Miklós Csürös, University of Montreal Endre Sebestyén, Agricultural Research Institute of the Hungarian Academy of Sciences Endre Barta, University of Debrecen Ádám

Novák, University of Oxford

More information: <http://www.renyi.hu/conferences/bngs2011/> miklosi@renyi.hu

Chioggia Italy

Marine Conservation Genetics Jul3-9

Second Summer School on Conservation Genetics of Marine Organisms

Organizers: Maria Berica Rasotto, Giorgio Bertorelle, Leonardo Congiu, Lorenzo Zane

When and Where: July 3-9, 2011, Chioggia (Venice), Italy

Application deadline: May 31, 2011

Fee: no registration fee is required; the financial support of the Regione Veneto (CLODIA project) covers also lunches, coffee breaks, and the social dinner for all the selected participants

Faculty: G. Bertorelle (University of Ferrara, Italy), M. Casiraghi (University of Milano-Bicocca, Italy), L. Congiu (University of Padova, Italy), J.C. Garza (NOAA Fisheries Service, Santa Cruz, USA), A. R. Hoelzel (Durham University, Durham, UK), C. van Oosterhout (University of Hull, UK), G. Procaccini (Stazione Zoologica A. Dohrn, Napoli), M.B. Rasotto (University of Padova, Italy), C. Sgro (Monash University, Melbourne, Australia), L. Zane (University of Padova, Italy)

The aim of the second summer school on conservation genetics is to increase the knowledge and disseminate the basic concepts in conservation genetics as an effective and modern tool for protecting and managing the biodiversity of marine environments. The school is designed for graduate and PhD students. A maximum of 25 students will be selected. Ten places will be reserved for students from the University of Padova. Basic lectures on general topics such as evolutionary and marine biology will be followed by specific lectures on conservation biology and conservation genetics. Six major themes in conservation genetics will then be discussed in more detail, covering both theoretical aspects and real examples. Lectures will be integrated with practical activities including genetic typing and data analysis. A few selected students will have the opportunity to present their projects during a special session. The summer school will be held at Palazzo Grassi, Chioggia.

Chioggia is a coastal town of the province of Venice in the Veneto region of northern Italy, situated on a small island at the southern entrance to the Lagoon of Venice about 25 km south of Venice (<http://en.wikipedia.org/wiki/Chioggia>).

The program and all the details for applying are available at: <http://chioggia.scienze.unipd.it/> (click on the News and go to the pages in English)

Giorgio Bertorelle Department of Biology and Evolution University of Ferrara <http://docente.unife.it/~giorgio.bertorelle> Phone +39 0532 455743 Fax: +39 0532 249761

Bertorelle Giorgio <ggb@unife.it>

Copenhagen PlantMarkerAnalysis

Course: Molecular marker analysis of plant population structure and processes

Copenhagen 22-08-2011 - 26-08-2011

This PhD course provides participants with practical and theoretical knowledge on analysis of genetic population structure, mating patterns, and population processes in plant populations, using molecular marker data. The course includes theoretical lectures, exercises and practicals with various computer programmes as well as discussions of student projects. The course is taught by staff at University of Copenhagen and other Danish Universities as well as Professor Peter Smouse, Rutgers University, one of the developers of GenA1Ex, a widely used software for population genetic analysis. Course content Estimation of genetic diversity, F-statistics, inbreeding level, gene flow, population and paternity assignment, population admixture, hybridization. Assumptions and limitations of methods, and practical exercises with relevant computer programmes, such as: GenA1Ex, Structure, Cervus, Two-gener, Population Graph, Geneland, Split tree, New Hybrids, AFLPOP, GeneClass2. Exact which programmes that will be used is to be decided. Discussion of selected student projects. Course credit 3 ECTS points. Requirement for obtaining credit: approval of a written synopsis of the course content. Course material Articles and lecture notes. All course material will be available through a restricted web site. Practical information Maximum number of participants is twenty. PhD students have preference, remaining seats are open to non-PhD students. The course will take place at University

of Copenhagen, Frederiksberg Campus (within Copenhagen). Computers with the relevant software will be available for all. Travel, lodging, and accommodation are to be organised and paid by the participants themselves; suggestions for hostels and hotels will be posted on the web. Course fee: 150 Euro Organisers and teachers Ole K. Hansen, Associate Professor in Forest Genetics; Erik D. Kj@r, Professor in Forest Genetics, Thure Hauser, Associate Professor in Plant Ecology; Gunter Backes, Associate Professor in Plant Breeding; Peter Smouse, Professor in Ecology, Evolution and Natural resources.

okh@life.ku.dk

Irapuato Mexico Evolutionary Genomics Jul19-22

REMINDER—APPLICATIONS TO RECEIVE FUNDING DUE MAY 13TH!!!

EVOLUTIONARY GENOMICS OF NON-MODEL SPECIES: NEXT GENERATION SEQUENCING, DATA MANAGEMENT, & HYPOTHESIS TESTING.

Announcing an NSF-Funded US-Mexico Workshop: Evolutionary Genomics of Non-Model Species: Next Generation Sequencing, Data Management, & Hypothesis Testing. http://www.theaga.org/2011/?page_id=3D207 To be held at the Laboratorio Nacional de Genómica para al Biodiversidad (Langebio) <http://www.langebio.cinvestav.mx/?pag=3D50> Irapuato, Mexico. July 19-22, 2011

Being held in conjunction with the 2011 AGA symposium, July 23-26, Guanajuato, Mexico. July 23-26, 2011. <http://www.theaga.org/2011/> OVERVIEW:

We have received NSF funding for a workshop to precede the AGA symposium 2011 “Genomics and Biodiversity.” The workshop is for graduate students and postdoctoral researchers looking to learn more about using next-generation sequencing technologies to address evolutionary questions with non-model organisms. There will be morning, afternoon, and evening sessions including hands-on computer sessions. We will cover a variety of topics and start with an introduction to NGS technologies and their applicability for different questions. We will also discuss hypothesis testing, data organization, data analysis pipelines with emphases on phylogeography, phylogenomics, and transcriptomics. In addition to the faculty listed below we will have guest

speakers from the AGA symposium present case studies. Please see our website to download a flyer and for more details on eligibility, funding, and application procedures. Applications are due by May 13, 2011!

FACULTY INCLUDE:

- Bryan Carstens, Louisiana State University
 - Ken Jones, University of Colorado School of Medicine
 - Ceil Abreu-Goodger, Langebio
 - Scott Edwards, Harvard University
 - Stacey Lance, UGA Savannah River Ecology Lab
- AND NOW ALSO: Rasmus Nielsen, University of California, Berkeley

ELIGIBLE APPLICANTS:

- Any US citizen or permanent resident currently enrolled in a MS or PhD program or working as a postdoctoral researcher in the US may apply to attend with funding to cover travel and lodging
- Any Mexican citizen currently enrolled in a MS or PhD program or working as a postdoctoral researcher in Mexico may apply to attend. Lodging will be covered via shared rooms with funded US participants.
- If space is available others may apply to attend but funding will not be provided

US PARTICIPANTS WILL BE EXPECTED TO:

- Share a hotel room with a Mexican student attending the workshop
 - Partner with a Mexican student to write & present a short research proposal using NGS technologies on a non-model organism
- Attend the AGA symposium 2011 “Genomics and Biodiversity” following the workshop

For more information and application procedures please see our website or contact Stacey Lance.

Sincerely,

Bryan Carstens, Ken Jones, Ceil Abreu-Goodger, Scott Edwards, Rasmus Nielsen, and Stacey Lance

Stacey L. Lance, Ph.D. Assistant Research Scientist
University of Georgia Savannah River Ecology Laboratory
PO Drawer E Aiken, SC 29802

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803.725.0988

lancestacey@gmail.com

KyotoU
ComputationalPhyloinformatics
Aug1-11

COMPUTATIONAL PHYLOINFORMATICS

August 1 2011 - August 11 2011

Bioinformatics Center of Kyoto University Application
Deadline: May 31, 2011[http://academy.nescent.org/wiki/-
Computational_phyloinformatics](http://academy.nescent.org/wiki/-Computational_phyloinformatics)

Computational Phyloinformatics is a 11-day international course (August 1-11, 2011) co-organized by the Computational Biology Research Center (CBRC/AIST), the Bioinformatics Center of Kyoto University, the Database Center for Life Science (DBCLS/JST), and the National Evolutionary Synthesis Center (NESCent). This course, which will take place at Kyoto University directly following the SMBE Meeting (<http://smb2011.com/>), aims to give participants practical knowledge and hands-on skills in phyloinformatics.

The venue in Kyoto is completely unaffected by the unfortunate events in Fukushima and the power shortages in Tokyo. We encourage biologists from other countries to participate in the SMBE meeting and/or this special international course, in solidarity with the scientific community of Japan in their effort to return to normalcy and to help minimize any negative impacts that the earthquake may have on scientific activities in Japan.

SYNOPSIS Biologists are faced with ever-larger datasets, more complex evolutionary models, and increasingly elaborate analytical methods. Seldom is it sufficient to run a dataset with an off-the-shelf program on a desktop PC; increasingly, biologists need to write scripts to interface with internet services and databases, build analytical pipelines, customize analyses, and distribute computation over multiple processors. This course is designed for graduate students, postdocs, faculty, and researchers in phylogenetics interested in receiving practical, hands-on training in the use of Perl and SQL for workflows and applications in phyloinformatics.

The course is divided into three parts:

- Part I: A tutorial review of of Perl, including object oriented programming and building packages -

- Part II: Introduction and practical use of BioPerl and Bio::Phylo, (e.g. scripting for large tree inference engines, automating model testing, genomic-scale data mining and acquisition, supertree assembly, rate smoothing and branch calibration, tree traversal, etc).
- Part III: Introduction and practical use of BioRuby for molecular evolution and functional genomics (e.g. scripting multiple sequence alignment, gene duplication inference, tree inference, etc.)
- Part IV: Introduction to SQL and database design; computing and querying nested sets and transitive closure; querying both large trees (e.g. NCBI) and large collections of trees (e.g. TreeBASE).

Participants will learn how to write basic phylogenetic or comparative analysis scripts, parse NEXUS files, traverse and compute over trees, and make practical use of phylogenetic software libraries. These skills will be learned in a biological context, touching on a diverse array of topics such as analysis of large datasets, automation of supertree assembly, querying for topological patterns in large collections of trees, etc. Participants will leave the course with a full set of installations and libraries on their computer ready to build phyloinformatic workflows for their own research projects, as well as continued access to a 50+ page wiki "textbook" containing step-by-step instructions, problem sets, and examples.

INSTRUCTORS AND COURSE ORGANIZERS
Christian Zmasek, Karen Cranston, Rutger A. Vos, Susumu Goto, Toshiaki Katayama, William H. Piel

APPLICATION DEADLINE May 31, 2011**TUITION** 40,000 (~\$500)

Participants are responsible for their own travel costs, including transportation and accommodation – see the website for more information. International participants will benefit by combining attendance with the 2011 SMBE meeting. A limited number of travel scholarships from NESCent are available for US-based students. Preference will be given to students from under-represented minorities.

PREREQUISITES

- Biology: A good understanding of phylogenetics - for example, having already taken the Workshop on Molecular Evolution (<http://www.molecularevolution.org/>) or equivalent coursework or experience.

- Computing: Prior experience with Perl or careful study of the suggested reading materials in advance of the class (see web site). Participants should have some experience with basic Unix shell commands.

- Equipment: Participants are expected to bring their

own Mac OSX computer or a LINUX computer, else they will be provided with an iMac. Participants who cannot bring their own computer and will be using a supplied iMac, should consider bringing their own portable firewire/usb drive so that they can also leave the course with a full suite of phyloinformatic software tools.

william.piel@yale.edu

KyotoU Phylogenetic Workflows Aug1-11 Deadline May31

COMPUTATIONAL PHYLOINFORMATICS August 1 2011 through August 11 2011 Bioinformatics Center of Kyoto University Application Deadline: May 31, 2011

http://academy.nescent.org/wiki/-Computational_phyloinformatics

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The course is divided into four parts:

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The Asia-Pacific Bioinformatics Network (APBioNet) is happy to provide travel assistance for a limited number of students/early career researchers from the Asia-Pacific region. Applicants are requested to contact Dr Asif Khan, APBioNet Secretariat: asif -@-bic.nus.edu.sg (replace -@- with @) for details.

PREREQUISITES

BIOLOGY: A good understanding of phylogenetics - for example, having already taken the Workshop on Molecular Evolution (<http://www.molecularevolution.org/>) or equivalent coursework or experience.

COMPUTING: Prior experience with Perl or careful study of the suggested reading materials in advance of the class (see web site).

— / —

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>

Lisbon GenomeBiolEvolution Aug1-19

Dear EvolDir

We would like to announce a summer school in Genome Biology and Evolution, to be held this summer (Aug 1-19) in Lisbon, Portugal. (www.igc.gulbenkian.pt/gbe2011)

This summer school targets mid MSc. students to interest them in this exciting research area - thanks to generous funding from the Volkswagen and Gulbenkian foundations, there will be excellent financial support for participants.

The summer school will include daily seminars by an international faculty - we are lining up an exciting list of speakers, including Sydney Brenner, Michael Lynch, Eduardo Rocha, Francois Balloux, Andrew Clark, among many others; open-ended experimental and/or bioinformatics research projects conducted in small groups with close support of faculty, leading to a scientific workshop where participants can discuss the results of their experiments; tutorials on basic concepts and methodologies used in genome analysis early in the summer school to enable full participation by students

from diverse scientific backgrounds. A rich social program is designed to maximize the exposure of students to the faculty.

The Summer school will happen at the Instituto Gulbenkian de Ciencia (www.igc.gulbenkian.pt) in Oeiras, a science-intensive sea-side village, located a few miles away from Lisbon (Portugal). It is being organized by Jose Pereira-Leal and Thiago Carvalho from the IGC, and Thomas Boehm from the Max Plank Institute.

Registrations open on May 15th and will remain open until June 15th - candidate will be selected on scientific merit and life experience.

We ask you to please forward this message to students whom you think can be interested, or lecturers in MSc. programs.

Thank you very much

Jose pereira-Leal

Jose Pereira Leal, PhD Computational Genomics Laboratory & Bioinformatics and Computational Biology Unit Instituto Gulbenkian de Ciência Apartado 14 P-2781-901 Oeiras Portugal

phone: +351 21 446 4528 fax: +351 21 440 7973

<http://www.evocell.org>

[http://-](http://-bioinformatics.igc.gulbenkian.pt)

[bioinformatics.igc.gulbenkian.pt](http://-bioinformatics.igc.gulbenkian.pt)

jleal@igc.gulbenkian.pt jleal@igc.gulbenkian.pt

Luebeck Germany SystemsBiology Sep5-9

Dear colleagues, researchers, and friends,

registration is now open for the

Workshop on Systems Biology together with the 2nd Baltic Autumn School

to take place in Luebeck during 5.-9.September 2011.

Invited speakers:

Tibor Antal (Edinburgh) Albert-Laszlo Barabasi (Notre Dame) Ofer Biham (Jerusalem) Angelika Börsch-Haubold (Plön) Stefan Bornholdt (Bremen) Theo Geisel (Göttingen) Bernhard Haubold (Plön) Marc-Thorsten Hütt (Bremen) Kunihiko Kaneko (Tokyo) Edda Klipp (Berlin) Jürgen Kurths (Potsdam) John Postlethwait (Eugene) Mamen Romano (Aberdeen) Kim Sneppen (Copenhagen) Peter Stadler (Leipzig) Marco Thiel (Aberdeen) Fred Turek

(Evanston) Olaf Wolkenhauer (Rostock)

Early registration and poster submission: 15. July 2011. A few number of contributions may be selected for oral presentation.

See the workshop webpage for details and registration: <http://www.inb.uni-luebeck.de/~as11/> We are looking forward to meet you in Luebeck!

Yours sincerely,

Jens Christian Claussen Amir Madany Mamlouk Katja Dau (GS-CMLS Events)

– PD Dr. Jens Christian Claussen claussen@inb.uni-luebeck.de Institut f. Neuro- und Bioinformatik Univ. Luebeck +49-451-5005412 <http://www.inb.uni-luebeck.de/~claussen/> Jens Christian Claussen <claussen@inb.uni-luebeck.de>

Messina Microbial Evolution Jun7-10

“this year the course is specifically design to address the issues of whom, using microbial systems, is addressing evolutionary theories. One of the three special guests is Alex Hall (Oxford University) is a world famous microbial evolutionary biologist, and he will follow the students for the whole week. It s lecture will address the use of experimental systems in evolutionary biology, as well as the other methodologies (cytometry, 454, cloning) are all suitable for evolutionary studies. I guess the course can be interesting for the evoldirs.”

We are glad to announce that the 3 SItEMICRO practical and theoretical course in Microbial Ecology will be held in Messina (Italy), from June 07 to 10 2011, at the University of Messina facility, Villa Pace. Such location, facing the charming scenario of the Strait of Messina, is equipped with both laboratory spaces and conference rooms. The course will provide insights in the new techniques applied in microbial ecology and evolution, focussing on their implications in the study of community ecology and experimental evolutionary microbiology. This year, 4 main scientific topics will be theoretically and practically described, also following the suggestions of the participants to the previous courses. 1-Cultivation Techniques in Microbial Ecology; 2-Quantitative analysis of Microbial Populations; 3-Clone Libraries: Opening the Diversity Book; 4-Estimating Prokaryotic Diversity: Fingerprinting and New-Generation Sequence-Based Techniques. More info on direct lectures by Stefan Bertils-

son (454 data Analysis - Uppsala University), Alex Hall (Microbial Systems in Evolutionary Biology - Oxford University), and Michail Yakimov (NGS techniques - IAMC-CNR Messina), as well as practical and theoretical lessons by Gian Marco Luna (Polytechnic University of Ancona), Gianluca Corno (CNR-ISE Verbania), Stefano Amalfitano (CNR-IRSA Rome), Manuela Coci (CNR-ISE Verbania), and Luigi Michaud (University of Messina) are available on our website. The course (inscription fee 200 Euro, extended deadline May 16) is designed for PhD students, but also “experienced” master students and young researchers are welcome. Keep tuned for news about deadlines, programme and lessons by clicking on www.sitemicro.it or email to: sitemicro@gmail.com

Dr. Gianluca Corno Microbial Ecology Group CNR - Institute of Ecosystem Study Largo Tonolli 50 - 28922 Verbania - Italy Tel. +39 0323 518 321 Fax +39 0323 556 513

SItE - Section of Microbial Ecology - <http://www.sitemicro.it/> Gianluca Corno <g.corno@ise.cnr.it>

Mount Desert Island Env Genomics Aug20-27

Second Annual Summer Course in Environmental Genomics at the Mount Desert Island Biological Lab

A technical course to guide research into how environmental conditions affect gene responses and the fitness of organisms

Date: August 20 to August 27, 2011. Number of participants: Restricted to 25.

http://www.mdibl.org/courses/-Environmental_Genomics/199/ The faculty at MDIBL is pleased to again offer a training course in Environmental Genomics, aiming to better understand technologies and approaches used to discover how gene function is influenced by environmental conditions while accounting for variation that exists within and among natural populations. This course is built on the paradigm that the research field will most effectively grow by properly designing large-scale experiments enabled by drastically increased sample-throughput and lower costs. Most importantly, the challenges of manipulating and analyzing population-level genomics data must be addressed.

This course is designed to train the next-generation of environmental scientists, which last year included five university professors, seven postdoctoral researchers, eight doctoral students and a government scientist, representing institutions from five countries and eight US states. All but two responded in the departure survey that the course curriculum, choice of technologies, and effectiveness provided sufficient training to either begin or enlarge an environmental genomics project in their own laboratories. All reported that they would recommend this course to a colleague.

This course trains researchers to design studies, and to collect and analyze state-of-the-art gene expression data. *Daphnia* is used for training because of its growing use as a model system for environmental genomics and for improving environmental health protection (see URL below), yet the skills learned during the course will be applicable to all study systems with mature genomics resources.

Nature News <http://www.nature.com/news/2011/110203/full/news.2011.71.html> Participants will also obtain hands-on training on the latest automation protocols for higher-throughput processing of next-generation sequencing samples, and will learn computational methods to manage and analyze genomics-scale data sets.

Ultimately, participants will be better positioned to incorporate these technologies into their own research laboratories, while better understanding how functional genomics and automation can be applied to ecology, evolution and toxicology.

Support for this training course is provided by The Indiana University Center for Genomics and Bioinformatics, Beckman Coulter Inc., Roche NimbleGen Inc., and Life Technologies Inc.

Please download the poster announcement at: https://wiki.cgb.indiana.edu/download/attachments/-22446089/MDIBL_Envngen_flyer_y2.pdf John Kenneth Colbourne The Center for Genomics and Bioinformatics Indiana University

jcolbour@cgb.indiana.edu

FIRST IV at CIBIO/UP - Teaching Workshops in Biology

Dates: 27 - 30 September 2011

Senior PhD students, postdoctoral researchers and faculty in any field of biology are invited to participate in Faculty Institutes for Reforming Science Teaching (FIRST IV) for Faculty and Postdoctoral Scholars. FIRST IV focuses on reform of undergraduate biology education through professional development of post-docs and faculty. Participants will design an inquiry-based, student-centered undergraduate biology course.

Key elements of FIRST IV include active learning, assessment and diversity in teaching. Participants will attend one workshop and a follow-up webinar during consecutive summers: a four-day workshop in 2011 followed by a webinar in 2012. During the academic year between the two workshops, participants will teach all or part of an introductory biology course (e.g., cell biology, genetics, ecology, organisms, populations, evolution) at their home institution using the course framework they designed during the workshop.

Who should apply?? Senior PhD students, postdoctoral researchers and faculty who have an interest in and commitment to teaching. We encourage individuals or teams of two participants from one institution to apply.

Cost? 360 euros. The course fee includes lunch, morning and afternoon coffee-breaks, room and instructional materials.

Application due: June 26, 2011 Notification of acceptance: July 4, 2011

Questions? Contact Rita Campos or Rui Faria, PopGen Research Group, CIBIO/UP, ritacampos@mail.icav.up.pt or rui.faria@upf.edu

Application is on the FIRST IV-like at CIBIO web site: <http://popgencibio.org/-web/> Please name your completed application file: **LastnameFirstname_FIRSTIVCIBIOapp.pdf

Send all application materials as one PDF document to: ritacampos@mail.icav.up.pt

Rui Faria <rui.faria@upf.edu>

Porto Portugal Teaching Evolution

Portugal.Teaching Workshops in Biology-
Porto.September.2011

Poznan Bioinformatics Jul11-15

9th Poznan Summer School of Bioinformatics

Faculty of Biology, Adam Mickiewicz University, Poznan, Poland

11th-15th July 2011

Advanced Techniques in Genome Analysis

Poznan Summer School of Bioinformatics is a comprehensive course of bioinformatics. The course is best prepared for those who have little knowledge in bioinformatics and find it necessary/interesting to learn more in this field. It is therefore aimed to give the opportunity to find out how to use some basic bioinformatic tools and how to perform bioinformatic analyses in your research.

The course consists of lectures (by scientists from Poland and abroad) and hands-on - this combination should fit best your needs as you have a chance to try the methods out yourself. We cover the following subjects (which we find most interesting and up-to-date):

* Population genetics in the genomic era * Next generation sequencing technologies * Sequence assembly * Genome wide association studies * miRNAs and their targets * Genome wide analysis of repetitive elements * Tools for genome annotations and analysis * Gene complexity and alternative splicing * Reactome - reactions, pathways and biological processes

Details can be found at the workshop website: <http://lemur.amu.edu.pl/bioinfo/> Please forward this announcement to anyone who might be interested.

Visit Poland! Enjoy bioinformatics!

Best regards,

PSSB Organizing Committee

Contact: genomics@amu.edu.pl

Bioinfo School <genomics@amu.edu.pl>

Poznan Poland Bioinformatics Jul11-15

Dear All,

Do you have some plans for the summer? Maybe you want to improve your skills and knowledge in bioinformatics, especially in Advanced Techniques in Genome Analysis?

We are happy to invite you for 9th Poznan Summer School of Bioinformatics (11-15 July 2011, Poznan, Poland, Adam Mickiewicz University)

The course consists of lectures (by scientists from Poland and abroad) and exercises - this combination should fit best your needs as you have a chance to try the methods out yourself.

We have a great pleasure to present you a list of invited speakers:

- Kenneth Weiss, Pennsylvania State University (Keynote speaker) - Maria Anisimova, Swiss Federal Institute of Technology, Zurich - Artemis Hatzigeorgiou, Al. Fleming BSRC, Athens - Robin Haw, Ontario Institute for Cancer Research, Toronto - Marcin Jakalski, University of Muenster, Muenster - Michal Kabza, Adam Mickiewicz University, Poznan - Antonio Marco, University of Manchester, Manchester - Anton Nekrutenko, Pennsylvania State University - Graziano Pesole, University of Bari, Bari - Andrzej Polanski, Silesian University of Technology, Gliwice - Monika Stoll, University of Muenster, Muenster - Yutaka Suzuki, University of Tokyo, Tokyo - Hadi Quesneville, INRA, Versailles Cedex - January Weiner, Max Planck Institute for Infection Biology, Berlin - Thomas Wiehe, University of Cologne, Cologne

This year we cover following subjects:

- Population genetics in the genomic era - Next generation sequencing technologies - Sequence assembly - Genome wide association studies - miRNAs and their targets - Genome wide analysis of repetitive elements - Tools for genome annotations and analysis - Gene complexity and alternative splicing - Reactome - reactions, pathways and biological processes

To read more and register, please visit our website: <http://lemur.amu.edu.pl/bioinfo/> Hope to see you in Poznan!

Best regards, PSSB Organizing Committee contact: genomics@amu.edu.pl

Bioinfo School <genomics@amu.edu.pl>

SantaBarbara MacroevolutionaryMethods in R Jun15

We are pleased to announce an intensive short course on using R to perform comparative methods to be held in Santa Barbara on July 31-Aug 5, 2011. This course is funded by the National Science Foundation, and a number of stipends to cover or defray travel, room,

and board are available to qualified students and post-docs. Topics covered will include an introduction to the R programming language, tree manipulation, independent contrasts and phylogenetic generalized least squares, ancestral state reconstruction, models of character evolution, diversification analyses, and community phylogenetic analysis. Course instructors will include Luke Harmon, Mike Alfaro, Todd Oakley, and Dan Rabosky.

If you are interested please submit your CV along with a short (maximum 1 page) description of your research interests, background, and reasons for taking the course. Admission is competitive, and the best applications come from students with data sets to analyze. International applicants are welcome. Applications should be submitted online at <http://bit.ly/liqVQ7> by 15 June 2011 (if you got a previous version of this message, please note the corrected date).

Thanks- Luke Harmon and Mike Alfaro

Luke Harmon Assistant Professor Biological Sciences
University of Idaho 208-885-0346 lukeh@uidaho.edu

Luke Harmon <lukeh@uidaho.edu>

Trento Italy ConsPopulationGenetics Sep20-22

It gives us great pleasure to announce that the INTERNATIONAL WORKSHOP 'Population Genetics for Animal Conservation III' will be held at the Congress Centre Panorama, Sardinia, Trento, Italy, September 20-22, 2011. This workshop will be organized by the Department of Biodiversity and Molecular Ecology, Fondazione Edmund Mach (S. Michele all'Adige, Trento, Italy) in collaboration with the European consortium ConGRESS.

ALL RELEVANT INFORMATION IS AVAILABLE AT <http://pgac3.fem-environment.eu/> The Third edition of the workshop will be focussed on a well-recognized, yet unsolved issue in conservation genetics: how to bridge the gap between scientists and end-users, i.e. non-scientists such as policymakers, administrators, or park rangers that are directly involved in animal conservation and would like to design, implement and/or apply management and conservation plans using the most modern strategies and tools

Therefore, this workshop intends addressing this gap by focussing on five main themes identified as top priori-

ties during a recent survey conducted by ConGRESS of 100 end-users from across Europe:

- 1) Identifying units for conservation
- 2) Population connectivity and isolation
- 3) Reconstructing past population dynamics
- 4) Detecting and planning translocations and reintroductions
- 5) Genetic diversity and adaptation

Each theme will be tackled in one 2-hour session (with lectures from invited speakers and contributions from attendees) with final-day round tables discussions where scientists and end-user will have the opportunity to examine, vis-a-vis, unresolved issues and possible solutions.

PGAC III hopes to bring together researchers from different fields (e.g. population genetics, ecology, conservation biology and related) and end-users with basic scientific knowledge and a strong desire to know more about applying population genetics tools to their particular conservation problem. The major aim will be to promote an effective interaction, using a common language, to fully exploit the potential of population genetics as applied to animal conservation.

Invited speakers: Giorgio Bertorelle (University of Ferrara, Italy) Josef Bryja (Academy of Sciences, Czech Republic) Mike Bruford (University of Cardiff, UK) Oscar Gaggiotti (Université J Fourier, Grenoble, France) Rus Hoelzel (University of Durham, UK) Jacob Hoglund (University of Uppsala, Sweden) Craig Moritz (University of California, Berkeley, USA) Richard Nichols (Queen Mary's College, UK) Craig Primmer (University of Turku, Finland) Gernot Segelbacher (University of Freiburg, Germany) Hans Siegismund (University of Copenhagen, Denmark) Per Sjögren-Gulve (Swedish Environmental Protection Agency) Carles Vilà (CSIC, Spain) Raj Whitlock (University of Liverpool, UK)

The Scientific Committee: Giorgio Bertorelle, University of Ferrara, Italy Mike Bruford, University of Cardiff, UK Heidi C. Hauffe, Fondazione Edmund Mach, S. Michele all'Adige, Trento, Italy Cristiano Vernesi, Fondazione Edmund Mach, Viote del Monte Bondone, Trento, Italy

DEADLINE for abstracts and registrations for PGAC III: 30 JUNE 2011.

Cristiano Vernesi Department of Biodiversity and Molecular Ecology Research and Innovation Centre - Fondazione Edmund Mach address: Centro di Ecologia Alpina, Viote del Monte Bondone - 38040 Trento - Italy

tel +390461939523 - fax +390461948190 - skype name:
cvernesi
vernesi@cealp.it

UHelsinki ClimateAdaptation Sep11-14

Workshop: ADAPTATION TO CLIMATE FROM A
SPATIAL PERSPECTIVE

11-14 September 2011 at Lammi Biological Station,
University of Helsinki, Finland

Short description:

Advancing our understanding how organisms adapt to environmental variation lies at the core of ecology and evolutionary biology, and has become especially relevant in the light of current human-induced environmental change as a major threat to global biodiversity. When predicting species' responses to climate change, including range shifts and adaptation, it is crucial to take into account spatial patterns of local adaptation and population dynamics at the regional and geographical scale.

We organize a conference (~60 participants) with a primary focus on adaptation to environmental variation, in particular climatic and thermal adaptation, from a spatial perspective at the regional and geographic level. We intend to bring together current high-quality research at multiple levels of investigation, including ecology, evolutionary genetics, physiology, theory and conservation. We aim to combine studies including a broad range of organisms, including plants, vertebrates and aquatic organisms, but with a main focus on ectotherms.

The conference will be organised around three main sessions:

Latitudinal and altitudinal clinal variation Landscape/metapopulation approaches to ecological and evolutionary dynamics Ecological and evolutionary dynamics at the range margins

Keynote speakers:

Dr. Jon Bridle (University of Bristol, UK) Prof. Steven Chown, Stellenbosch University, South Africa) Prof. Klaus Fischer (Greifswald University, Germany) Prof. Ilkka Hanski (University of Helsinki, Finland) Prof. Pär Ingvarsson (Umeå University, Sweden) Prof.

Volker Loeschcke (Aarhus University, Denmark) Prof. Juha Merilä (University of Helsinki, Finland) Prof. Patricia Schulte (University of British Columbia, Canada) Prof. Chris Thomas (University of York, UK)

Organizers:

Maaïke de Jong & Marjo Saastamoinen

Metapopulation Research Group, Department of Biosciences, University of Helsinki

For more information and online registration (registration deadline is June 30th 2011):

< <http://www.helsinki.fi/science/metapop/-workshop/> > <http://www.helsinki.fi/science/-metapop/workshop/> Marjo Saastamoinen, PhD Metapopulation Research Group Department of Biological Sciences PO Box 65 (Viikinkaari 1) FI-00014 University of Helsinki FINLAND

Phone +358 9 191 57741

“Saastamoinen,
<marjo.saastamoinen@helsinki.fi>

Marjo”

Venice EvoDevo Sep19-22

Summer School on Evolutionary Developmental Biology Conceptual and Methodological Foundations

2nd Edition: From Gene Networks to Organismal Systems

Venice, 19 - 22 September 2011

Organizers: Alessandro Minelli, Gerd B. Müller and Giuseppe Fusco School director: Johannes Jaeger

School sponsors: Istituto Veneto di Scienze, Lettere ed Arti, Venice and Konrad Lorenz Institute for Evolution and Cognition Research, Vienna. Location: Istituto Veneto di Scienze, Lettere ed Arti, Palazzo Franchetti, Venice

Taching panel: J. Jaeger (School Director, CRG Barcelona), P. Beldade (Gulbenkian Institute, Lisbon), C. Braendle (CNRS and Université de Nice - Sophia Antipolis), G. E. Budd (University of Uppsala), G. Fusco (University of Padova), A. Hejnol (Sars International Center for Marine Molecular Biology, Bergen), R. Jenner (Natural History Museum, London), A. Minelli (University of Padova), G. B. Müller (Konrad Lorenz Institute, Vienna), S. A. Newman (New York Medical College)

Deadline for applications: May 30th 2011.

For details, visit <http://www.istitutoveneto.it/-EDB2011/> Giuseppe Fusco Department of Biology University of Padova Via U. Bassi 58/B I-35131 Padova Italy tel. +39.049.827.6238 fax +39.049.827.6230 e-mail giuseppe.fusco@unipd.it webpage <http://dept.bio.unipd.it/fusco>

Giuseppe Fusco <giuseppe.fusco@unipd.it>

West Virginia Malaria Evolution Aug1-4

SECOND ANNOUNCEMENT

International Workshop on Malaria and Related Haemosporidian Parasites of Wildlife

Monday August 1st V Thursday August 4th, 2011

National Conservation Training Center, Shepherdstown, West Virginia

Sponsored by the NSF Research Coordination Network for Haemosporida of Terrestrial Vertebrates¹

**The workshop is likely to be of interest to evolutionary biologists as it will center around the systematics of a very successful and diverse group of parasites of natural vertebrate populations and include laboratory exercises involving phylogenetic analysis of parasite lineages and readings and discussions on the evolutionary history of the parasites including cospeciation of hosts and parasites as well as the evolution of virulence.

Dear Colleagues,

The NSF-sponsored Research Coordination Network for Haemosporida of Terrestrial Vertebrates (MalariaRCN) is pleased to announce our first annual workshop on the malaria parasites and closely related haemosporidians of natural populations of vertebrates. The four day workshop will include both field and laboratory exercises as well as lectures and discussions led by RCN members².

Topics to be covered through the workshops exercises include vertebrate and invertebrate field capture techniques, blood sampling and preparation of blood smears, vector identification and salivary gland preparation, sample vouchering and cryopreservation, light microscopy for parasite species identification and parasite and cell counts, DNA extraction and PCR screening of parasites, sequence data analysis including phy-

logenetics, and databasing. Discussion topics will include, but are not limited to, the basic biology, phylogenetics and systematics of Haemosporida, community ecology of parasites, coevolution of parasites and hosts, the evolution of virulence, and conservation and disease.

The workshop will commence on Monday morning, August 1st, and continue through until the afternoon of Thursday, August 4th. The workshop will be followed by a three day meeting on the malaria and related haemosporidian parasites of wildlife, organized by the same RCN group.

All food, lodging and workshop events will take place at the US Fish & Wildlife Services National Conservation Training Center in Shepherdstown, West Virginia, a site easily accessible through Washington, D.C., area airports.

The workshop is geared towards graduate students, postdoctoral researchers, and other investigators new to the field of wildlife haemosporidians. We are currently accepting applications and encourage individuals from outside the United States, particularly from developing countries. Funding is available to cover the workshop cost, accommodation at the Shepherdstown facility, transportation from the Washington Dulles International airport (IAD), and meals for all participants. Additional funds may be available to help with travel costs. Application forms can be requested from the workshop organizers (email: MalariaRCNWorkshop@gmail.com). Additional information on the workshop including an overview of the four days of events will soon be made available on the official workshop website (<http://malariarcn.org/>). Decisions on participation will begin on Monday May 30th and continue until the workshop is filled. If interested, you are encouraged to apply for the workshop as soon as possible.

¹ The Research Coordination Network for Haemosporida of Terrestrial Vertebrates (RCN), sponsored by the U. S. National Science Foundation and funded through 2015 at the University of Missouri-St. Louis, was established to promote communication among researchers working on the ecology and evolution of haemosporidian parasites of vertebrate wildlife populations.

² Workshop organizers include Ellen Martinsen (Smithsonian Institution), Staffan Bensch (Lund University), Ravinder Sehgal (San Francisco State University), Carter Atkinson (USGS), and Gediminas Valkiunas (Nature Research Center, Vilnius). Other members of this RCN include Robert Ricklefs and Patricia Parker (University of Missouri V St. Louis), Robert Fleischer (Smithsonian Institution), Susan Perkins (American

Museum of Natural History), Tom Smith(University of land Museum).
California, Los Angeles), and Robert Adlard (Queens- “Fleischer, Robert” <FleischerR@si.edu>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

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

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

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

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 L^AT_EX do not try to embed L^AT_EX or T_EX in your message (or other formats) since my program will strip these from the message.