
E v o l D i r

August 1, 2012

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

Foreword

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

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

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



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Conferences

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Brussels BarcodeOfLife ECBOL3 Sep17-20 NEW DEADLINES

Dear colleague,

As you may know already the Third European Consortium for the Barcode of Life conference (ECBOL3) will take place from 17-20 September 2012 in Brussels (Belgium). The conference will be organised by the Royal Museum for Central Africa (RMCA), the Royal Belgian Institute of Natural Sciences (RBINS) and ECBOL.

This reminder is to notify you that the EXTENDED deadline of early-bird registration for the conference (5 AUGUST 2012) is approaching fast! Please note that we have excellent invited speakers for each of the five major themes of the conference!

Registration for the conference and abstract submission is open. More information on the conference can be found at <http://ecbol3.myspecies.info/> and in the attached second circular. We hope to see you in Brussels!

Yours sincerely,

Thierry Backeljau and Marc De Meyer - conference coordinators

ecbol3 <ecbol3@africamuseum.be>

lustimaci@yahoo.com

Bulgaria Bioinformatics Sep19-21 CallAbstracts

Only 1 month left to submit your abstract to BIOCOMP BG 2012!

International Conference on Bioinformatics and Computational Biology - BIOCOMP BG 2012 (<http://biocomp.bio.uni-plovdiv.bg/>).

Topics

Topics of interest include, but are not limited to:

High-performance bio-computing High-throughput sequencing data analysis (NGS) Bio-ontologies Molecular evolution Comparative genomics Molecular modeling and simulation Computational genetics Computational proteomics Data mining and visualization Software tools and applications Gene expression analysis Gene networks Structural biology Genome analysis Databases Systems biology

Publications

All accepted abstracts will be published in the conference abstract book. Best 20 abstracts will be peer-reviewed and published as full text manuscripts in a Special Issue of Springer and Elsevier journals: Interdisciplinary Sciences: Computational Life Sciences

(ISSN: 1867-1462). Journal of Computational Science
(ISSN: 1877-7503)

Venue

The venue of the conference is 4-star All-inclusive Sunny Day Black Sea resort, Bulgaria

Registration and abstract submission

All the actions related to the BIOCAMP 2012 (abstract submission, registration etc) may be completed via the Conference website at <http://biocomp.bio.uni-plovdiv.bg/> Accommodation

IMPORTANT: Accommodation is included in the conference registration fee.

Important dates

Abstract Submission Deadline - 20 August 2012 (submitted abstracts will be notified for acceptance after 48h of submission)

Early Registration Fee Payment Deadline - 20 August 2012

Arriving, Poster set up, Registration V 19 September 2012

Plenary and Poster Sessions V 20-21 September 2012

You may find details of the Conference visiting the Conference website at <http://biocomp.bio.uni-plovdiv.bg/> Looking forward to see you in Bulgaria!

Dr. Vesselin Baev Research Assistant Professor

University of Plovdiv Dept. Plant Phys. and Molecular Biology Bioinformatics SMART Group

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CUNewYork
PhilosophyEvolutionTheory
Apr12-14

CUNY Graduate Center CFP: Philosophy & Theory in Biology Young Investigators Symposium Theorists have long probed, and often crossed, the boundaries between biology and philosophy through conceptual reflection, mathematical modeling, and the analysis of complex empirical patterns.

>From Aristotle to Darwin and beyond the growth

of biological theory has gone hand-in-hand with philosophical inquiry into biological phenomena. The work done at these frontiers by theoretically-minded biologists and scientifically-informed philosophers is of mutual benefit to both disciplines.

These frontiers are often most evident in the next generation of researchers who are open to new possibilities and aware of novel perspectives or innovative tools. We therefore invite the emerging next generation of theorists to catalyze this dialogue with a symposium in New York City, one of the nations thriving centers of research in both biology and philosophy of biology, to be held on April 12-14, 2013 at Lehman College, part of the City University of New York.

Attendance is open to all, but we accept papers by young investigators in theoretical biology or philosophy of biology, defined as graduate students, postdocs, or non-tenured faculty. Papers should be of a maximum length of *5,000 words* (including references) and need to be submitted at the latest by *November 25, 2012*. Information, registration and instructions to submit papers can be found at <https://sites.google.com/site/philobiosymposium/> Leonard Finkelman

Leonard Finkelman <lfinkelman@gc.cuny.edu>

Cambridge InsectGenomics Nov26

Registration is now open for the Royal Entomological Society Special Interest Group on Insect Genomics, to be held on Monday 26th November 2012 at St John's College Cambridge: <http://www.royensoc.co.uk/content/genomics-special-interest-group-26th-november-2012> The goal is to bring together both genomics practitioners and those who are just starting out or planning to use genomics techniques in Entomology. Invited speakers will be Mark Blaxter (The GenePool, Edinburgh), Dan Lawson (European Bioinformatics Institute and i5k initiative) and Lin Field (Rothamstead Research). We hope to cover a range of topics including new technologies, bioinformatic challenges and specific projects across entomology that involve genomic techniques.

Participants are encourage to register and pay the £10 registration fee by November the 12th at the latest.

If you are interested in giving a talk please send a proposed title and abstract to me (njn27@cam.ac.uk) by the 28th of September. This is a one-day meeting so

we may not be able to accept all proposed talks. If you would be interested in presenting a poster instead please let us know.

Chris Jiggins and Nicola Nadeau

– Dr Nicola Nadeau Butterfly Genetics Group
Department of Zoology University of Cambridge
Downing Street Cambridge, CB2 3EJ Phone: 01223
336644 Email: njn27@cam.ac.uk Web: <http://heliconius.zoo.cam.ac.uk/2009/nicola-nadeau/>
njn27@cam.ac.uk

DrexelU Biodiversity Oct11-12

Please join the Academy of Natural Sciences of Drexel University in Philadelphia October 11 - 12, 2012 as we explore current and future research on the diversity of life with a focus on evolutionary history, ecology, and environmental quality.

Biodiversity: From Evolutionary Origins to Ecosystems Function A Bicentennial Symposium to Celebrate 200 Years of Research at the Academy of Natural Sciences

www.ansp.org/symposium The two-day conference will open at 2 p.m. on Thursday, October 11, with tours of the Academy's collections and environmental labs. We will close with a poster session and reception on the evening of Friday, October 12.

Visit www.ansp.org/symposium or email symposium200@ansp.org for meeting information, registration, and details about submitting to the student poster session. *Please note that students who submit poster abstracts to symposium200@ansp.org prior to Aug 31 will be eligible for a fee-waiver*

SPEAKERS

DOUGLAS J. FUTUYMA, Stony Brook University
SANDRA KNAPP, Natural History Museum in London, England
J. PATRICK KOCIOLEK, University of Colorado
Museum of Natural History
WAYNE P. MADDISON, University of British Columbia and Beaty Biodiversity Museum
LUCINDA A. MCDADE, Rancho Santa Ana Botanic Garden
DANIEL OTTE, The Academy of Natural Sciences of Drexel University
SHAHID NAEEM, Columbia University
DAVID TILMAN, University of Minnesota

SYMPOSIUM SCHEDULE Thursday, October 11, 2012
The Academy of Natural Sciences of Drexel University, Philadelphia, PA USA
The conference opens

with an opportunity to tour the Academy's historic collections and environmental labs. All departments will be open for registrants to visit. The presentation of the Academy's prestigious Joseph Leidy Award and an address by its recipient Douglas Futuyma, Distinguished Professor of ecology and evolution at Stony Brook University, will be followed by a welcome reception in the museum.

Friday, October 12, 2012
Papadakis Integrated Sciences Building (PISB), Drexel University, Philadelphia, PA USA
Friday is filled with speaker sessions in PISB, Philadelphia's newest landmark for scientific research and the future of integrated science at Drexel. The day ends with a closing reception and poster session.

CALL FOR POSTERS Undergraduate and graduate students are encouraged to present their research.

On behalf of the organizing committee,

John G. Lundberg Chaplin Chair and Curator of Ichthyology
Academy of Natural Sciences
1900 Benjamin Franklin Pkwy Philadelphia, PA 19103 USA
215-405-5069

ilves@ansp.org

Frankfurt Adaptive Genomics Ecological Niches Oct12

The Biodiversity and Climate Research Centre Frankfurt/M, Germany invites to a

Symposium: Genomic Adaptation to Ecological Niches.
12.October.2012

Invited speakers: Prof. Diethard Tautz - MPI for Evolutionary Biology, Plön. Prof. Walter Salzburger - Evolutionary Biology, U. of Basel.

Hosts: Prof. Markus Pfenninger - BiK-F, Frankfurt/M.
Prof. Axel Janke - BiK-F, Frankfurt/M.

We are organizing a one-day workshop to discuss current projects and possibly common interests in the rapidly expanding field of adaptive genomics of ecological niches. Adaptation is one of the corner stones of evolutionary and adaptation to different niches provides the bridge to ecology. Rapidly falling sequencing prices make it possible to study this process at the genome level, triggering a methodological revolution extending also to non-model organisms. However, bioinformatics

and research strategies are becoming increasingly challenging for single groups and therefore progress may benefit from coordinated efforts.

The aim of the symposium is bringing researchers together to present and discuss current developments in this field, and possibly find common strategies concerning infrastructure and funding. Besides for the presentations of the invited speakers a number of short talks will be available for presenting own research and projects. We invite the submission of abstracts with the registration. Attendance is free.

The symposium is organized by the project area D (Laboratory Centre & Adaptive Genomics) of the BiK-F centre (www.bik-f.de) and is aimed at everyone - student to professor - interested in this rapidly expanding field.

The meeting starts at 9 o'clock and is planned to end in the late afternoon (ca. 5 o'clock), with a possible extension to discuss projects over dinner.

Venue: BiK-F seminar room 306 Jügelhaus Mertonstrasse 17-21 60325 Frankfurt /M

Registration: Christina.reisert@senckenberg.de Information: Pfenninger@bio.uni-frankfurt.de, or axel.janke@senckenberg.de

pfenninger@bio.uni-frankfurt.de

KansasStateU Genomics Oct26-28

The 10th Annual Ecological Genomics Symposium

This year marks the 10th anniversary of the Ecological Genomics Symposium and we have put together an outstanding and extended lineup of thirteen speakers that will cover the latest research results as well as a retrospective on progress in Ecological Genomics over the last 10 years and challenges and opportunities for the future. Symposium details can be found at ecogen.ksu.edu/symp2012.

FEATURED SPEAKERS: Jennifer Brisson - University of Nebraska William Cresko - University of Oregon Scott Edwards - Harvard University Martin Feder - University of Chicago Loretta Johnson - Kansas State University Jan Kammenga - Wageningen University Thomas Mitchell-Olds - Duke University Jeanne Serb - Iowa State University Jack Schultz - University of Missouri Emilie Snell-Rood - University of Minnesota John Werren - University of Rochester Christopher Wheat -

Stockholm University Tom Whitham - Northern Arizona University Patricia Wittcop - University of Michigan

POSTER SESSIONS: A poster sessions will be held on Friday evening and Saturday afternoon. Poster topics should be related to the field of Ecological Genomics. A LIMITED NUMBER OF SUBMITTED POSTER ABSTRACTS WILL BE SELECTED FOR ORAL PRESENTATIONS.

Funding for this symposium is provided by The National Science Foundation and Kansas State University.

Kansas State University, Division of Biology, 116 Ackert Hall, Manhattan, KS 66506-4901 ecogen.ksu.edu

Theodore J Morgan, Associate Professor Mail: Division of Biology, 116 Ackert Hall, Kansas State University, Manhattan, KS 66506 Office: 785.532.6126, Molecular Lab: 785.532.6074, Fly Lab 785.532.6416, Fax: 785.532.6653 Email: tjmorgan@ksu.edu, Skype: morganlab.ksu, www.ksu.edu/-morganlab tjmorgan@ksu.edu

KansasStateU Genomics Oct26-28 TravelAwards

The Ecological Genomics Institute at Kansas State University is pleased to announce funding for student and postdoc travel fellowships to attend the 10th Annual Ecological Genomics Symposium. Application and symposium details are below or can be found at ecogen.ksu.edu/symp2012. We look forward to seeing everyone October 26th to the 28th in Kansas City.

Travel Fellowships for the 10th Annual Ecological Genomics Symposium

The Ecological Genomics Institute (ecogen.ksu.edu) at Kansas State University has funds to support student and postdoc travel fellowships to attend the 10th Annual Ecological Genomics Symposium (ecogen.ksu.edu/symp2012) in Kansas City from October 26th to the 28th 2012.

The fellowships are supported by the U.S. National Science Foundation (IOS-1244871) with the goal of increasing the cultural and scientific diversity of the young scientists at the symposium.

Your application packet must include each of the following:

1. A statement that you are a United States citizen or permanent resident who is currently enrolled in a MS or PhD program or working as a postdoctoral researcher in the United States.
2. A title and abstract for a poster to be presented by the applicant.
3. A short CV/resume. Please include your gender and race and ethnicity for NSF reporting.
4. A paragraph on why you are interested in attending the symposium.
5. A brief letter of recommendation from your advisor submitted under separate cover. The letter should be sent to dmerrill@k-state.edu by Monday, September 17, 2012.

Complete application (items 1 to 4) should be submitted as a single pdf document to dmerrill@k-state.edu. The deadline for submission is Monday, September 17, 2012

For questions about the application contact Ted Morgan at tjmorgan@ksu.edu or 785-532-6126

Theodore J Morgan, Associate Professor Mail: Division of Biology, 116 Ackert Hall, Kansas State University, Manhattan, KS 66506 Office: 785.532.6126, Molecular Lab: 785.532.6074, Fly Lab 785.532.6416, Fax: 785.532.6653 Email: tjmorgan@ksu.edu, Skype: morganlab.ksu, www.ksu.edu/-morganlab tjmorgan@ksu.edu

Madison EvoSysBio Jul30-Aug1

Dear All,

For those with an interest in interdisciplinary meetings, here is a perfect excuse to visit beautiful Madison, Wisconsin at short notice.

>From July 30 to Aug 1, 2012 will be the first meeting on Evolutionary Systems Biology with an associated workshop on modeling languages at the University of Wisconsin-Madison:

<http://evolutionarysystemsbiology.org/meeting/2012-Madison/> The purpose of the EvoSysBio meeting is to explore, how to best bring together evolutionary biology and current systems biology and what new insights might result from this. Evolutionary systems biology analyses critically depend on our ability to build and analyze quantitative models of dynamical

systems. Many important questions will require such quantitative analyses on scales that demand full automation. Appropriately designed problem specific programming languages are a powerful way for achieving such automation. The purpose of the associated workshop on modeling languages is to collect examples for what analyses might be desirable and how a modeling language might look like that could facilitate this. This is a place where you can say what you want! This discussion will inform future development of evolix, a new user friendly model description language currently under development in the Evolutionary Systems Biology Group at UW-Madison.

The meeting is free, but registration is required for catering and other reasons. Registration will be open until July 21 and is easy, see link on website.

Posters can be contributed until July 21 and there is still the possibility to compete for a very small number of talks.

We expect many exciting interdisciplinary discussions and look forward to seeing you in Madison!

All the best, Laurence Loewe

– Laurence Loewe Assistant Professor Evolutionary Systems Biology Group Laboratory of Genetics and Wisconsin Institute for Discovery University of Wisconsin-Madison 330 North Orchard Street, Madison, WI 53715, USA <http://evolution.ws/people/loewe>
Tel: +1-608-316-4324

loewe@wisc.edu

Mainz Germany PlantEvol Sep16-19 DeadlineExt

Dear Colleagues,

This is to inform you that registration and abstract submission for the

21st International Symposium Biodiversity and Evolutionary Biology of the German Botanical Society

(16th - 19th September at Mainz/Germany) - <http://www.biodivevol2012.uni-mainz.de/> has been extended to 15 July.

We are looking forward to seeing you in Mainz!

Joachim W. Kadereit

Prof. Joachim W. Kadereit, Ph.D. Institut für Spezielle

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3923524

gehrke@uni-mainz.de

Marseilles 16thEBM Sep18-21 FinalProgram

The “16th Evolutionary Biology Meeting at Mar-
seilles ” final program is available: [http://sites.univ-
provence.fr/evol-cgr/](http://sites.univ-provence.fr/evol-cgr/) Few spots (4) for poster presen-
tations are available

Best regards

Pierre Pontarotti

Pierre PONTAROTTI <Pierre.Pontarotti@univ-
provence.fr>

Marseilles 16thEBM Sep18-21 Program

The 16th Evolutionary Biology Meeting at Marseilles
program will be available the 07/06 see : [http://-
sites.univ-provence.fr/evol-cgr/](http://sites.univ-provence.fr/evol-cgr/) few spots are available
for poster presentation

best regards Pierre Pontarotti

Pierre PONTAROTTI <Pierre.Pontarotti@univ-
provence.fr>

Miami IntlBiogeographySociety Jan9-13

Registration is now OPEN for the 6th Biennial Confer-
ence of the International Biogeography Society Miami,
Florida, USA; 9-13 January, 2013

For more information about the conference, and to reg-
ister, please visit [http://www.biogeography.org/html/-
Meetings/2013/index.html](http://www.biogeography.org/html/-Meetings/2013/index.html) .

The meeting has four successive SYMPOSIA (10th &
11th January) on broad foundational and cutting-edge
topics and approaches in biogeography and macroecol-
ogy, each with a suite of leading international scientists
and *openings for contributed papers*:

1. Island Biogeography: New Syntheses (Organizers:
Robert Whittaker & Kostas Triantis).
2. Beyond
Bergmann: New Perspectives on the Biogeography of
Traits (Organizers: Adam Algar & Nathan G. Swen-
son).
3. The Convergence of Conservation Paleontol-
ogy and Biogeography (Organizers: Jenny McGuire &
Edward Davis).
4. Predicting Species and Biodiversity
in a Warmer World: Are We Doing a Good Job? (Or-
ganizers: Antoine Guisan & Niklaus E. Zimmermann).

Keynote lectures will be given by Dr. James H. Brown,
after receiving the Alfred Russel Wallace Award in
recognition of his lifetime of outstanding contributions
to biogeography, and Dr. Miguel B. Araújo, after re-
ceiving the MacArthur & Wilson Award in recognition
of his innovative early career contributions to biogeog-
raphy.

The meeting also has 12 sessions of CONTRIBUTED
PAPERS (12th January) and continues to feature its
priority POSTER SESSIONS (10th & 11th January)
sampling the widest diversity of research in biogeogra-
phy.

In addition, before the meeting, on 9th January, five
WORKSHOPS will be held: 1. Biodiversity Informat-
ics 2. Communicating Biogeography 3. Biogeography
of Stress 4. Popular Science Writing 5. Bayesian Sta-
tistical Analysis.

On 9th & 13th January arranged FIELD EXCUR-
SIONS will visit sites of Florida’s characteristic bio-
diversity.

Check out the IBS meeting website for more details
and to register ([http://www.biogeography.org/html/-
Meetings/2013/index.html](http://www.biogeography.org/html/-Meetings/2013/index.html))

The INTERNATIONAL BIOGEOGRAPHY SOCI-
ETY (IBS; <http://www.biogeography.org/>) is a non-
profit organization, founded in 2000, with the mis-
sion to: - Foster communication and collaboration be-
tween biogeographers in disparate academic fields. -
Increase both the awareness and interests of the sci-
entific community and the lay public in the contribu-
tions of biogeographers. - Promote the training and
education of biogeographers so that they may develop
sound strategies for studying and conserving the world’s

biota. + As part of this mission, the IBS publishes the Open Access journal *Frontiers of Biogeography* (<http://www.escholarship.org/uc/fb>).

Michael Dawson <mdawson@ucmerced.edu>

dawson.mn@gmail.com

UCalifornia SantaBarbara EvolutionMulticellularity Feb4-8

Cooperation and Major Evolutionary Transitions
DATES: Feb 4, 2013 - Feb 8, 2013

Registration deadline is: Jan 7, 2013

Conference begins: 8:00am Feb 04, 2013 with registration.

Registration includes: Daily refreshment breaks, lunches and two Special Events Dinners.

Registration Fee: \$300 Fee Due: Jan 4, 2013 Late Registration Fee: \$350

Contact Information: kitpconf@kitp.ucsb.edu

Cooperation and the Evolution of Multicellularity Coordinators: David Bensimon, Pierre Durand, Cassandra Extavour, Greg Huber

Cooperation between individuals occurs throughout the biological world. It is one of the most intriguing and least understood phenomena despite its profound consequences and its enduring impact on the history of life. Strikingly similar patterns of cooperative behavior appear across the hierarchies of biological structures: genes have cooperated to form genomes, cells can be organized into multicellular organisms, organisms into societies, and species into ecologies. While analogies between mechanisms of cooperation at different levels of organization suggest themselves, general principles have been difficult to pin down. The evolution of biological complexity, the premier example of which is the origin of multicellularity, involves countless interactions between individuals and the fundamental question remains: Why and how do individuals at one level cooperate to form increasingly more complex levels of biological organization?

There are signs that the study of cooperation and its evolution is entering a new period, as theoretical advances meet with advances in molecular biology, genomics and cell biology. The new tools and technologies available to observe and manipulate genes, cells,

microorganisms and collectives have resulted in new experimentally tractable systems and new data to probe classical ideas of fitness, the structure of communities, and the evolution of cooperation. To integrate these advances, this conference brings together eminent researchers in a variety of disciplines; from philosophers and theorists, to genomicists, physicists and molecular biology empiricists. The aim is to draw on a range of expertise revolving around the central notion of cooperation, where we hope the interplay of theory and experiment can provide the foundation for new collaborative work in the field. The conference is provisionally divided broadly into 5 groupings: (i) Cooperation and major evolutionary transitions; (ii) Origin and evolution of genomes: selfish genes, cooperative genes and the origin of life; (iii) Co-evolution of protein interactions; (iv) Mutualisms and molecules: Mitochondria and chloroplasts; and (v) Evolution of sex/ insect societies.

KAVLI INSTITUTE FOR THEORETICAL PHYSICS
KOHN HALL UNIVERSITY OF CALIFORNIA
SANTA BARBARA CA 93106-4030

Phone: (805) 893-6306

<http://www.kitp.ucsb.edu/activities/dbdetails?acro=-multicell-c13> Jocelyn Quick, jocelyn@kitp.ucsb.edu
Jocelyn Quick, jocelyn@kitp.ucsb.edu

ULisbon PrimateEvolution Sep10-12 ExtDeadline

Extended Deadline, Final Call for abstracts

>From grooming to speaking: recent trends in social primatology and human ethology

Centre for Philosophy of Science, University of Lisbon, Portugal | September 10-12th, 2012.

Conference website http://cfcul.fc.ul.pt/linhas_investigacao/-Philosophy%20of%20Life%20Sciences/int_col/-index.htm Plenary talks Johan Bolhuis, Constança Carvalho & Luis Vicente, Augusta Gaspar, Nathalie Gontier, Mary Lee Jensvold, Simone Pika, Tim Racine, Jeroen Stevens, Jordan Zlatev.

Abstracts of the talks are now available online.

CFA: deadline July 8th We call for primatologists, ethologists, anthropologists, sociobiologists, evolutionary, cognitive and comparative psychologists, biolin-

guists, evolutionary linguists, bio-ethicists, philosophers and historians of science, to provide talks on: 1. Historical reviews on the introduction and use of primate studies to acquire knowledge on the origin and evolution of communication and language 2. Methodologies of primate communication and language research 3. Theories on primate communication and the evolution of language 4. Ethical issues in social primatology and human ethology

Abstracts can be send to Ricardo Santos: rssantos@fc.ul.pt

The author of the best abstract will be awarded a Springer Book Voucher for the worth of 180 euro. And a selection of talks will be published in an anthology for the Springer Book Series "Interdisciplinary Evolution Research".

Scientific committee Rod Bennison, Rudie Botha, Massimiliano L. Cappuccio, Daniel Dor, Luc Faucher, Nathalie Gontier (chair), David Leavens, Robert Lickliter, Jorge M.L. Marques da Silva, Mark Nelissen, Eugenia Ramirez Goicoechea, Emanuele Serrelli, Chris Sinha, James Steele, Ian Tattersall, Natalie Uomini, Arie Verhagen, Luis Vicente.

nathalie.gontier@vub.ac.be

Vigo Spain Phylogenomics Sep13-14

Dear all,

Thanks to additional funds, REGISTRATION IS FREE now for the

Computational and Statistical Phylogenomics meeting Vigo, Spain, September 13-14, 2012

<http://csphylo12.uvigo.es/> EXTENDED DEADLINE: 29 JULY

There will be invited talks by some of the most relevant scientists in the field, but no contributed talks. Confirmed speakers are: Guy Baele (Belgium), Bastien Boussau (USA), Oliver Eulenstein (USA), Olivier Gasuel (France), Lars Jermin (Australia), Laura Kubatko (USA), Jens Lagergren (Sweden), Nicolas Lartillot (Canada), Leo Martins (Spain), Luay Nakleh(USA), Alexis Stamatakis (Germany), Tandy Warnow (USA) and Ziheng Yang (UK).

Besides the science, we will organize some social activities, like a visit to a National Park nearby at the astonishing Cies Islands. For any questions, please contact us at csphylo12@gmail.com.

All the best,

David Posada University of Vigo Spain

dposada@uvigo.es

Fax: +34 986 812556 Email: dposada@uvigo.es Web: <http://darwin.uvigo.es> dposada@uvigo.es

GradStudentPositions

AarhusU PrimateEvolutionaryGenomics	10	UAntwerp EvolutionaryEcolBegging	16
Amsterdam EvolutionaryBiol	10	UBasel EvolutionarySociogenomics	17
BangorU Metagenomics	12	UBourgogne AvianSexualSelection	18
Berlin AmphibianSexChromosome evolution	12	UEastAnglia EvolutionFruitflies	19
ETH Zurich TropicalConservationGenetics	13	UEdinburgh HostParasiteInteractions	19
Ireland MetagenomicsBioinformatics	14	UEdinburgh NextGenGenomics	20
McGillU 2 EcolGenomics	15	UFZ Halle Germany PopGenetics	21
MemorialU MarinePopulationGenomics	15	UGeneva EvolutionaryBiol	22
RyersonU PlantEvolution	16	UGottingen EvolutionMolluscPigments	23

UHalle HostParasiteEvolution	23	UStirling 2 MusselOrigins	27
ULausanne EvolutionParthenogenesis	24	UUppsala MolEvol	27
ULouvainLaNeuve BehaviourEvol	24	UValencia EvolutionaryBiology	29
UMassey Auckland YeastSpeciesInteractions	25	UZurich EvolutionaryBiology	29
UPolitecnicaMadrid ViralEvolution	26	UmeaU ForestPopulationGenomics	29
UStAndrews ChordateEvolution	26		

AarhusU PrimateEvolutionaryGenomics

PRIMATE EVOLUTIONARY GENOMICS Applications are invited for a PhD fellowship/scholarship at the Graduate School of Science and Technology, Aarhus University, Denmark, within the Computer Science programme available from 1 November 2012.

Research area and project description:

A PhD position is vacant for a candidate with an interest in evolutionary genomics of humans and other primates and its application to gene function and human health. Full genome sequences are available for population samples of all great ape species/subspecies. Projects are available in modelling and inferring patterns of natural selection, e.g. on non coding RNAs, in contrasting selection on the sex chromosomes and the autosomes, and in applying evolutionary thinking to the field of association mapping, all with many possible collaborative links with wet labs at the Faculty of Health and the Faculty of Science and Technology. Candidates with an interest in taking the results of analysis to functional experiments are encouraged to apply.

Place of Employment and Place of Work:

Bioinformatics Research Center and, iSEQ interdisciplinary sequencing centre, Aarhus University, DK-8000 Aarhus C, Denmark.

Contacts:

Applicants seeking further information are invited to contact:

Professor Mikkel Heide Schierup, Bioinformatics Research Center and, iSEQ interdisciplinary sequencing centre, Aarhus University, DK-8000 Aarhus C, Denmark, Tel.: +45 27782889, e-mail mheide@cs.au.dk

Application procedures:

Please apply for this specific project here:

<http://talent.au.dk/phd/scienceandtechnology/>-

opencalls/ Choose August 2012 Call with deadline 1 August 2012.

You will be directed to the call, and must choose the programme 'Computer Science' Then you must fill out the information regarding:

Personal information Academic background Admission Financing (if any) Study: In the dropdown menu you must choose the project: "Primate evolutionary genomics"

Source (how you found out about the call) References (as a minimum 1 must be uploaded) Application material (pdf only, max 20 MB, no zip): Motivation, CV, Diploma and transcript of records, project description

Please be aware that you cannot save the application and continue working on it later. Therefore, you must have all relevant appendices, attachments, addresses for referees, etc. ready when you apply, as the entire application must be uploaded to the system in one go.

As a minimum you need to upload the application material:

one reference letter curriculum vitae, motivation (max. 1 page) transcripts and diploma(s) in one merged file. Please enter your unweighted grade average calculated and based on your transcript's grading scale, BSc and MSc separately. project description (1½-2-4 pages) For technical reasons, you must upload a project description. When - as here - you apply for a specific project, please simply copy the project description above, and upload it as a PDF in the application

You cannot submit the application if one or several of these documents have not been uploaded.

Mikkel Heide Schierup <mheide@birc.au.dk>

Amsterdam EvolutionaryBiol

PhD Position in Evolutionary Biology (f/m)

For 1,0 fte (full time) Vacancy number 1.2012.00171

Project title 'Promiscuous snails with complex weaponry: Physiology and evolution of love dart shooting'

Available position A 4-year NWO-funded PhD position is available in the department of Ecological Science of Faculty of Earth and Life Sciences (FALW). The project is funded by the Netherlands Organisation for Scientific Research (NWO) and is a collaboration between VU University Amsterdam (group of Dr. Joris M. Koene) and the Netherlands Centre for Biodiversity 'Naturalis' in Leiden (group of Prof. Menno Schilthuizen). The PhD candidate will be based in Amsterdam but will also spend time in Leiden (e.g., for use of the collection) and abroad (for field work).

Description of the project Sexual conflict plays a crucial role in shaping the evolution of many behaviours and processes involved in reproduction. The project will take an integrative approach to investigating the effect of sexual conflict on reproductive processes in simultaneous hermaphrodites. The focus will lie on one of the most prominent examples of extreme mating behaviours in hermaphrodites, the shooting of love darts in lands snails. We aim to investigate simultaneously physiology, sperm transfer, dart shooting behaviour, and reproductive anatomy of different species. In doing so, we will examine the generality of the function of the love dart and integrate this with behavioural and morphological data. We expect the results to contribute significantly to our understanding of sexual conflict in hermaphrodites as well as the evolution of bizarre reproductive strategies in general.

Tasks Executing scientific research as detailed in the project description; publishing results of the research in peer-reviewed scientific journals as well as in a thesis; assisting in undergraduate courses given within the department of Ecological Science; following the PhD educational programme as prescribed by the department.

Requirements MSc degree in Biology; advanced courses in molecular biology, evolution, animal physiology or equivalent; proficiency in both written and spoken English; ability to work efficiently, independently as well as in collaboration, and high motivation will be assets.

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. E.g., remuneration of 8,3% end-of-year bonus and 8% holiday allowance; possibilities to save up holidays for sabbatical leave; generous contribution (70%) commuting allowance based on public transport.

Faculty FALW offers a range of Bachelor and Master programmes. Research at the faculty focuses on the fields of the life sciences, health sciences, environmental sciences and earth sciences. World-class teaching and cutting-edge research activities go hand in hand. FALW works together with other faculties like medicine, exact sciences, economics, psychology and social sciences. The faculty's research facilities can be categorized as excellent. The faculty's international focus fosters cross-border collaboration, leading to substantially improved quality and greater impact of our research results

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 85) based on a full-time employment.

Information Further information and the complete project description can be obtained from the project leader, Dr. J.M. Koene, joris.koene@vu.nl

Application Applicants are requested to write a letter in which they describe their abilities and motivation, accompanied by a curriculum vitae and two references with contact details before August 15, 2012. If possible a copy of your graduate work and/or reprints of published work can be included. Only complete applications will be considered and should be sent (preferably in one single digital pdf file) by e-mail to vacature.falw@vu.nl Only if absolutely necessary, the application can be sent via regular mail to: VU University Amsterdam, Faculty of Earth and Life Sciences, attn.: Dr. Y.K.M. Kops, managing director, De Boelelaan 1085, 1081 HV Amsterdam, The Netherlands.

Please mention the vacancy number in the e-mail header or at the top of your letter and on the envelope.

Dr. Joris M. Koene <http://www.joriskoene.com> VU University - Ecological Science De Boelelaan 1085, 1081 HV Amsterdam, THE NETHERLANDS tel: +31 (0)20 5987095 joris.koene@vu.nl

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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>

PhD position: Understanding the microbial (metagenomic) biodiversity underpinning the release of carbon from peatland ecosystems.

Applications are invited for a PhD studentship, fully funded for three years by the HPC Wales/Fujitsu collaboration (<http://www.hpcwales.co.uk/>) for full-time study based in the Molecular Ecology and Fisheries Genetics Laboratory (<http://mefgl.bangor.ac.uk>), School of Biological Sciences, supervised by Dr Simon Creer (<http://mefgl.bangor.ac.uk/si.php>) in collaboration with Prof. Peter Golyshin, Prof. Chris Freeman, Dr. Nathalie Fenner and Dr. James McDonald, to start on the 1st October 2012.

Summary of project: Peatlands constitute the most important, long-term, terrestrial organic carbon store on our planet. Moreover, because production rates exceed decomposition rates, peatlands in many regions are still actively sequestering carbon, highlighting both the historical and contemporary global ecological importance of these fragile ecosystems. Thus, in their natural waterlogged, low-oxygen state peatlands represent an unrivalled terrestrial carbon store. However, it has been shown that under cycles of drought conditions, the stored carbon is released as gaseous CO₂ into the atmosphere and dissolved organic carbon (DOC) into surrounding waterways, contributing to global warming, net loss of C from peatland and reduced drinking water quality. Although it has been shown that the microbial community underpins the cascade of events responsible for drought-induced carbon emission, the composition of microbial communities driving the mineralization of organic matter and the underlying mechanisms responsible for the biogeochemical cascade remain unknown.

Aims and objectives In this PhD programme, we will use combinations of shotgun environmental metagenomic Illumina sequencing (<http://www.illumina.com/index.ilmn>) and biogeochemical assays to identify links between both the taxonomic composition and functional diversity of the microbial communities and drought-driven carbon loss from a range of experimental peatland ecosystems.

Summary of research environment The successful applicant will join the large, thriving team in the MEFGL (<http://mefgl.bangor.ac.uk/>) 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 and close proximity to the Wolfson Carbon Capture Laboratory (<http://wcc.l.bangor.ac.uk/index.php>), second and third gen-

eration sequencing capability at the Liverpool Centre for Genome Research (<http://www.liv.ac.uk/genomic-research/>) and access/bioinformatic development capability on the HPC Wales supercomputing genomics gateway.

Area 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.

Funding and eligibility The studentship is open to all applicants and includes a tax-free maintenance grant of £14k per annum, but with full-time fees paid for UK and European residents only. International fee applicants will be required to pay the difference between the UK/EU fee of £4,009 per annum and the international fee of £12,800 per annum.

Further details are available here <http://mefgl.bangor.ac.uk/opportunities.php> Informal enquiries 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 17th August 2012 and the proposed assessment schedule is as follows: short-listed applicants will be notified by 20th August to attend an interview (physical or electronically), initially scheduled to occur on the 24th August, with an anticipated start date of 1st October 2012.

With thanks and best wishes Brian, as always

Simon

– Simon Creer Lecturer 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://mefgl.bangor.ac.uk/si.php> “Creer,Simon”
 <s.creer@bangor.ac.uk>

Berlin AmphibianSexChromosome evolution

The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) invites applications for a:

PhD position on amphibian sex chromosome evolution

A three-year-PhD position in evolutionary biology is available at the Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) in Berlin, funded by the German Research Foundation (DFG). The PhD student will be affiliated with the Humboldt University of Berlin, and working with Matthias Stoeck on the evolution of sex chromosomes of amphibians. We use next generation sequencing (NGS) genome data to develop molecular genotyping and sequence markers that will be applied in sibship and population genetics analyses to study the evolution of homomorphic sex chromosomes. Applications to endocrine disruptive substances of none-model anuran species are planned.

Requirements: We are looking for an enthusiastic, empirical and "organismal" PhD student with a master or diploma in (evolutionary) biology, experience with molecular wet lab approaches (PCR, genotyping, cloning), population genetics analyses, ideally experience with bioinformatics analyses of NGS data, and experience to work with live amphibians or fish.

Salary will be paid according to the TVöD for a 50% position. In keeping with the IGB's policy regarding gender equity, female applicants are particularly encouraged; disabled people with identical qualifications will be favored.

Please, send a motivation letter including research interests and experience, CV, and the email-addresses of at least two referees via email to: matthias.stoeck@igb-berlin.de by August 10, 2012.

Leibniz-Institute of Freshwater Ecology and Inland Fisheries in the Forschungsverbund Berlin e.V. Department of Ecophysiology and Aquaculture Dr. Matthias Stoeck Müggelseedamm 310, D-12587 Berlin, Germany

The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) is the largest freshwater ecology research institute in Germany. It is a member of the Forschungsverbund Berlin e.V. and the Leibniz-Association (www.wgl.de). The FVB manages eight large research institutes in Berlin that have close links to all three universities in the German capital. IGB offers excellent laboratory and field facilities for interdisciplinary research, large-scale experimental facilities, long-term research programs and data sets.

References: Colliard C., Sicilia A., et al., and M. Stoeck (2010): Strong reproductive barriers in a narrow hybrid zone of West-Mediterranean green toads (*Bufo viridis* subgroup) with Plio-Pleistocene divergence. *BMC Evolutionary Biology* 10: 232 (19 pp).

Stoeck M., Horn A., Grossen C., et al., and N. Perrin

(2011): Ever-young sex-chromosomes in European tree frogs. *PLoS Biology* 9 (5): e1001062.

Stoeck M., Croll D., Dumas Z., Biollay S., Wang J., and N. Perrin (2011): A cryptic heterogametic transition revealed by sex-linked DNA markers in Palearctic green toads. *J. Evol. Biol.* 24: 1064-1070.

Links: <http://www.igb-berlin.de/> <http://www.unil.ch/dee/page40037.html>
<http://www.unil.ch/dee/page40038.html>

Matthias Stoeck <matthias.stoeck@unil.ch>

ETH Zurich TropicalConservationGenetics

A fully funded PhD studentship in tropical plant ecology and conservation genetics, ETH Zurich, Switzerland

Project: Demographic and genetic processes underlying regeneration in coco de mer (*Lodoicea maldivica*) the largest seeded plant in the World

Start Date: November 1st, 2012

Summary: The endangered Seychelles palm *Lodoicea maldivica* (coco de mer), is a truly remarkable plant species, producing the largest seeds in the plant kingdom. The nuts are traded commercially being the most valuable in the world, with virtually all nuts harvested for commercial use. Despite its extraordinary ecological and economic significance, very little is known about the reproductive ecology and regeneration of the coco de mer. With virtually no seed dispersal (the seeds fall directly below the mother plant), it can be seen as an evolutionary endpoint in a spectrum of dispersal strategies among higher plants. This project will apply molecular ecological methods and detailed field ecological surveys to investigate the role of dioecy, pollen dispersal and restricted seed dispersal in shaping the patterns of genetic diversity, demographic structure and fitness in this extraordinary species. The results of this study will contribute directly to the conservation and management of coco de mer, but will also have broader relevance to our understanding of the genetic consequences of habitat fragmentation in plant species with limited seed dispersal.

Location: ETH Zurich, Switzerland, with fieldwork on Praslin Island, Seychelles. The Primary affiliation of this project will be the Ecosystem management Group,

ETH, Zurich.

Supervisors: Dr. Chris J Kettle (Ecosystem Management, ETH Zurich), Prof. Dr. Peter Edwards (Plant Ecology, ETH Zurich), Dr Christopher Kaiser-Bunbury (Aarhus University, Denmark). The project will be conducted in close collaboration with the Seychelles Islands Foundation (SIF < <http://www.sif.sc/> >), with local co-supervision from Dr Frauke Fleischer-Dogley.

Requirements: Highly motivated, with a desire to work on tropical plant ecology and conservation as part of a dynamic team. You will have a good B.Sc and M.Sc degree, in Ecology, Evolutionary biology, or a related field, with experience in experimental ecology, statistics, and molecular laboratory work. Spoken and written English required, knowledge of German and French would be advantageous. Applicants should enjoy working in a challenging tropical field conditions as well as in the lab. Climbing skills would be an advantage. Independence and self-reliance in often difficult working conditions, are essential, as well as an ability to interact well with a team of local and international staff.

The Group: We offer a dynamic and stimulating scientific environment with world-class facilities. Our group of scientists and students is international in composition, and tackles a range of multi-disciplinary topics relating to plant ecology, conservation and ecosystem management. See our web site for more details (www.ecology.ethz.ch). The successful candidate will also be embedded in the scientific and conservation community in the Seychelles, hosted and supported by SIF.

Conditions of Employment: Three years appointment at ETH, Zurich (funded at the ETH Zurich PhD student salary scale). The position is to be based in Zurich with extended periods of field work in the Seychelles. The PhD student may be required to do some course work at ETH Zurich as part of the entry requirement. This position is open to suitable candidates of all nationalities.

Application: Please send a letter of motivation, outlining why you are interesting in this PhD, full CV and names and addresses of two academic referees to Ankara Chen by e-Mail (info.em@env.ethz.ch). Please quote CDM in the subject line. Closing date for applications is 15 August 2012. We expect to interview short-listed candidates in early September

For informal enquires contact Chris Kettle chris.kettle@env.ethz.ch or further details click here < <http://www.ecology.ethz.ch/-ETH.PhD.ad.CDM.2012.pdf> >

Dr Chris J Kettle < <http://www.ecology.ethz.ch/-people/obass/ckettle> > Lecturer and Senior Sci-

entist Department of Environmental Systems Science < http://www.usys.ethz.ch/index_EN > ETH Zurich < http://www.ethz.ch/index_EN > Switzerland www.chris-kettle.com < <http://www.chris-kettle.com/> >

Kettle Chris <chris.kettle@env.ethz.ch>

Ireland Metagenomics Bioinformatics

PhD Studentship in Ireland - Metagenomics / Bioinformatics

Research area: Metagenomic analysis of rumen microbial communities.

A Walsh Fellowship (4-year) is available to work on an inter-institutional project between Teagasc (Animal & Bioscience Research Department, Grange, Co. Meath, Ireland) and The Institute of Biological, Environmental and Rural Sciences (IBERS), Aberystwyth University, Wales. The project is part of a consortium funded by The New Zealand Fund for Global Partnerships in Livestock Emissions Research.

This PhD project will involve the application of network-based approaches to analyse metagenomic sequencing data from rumen microbial communities. The primary focus of the study will be to understand the interactions in the rumen microbial community that effect changes in methane production. The appointee will join a strong interdisciplinary team of computational and molecular biologists in the new Animal and Bioscience Research Department in Teagasc.

Ideal candidates should have a science related degree (2.1-1st) in a molecular biological, microbiological, agricultural or computational subject, preferably with experience in multiple disciplines. Candidates should be enthusiastic and willing to work as part of a multi-disciplinary team of scientists. Candidates with experience in programming in perl/python/C/C++/java are desired, but students with a strong molecular biology/genetics/microbiology background and a demonstrable willingness to learn computational approaches/programming are also encouraged to apply.

The stipend is valued at euro 21,000 per annum (including fees). Those appointed will be based at the Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath, Ireland.

The Animal and Bioscience Research Department, is

a major new initiative to expand Teagasc's capacity for bioscience research within its animal science research programme. For more information see <http://www.teagasc.ie/animalbioscience/> The closing date for applications is 17st August 2012.

Interested candidates should forward a letter of interest and curriculum vitae including the names and addresses of at least two referees by e-mail to:

Dr Chris Creevey, Animal and Bioscience Research Department Teagasc, Grange, Dunsany, Co. Meath, Ireland. chris.creevey@teagasc.ie

chris.creevey@gmail.com

McGillU 2 EcolGenomics

McGill University. 2. Ecological Genomics

Two PhD positions in Ecological Genomics beginning January 2013 are available in the Biology Department at McGill University. The projects will involve studying multiple stressors in aquatic environments (e.g., metals, calcium decline, invasive species) with special emphasis on the genetics of local adaptation and habitat transitions. We are using a combination of ecological and genomics approaches to address broad environmental and evolutionary questions related to the evolutionary forces that shape biodiversity and the health of freshwater ecosystems.

We are looking for highly motivated graduate students. Candidates should have strong background in ecology, evolution, strong quantitative skills and demonstrate interest in team-based, interdisciplinary projects. International students with high academic achievements will also be considered.

We offer competitive stipend as well as versatile professional development under the NSERC CREATE training program in Aquatic Ecosystem Health housed at the University of Windsor, the Great Lakes Institute for Environmental Research: <http://www.uwindsor.ca/erasmus-create/> Interested student should send their CV, a brief statement of research interest, and a list of 3 references to Dr. Melania Cristescu at Email: mcris@uwindsor.ca.

Melania E. Cristescu Associate Professor Director, NSERC CREATE Training Program in Aquatic Ecosystem Health University of Windsor Great Lakes Institute for Environmental Research/Biology 401 Sun-

set Ave Windsor Ontario Canada N9B 3P4

Phone: (519) 253-3000 Ext. 3763 FAX: (519) 971-3616

E-Mail: mcris@uwindsor.ca www.uwindsor.ca/glier/-melania-cristescu

www.uwindsor.ca/erasmus-create

Melania Cristescu <mcris@uwindsor.ca>

MemorialU MarinePopulationGenomics

Graduate student positions (MSc and PhD) and post-doctoral fellowship in population genomics and molecular ecology of marine organisms

Join a team investigating the genomic basis of population structure and adaptation in anadromous and marine species in the western North Atlantic based in St. Johns Newfoundland, Canada. This funded program will use RAD-seq to examine adaptive divergence in Atlantic salmon, green crab, sea scallop (and possibly others). This project is a joint venture of Memorial University, the Bedford Institute of Oceanography, and the Northwest Atlantic Fisheries Centre. The main project goal is the development and application of genomic resources for the conservation and management of aquatic resources.

Possible PhD projects include (1) the genomic architecture of divergence in threatened Atlantic salmon populations. (2) Evaluation of outbreeding and temporal changes in SNP allele frequency in salmon using archived and recent samples following contact with farm escaped salmon. Potential MSc projects include (1) Green Crab SNP development, genotyping and identification and characterization of genomic areas associated with invasion success and thermal tolerance and (2) Scallop SNP development, genotyping, and identification of genes associated with latitudinal variation in life history and climate. Other RAD-seq projects and species may be possible depending on the success of current funding applications. In addition to SNP work, microsatellite based mixed stock fishery analysis in Atlantic salmon is ongoing and suitable for student projects (PhD or MSc) on migration routes of Atlantic salmon at sea.

The proposed student experiences represent training in state of the art genomic tools and techniques while experiencing both university and government laboratory environments. Graduate students will have access to technical support both in the field and labora-

tory through government staff and expertise. Student projects are designed to address topical issues and result in peer-reviewed journal publications and student presentations at national and international meetings. This proposal represents excellent student opportunities for training and career development in biotechnical sciences and evolutionary ecology.

For details contact Dr. Ian Bradbury via email to ian.bradbury@dfo-mpo.gc.ca

Ian Bradbury <ibradbur@me.com>

RyersonU PlantEvolution

2013 Reply-To: lesley.g.campbell@ryerson.ca

Graduate Assistantship available in Plant Evolutionary Ecology and Conservation Biology

Description:

My lab is broadly interested in the evolution and conservation of plants, often focusing on plant hybridization and mating patterns. My research program broadly aims to understand the evolutionary consequences of global climate change, species invasions, and species rarity. More specifically, I study (1) the mechanisms regulating genetic diversity, phenotypic evolution, and population demography in rare and invasive plants and (2) how evolutionary processes (hybridization, adaptation) and properties (mating systems, genetic diversity) affect the ecological function of plant populations (e.g., reproduction, extinction). As such, my research touches on a variety of sub-disciplines, including conservation biology, agricultural ecology, and population dynamics using a combination of field, greenhouse, and eco-informatic approaches. Students are expected to develop their own independent projects but will also have opportunities to collaborate on funded investigations of hybridization, plant evolution, and ecological conservation in North American agricultural and natural plant ecosystems.

Ryerson's Chemistry and Biology department program boasts an exceptionally active and growing faculty. Areas of emphasis include environmental and molecular biology. Year-round financial support is available for graduate students. Toronto is an exceptionally diverse community and a wonderful place to live.

Applications: I am accepting applications from prospective MSc or PhD students to start a graduate

program in January 2013. If you are interested, please email me (lesley.g.campbell@ryerson.ca) a statement of your research interests with your CV and the names and email addresses of at least 2 references.

lesley.g.campbell@ryerson.ca

UAntwerp EvolutionaryEcolBegging

The Faculty of Sciences of the University of Antwerp is seeking to fill the following full-time (100 %) vacancy in the Department of Biology-Ethology

PhD student by the University Research Fund (BOF) in the area of Behavioural and Evolutionary Ecology

Job description You prepare a doctoral thesis in the field of Behavioral Ecology. The PhD project focuses on the evolutionary ecology of begging at the interface between mechanisms and function/evolution using avian model species (e.g. blue tits, gulls, starlings, canaries). Begging, the solicitation of food from parents the offspring, has a direct and significant effect on growth, survival, and thus ultimately on fitness. Obviously, begging for food from parents should elicit the transfer of resources, typically a greater amount than parents are selected to provide, since parents and offspring are, at least in birds, not genetically identical. Furthermore, when offspring seeks parental investment, their begging exerts a selective pressure on the parents. But begging is at the same time also a target of selection, because it is influenced by the parental response. Both behaviours should, therefore, ultimately become co-adapted. Being a agent and a target of selection, begging follows a complex evolutionary trajectory, flavoured by evolutionary conflicts of interest. Possible lines of research are: - To test important evolutionary ecological predictions in the context of evolutionary conflicts of interest, scramble competition and the honest signalling of offspring requirement - To impose (artificial) selection on begging (a) to investigate genetic covariances and correlated responses in traits that generate trade-offs or that are co-adapted and (b) to identify underlying control mechanisms via a correlated selection on physiological traits - To study the regulating role of testosterone and corticosterone, since physiological mechanisms may affect or even constrain the response to selection by linking the expression of different traits across contexts or life-history stages - To investigate what mechanisms make begging adaptive and thus improve our understanding of the evolutionary ecology of life- history traits

and fitness components Profile and requirements You hold a master degree in Biology; You are an enthusiastic, highly motivated student with a strong interest in Behavioral and Evolutionary Ecology, preferentially with previous experience in related research; You have good organizational, writing and presentation skills and should be able to work well both independently and in a team environment; We offer

A doctoral scholarship for a period of two years, with the possibility of renewal for a further two-year period after positive evaluation; The start date of scholarship will be October 1st, November 1st, December 1st 2012 or January 1st 2013; A monthly salary ranging from 2.070 - 2.120; A dynamic and stimulating group of researchers working on the interface of all 4 major aspects of animal behaviour (causation, development, function, evolution), with particular emphasis on bird family life (maternal effects, phenotypic plasticity, parent-offspring conflict & co-adaptation).

Interested? Applications may only be submitted online <<http://solliciteren.ua.ac.be/Default.aspx?vid01320&fac=7&empl0&typep&lang=en>> (vacancy number 2012AAPDOCPROEX115) and need to include a letter of motivation (approx. 250 words) and contact information of up to two referees, closing date August 12th 2012; A pre-selection will be made from the submitted applications. The remainder of the selection procedure is specific to the position and will be determined by the selection panel; The interviews will take place from August 20th until August 31st 2012; Ellen Huijser (TEL 03 265 31 45); see also www.ua.ac.be/vacatures; for questions about the profile, please contact Prof. Wendt Müller (wendt.muller@ua.ac.be), see also <http://www.ua.ac.be/wendt.muller> Wendt Müller University of Antwerp Department of Biology-Ethology Campus Drie Eiken C-127 Universiteitsplein 1 2610 Antwerp (Wilrijk), Belgium

e-mail: Wendt.Muller@ua.ac.be web: <http://www.ua.ac.be/wendt.muller> tel +32 32652292 fax +32 32652271 mobile:+32 473567276

Müller Wendt <wendt.muller@ua.ac.be>

UBasel EvolutionarySociogenomics

A fully funded PhD-position (3 years) is available at the Department of Environmental Sciences, University of Basel, Switzerland. The project is on the so-

ciogenomics of parent-offspring co-adaptation in insect families using the European earwig (*Forficula auricularia*) as experimental system. In many organisms, parental care can affect development, behavior, and fitness of offspring while the offspring can in turn influence parental care, reproduction and life-history. Such reciprocal feedback leads to selection for traits that reflect optimal - co-adapted - combinations of parent and offspring traits. The project will test this key prediction of co-adaptation models at the level of gene expression in earwigs, and it will combine manipulative experiments with modern genetic technologies (RNA-Seq and gene expression analysis)

We are seeking a highly motivated PhD-student who is fascinated by working and thinking scientifically, and who has a keen interest in the research topic and the involved experimental, molecular, bioinformatics, and statistical methods. The successful candidate should have experience working experimentally, be skilled in applied basic molecular methods (DNA/RNA isolation, PCR), be motivated to apply and further learn quantitative methods (statistics, bioinformatics), and have excellent communication and scientific writing skills in English. He/she should also be able to work independently while enjoying being part of a closely collaborating research group.

The project will be carried out in collaboration with Jean-Claude Walsler (Genetic Diversity Centre GDC, ETH Zürich) and Barbara Taborsky (Institute of Ecology and Evolution, University of Bern). The PhD-candidate will be part of a graduate research program (ProDoc) on "Proximate and ultimate causes of cooperation" funded by the Swiss National Science Foundation. This program connects research groups from five Swiss Universities in their joint venture to better understand the evolution of cooperation and social interactions. See www.prodoc-evolcoop.uzh.ch for more information.

The position requires an MSc (or equivalent) in biology, ideally with specialization in an evolutionary or genetics area. To apply, please send your application documents (preferably by e-mail and in one pdf-document) to: Prof. Mathias Koelliker, Department of Environmental Sciences, Zoology and Evolution, University of Basel: mathias.koelliker@unibas.ch.

The application should include: 1) motivation letter, 2) curriculum vitae, 3) copy of your MSc-certificate (or equivalent) including grades (or the expected date of graduation with BSc-certificate/grades if the MSc-exam is forthcoming), 4) a passage/copy of your MSc-thesis, and 5) the names and contact details of two referees.

Applications received by 29. July 2012 will receive full consideration. The preferred starting dates are 1. September or 1. October 2012.

For additional information about our group and research, please visit our website at www.evolution.unibas.ch/koelliker; you may also contact M. Koelliker directly before 18. July. phone: ++41 (0)61 267 03 79; e-mail: mathias.koelliker@unibas.ch

mathias.koelliker@unibas.ch

UBourgogne AvianSexualSelection

PhD PROPOSAL

Post-copulatory sexual selection in the houbara bustard

/A three year PhD position is available to work on a collaborative project dealing with the post-copulatory sexual selection in the houbara bustard./

In most animal species, females mate with multiple males giving rise to the potential for sperm competition and cryptic female choice. These post-copulatory components of sexual selection add to those acting on males to attract mates (pre-copulatory sexual selection).

Although the study of post-copulatory sexual selection has flourished in the last decade, there are very few biological systems that are amenable to the experimental study of sperm competition and cryptic choice.

Houbara bustards are endangered bird species living in North Africa (/Chlamydotis undulata/), Middle East and Central Asia (/Chlamydotis macqueeni/). In order to restore and reinforce natural populations of houbara in Middle East, the National Avian Research Center (NARC) has promoted a captive breeding program in Abu Dhabi (EAU) under the leadership of the International Fund for Houbara Conservation. This breeding program is based on the collection of sperm which is subsequently used to artificially inseminate females under standardized conditions (Saint Jalme et al. 1994). This allows investigating several aspects related to sperm competition and cryptic choice, in a species where both pre- and post-copulatory sexual selection is supposed to be a strong selective force. Indeed, males harbor extravagant sexual displays (Chargé et al. 2010, 2011; Preston et al. 2011) and females have been shown to mate with multiple males in the wild, where the pro-

portion of clutches sired by multiple fathers is fairly high (60%) (Lesobre et al. 2010).

In the first stage of the PhD thesis, we expect to better characterize sperm traits that determine the likelihood to successfully fertilize eggs. Then, experimental work could be conducted to explore the following questions:

- 1) Is there a trade-off between pre- and post-copulatory components of sexual selection?
- 2) Is fertilization success mostly driven by sperm competition or cryptic choice?
- 3) Is there a scope for sexual conflict in this system?

In addition to their fundamental interest, the obtained results could also be valuable with respect to the genetic management of the captive breeding. On one hand, inseminating with a mix of semen could facilitate insemination procedure by reducing the time spent to select precise pedigree and by optimizing semen utilization (mixture of small ejaculates that are usually discarded could be easily used). On the other hand, sperm competition might result in severely biased paternity with a potential for strong involuntary selection acting on breeding males.

This is a collaborative project involving the NARC (Yves Hingrat, Loic Lesobre, Tony Chalah) where all the experimental work will be carried out and where the successful applicant will spend most of the time, the French CNRS in Dijon (Gabriele Sorci) and the Museum of Natural History in Paris (Michel Saint Jalme).

Interested applicants should send a CV and the name of three references to Gabriele Sorci (gabriele.sorci@u-bourgogne.fr) and Michel Saint Jalme (mstjalme@mnhn.fr).

Salary: 1,250 euros per month. Accommodation and food is provided by the NARC with no fees for the student.

Selected articles published by the group related to the project

Chargé R. et al. 2011. Immune-Mediated Change in the Expression of a Sexual Trait Predicts Offspring Survival in the Wild. PLoS ONE 6: e25305.

Preston B. et al. 2011. Sexually extravagant males age more rapidly. Ecology Letters 14: 1017-1024.

Chargé et al. 2010. Male health status, signalled by courtship display, reveals ejaculate quality and hatching success in a lekking species. Journal of Animal Ecology 79: 843-850.

Lesobre L. et al. 2010. Conservation genetics of Houbara Bustard (Chlamydotis undulata undulata):

population structure and its implications for the reinforcement of wild populations. *Conservation Genetics* 11: 1489-1497.

Lesobre L. et al. 2010. Absence of male reproductive skew, along with high frequency of polyandry and conspecific brood parasitism in the lekking Houbara bustard *Chlamydotis undulata undulata*. *Journal of Avian Biology* 41: 117-127.

Saint Jalme M. et al. 1994. Artificial insemination in Houbara bustard (*Chlamydotis undulata*): influence of the number of spermatozoa and insemination frequency on fertility and ability to hatch. *Journal of Reproduction and Fertility* 100: 93-103.

Gabriele Sorci <gabriele.sorci@u-bourgogne.fr>

UEastAnglia EvolutionFruitflies

Novel Routes for Environmentally Benign Control of Agricultural Food Insects

A NERC CASE PhD studentship is available for October 2012 start with Tracey Chapman in the School of Biological Sciences at UEA (<http://www.uea.ac.uk/bio>) with CASE partner Oxitec (<http://www.oxitec.com>) funded through the NERC open CASE award scheme.

INTRODUCTION: Safeguarding world food supplies is a grand challenge. Central to this is the need to develop new methods for tackling pests of agriculturally important crops such as the medfly (*Ceratitis capitata*). Traditional approaches include pesticides, integrated pest management and biological control. However, each has serious drawbacks. In light of this there has been increasing interest in applying genetic modification (GM) techniques for insect control, such as the promising Release of Insects with a Dominant Lethal (RIDL) invented by the CASE partner (Oxitec). RIDL efficacy is expected to vary with key environmental (e.g. food and water availability, temperature) and intrinsic (e.g. sex ratio, frequency of resistance) factors of known importance encountered in the field. The aim of the studentship is to test hypotheses of the effect of these key factors on control via RIDL, using laboratory, glasshouse and field cage experiments.

RESEARCH PROGRAMME: Effect of diet, temperature, sex ratio and resistance on the efficacy of RIDL. The student will test in laboratory (atUEA) in glass house (at Oxitec) and in field cage experiments (in

Greece), the predictions that (i) reductions in resource levels (diet and water) will alter RIDL suppression, (ii) rising temperature will elevate then decrease male suppression potential, and (iii) a male biased sex ratio will decrease control when wild type competitor males are present. The student will also conduct novel tests for (iv) the evolution of biochemical resistance to lethal RIDLtransgenes. It is anticipated that the student will spend years 1 and 3 based at UEA and year 2 based with the CASE partner, Oxitec.

TRAINING: The studentship provides a wide-ranging, topical and challenging project with excellent training potential. Training in technical and generic skills will be supported by UEA's Personal and Professional Development (PPD) programme.

FUNDING STATUS: Directly Funded Project (UK Students Only)

SOURCE OF FUNDING: Funding is available for UK students and will cover tuition fees and provide a stipend. European Union (EU) citizens may apply but you will be eligible for a fees-only award. Please refer to the full NERC eligibility criteria at: <http://www.nerc.ac.uk/funding/available/-postgrad/eligibility.asp> **APPLICATION DEADLINE:** Position open until filled.

ACCEPTABLE FIRST DEGREE: Biological Sciences, ideally with Evolution, Genetics, Ecology focus.

CONTACT: informal enquiries to tracey.chapman@uea.ac.uk

APPLY ONLINE: <http://ueasciweb.uea.ac.uk/-Resproject/show.aspx?ID=224> Prof Tracey Chapman School of Biological Sciences University of East Anglia Norwich Research Park Norwich, Norfolk NR4 7TJ UK

Phone: + 44 (0)1603 593210 FAX: +44 (0)1603 592250 Web: <http://www.uea.ac.uk/bio/People/-Academic/Tracey+Chapman> "Tracey Chapman (BIO)" <Tracey.Chapman@uea.ac.uk>

UEdinburgh HostParasiteInteractions

The evolutionary ecology of biological rhythms in host-parasite interactions

http://www.ed.ac.uk/schools-departments/-biology/postgraduate/phdproj?tags=2&cw_xml=-

[projects.institute.php#SReece_7](#) The discovery of biological rhythms, such as circadian rhythms, in parasite behaviours [1] and host immune responses [2] suggests that timing matters for how hosts and parasites interact with each other. However, to date, the study of parasite biological rhythms has rarely considered whether parasites are organising their own schedules or whether parasites are passive and scheduled by aspects of host physiology with circadian rhythms. Furthermore, the study of circadian immune responses has largely occurred without involving disease or links to parasite behaviours. This project will bridge this divide to investigate 'what roles do the rhythms of hosts and parasites play in disease' and 'what are the consequences for host-parasite co-evolution'?

Specifically, the project will use an established disease model (rodent malaria [3-5]) to link parasite and host biological rhythms to ask the following questions: (a) What impact do circadian rhythms in immune factors have on protecting the host from disease? (b) How do host rhythms influence how successfully parasites exploit their hosts and transmit to new hosts? (c) Have parasites evolved time-keeping mechanisms to better exploit host resources or to evade immune killing? (d) Do the developmental schedules of parasites influence the outcome of competitive interactions between co-infecting parasites?

This project will synergise several disciplines across biology including the systems biology of circadian rhythms, behavioural and evolutionary ecology, evolutionary immunology. The approach will begin by collecting data from conducting experiments in the lab [e.g. 1] to elucidate the daily schedules of host-parasite interactions during infection. Depending on the student's interests, the project could develop into focusing on further experiments and/or could involve using computational biology to undertake statistical inference of disease processes [e.g. 6] to quantify the costs and benefits of rhythms to hosts and parasites, and investigate whether host rhythms drive the evolution of parasite rhythms and vice-versa.

[1] O'Donnell A.J., Schneider P., McWatters H.G. & Reece S.E. (2011) Fitness costs of disrupting circadian rhythms in malaria parasites, *Proceedings of the Royal Society of London, Series B*, 278(171): 2429-2436

[2] Keller M., Mazuch J., Abraham U., Eom G.D., Herzog E.D., Volk H.D., Kramer A. & Maier B. (2009) A circadian clock in macrophages controls inflammatory immune responses. *Proceedings of the National Academy of Sciences, USA*, 106(50):21407-12.

[3] Reece S.E., Ramiro R.S. & Nussey D.H.N. (2009)

Plastic parasites: sophisticated strategies for survival and reproduction? *Evolutionary Applications* 2(1): 11-23

[4] Pollitt L.C., Mideo N., Drew D., Schneider P., Colegrave N. & Reece S.E. (2011) Competition and the evolution of reproductive restraint in malaria parasites. *American Naturalist*, 177(3): 358-367

[5] Mideo N. & Reece S.E. (2012) Plasticity in parasite phenotypes: evolutionary and ecological implications for disease. *Future Microbiology* 7(1): 17-24

[6] Miller M.R., Raberg L., Read A.F. & Savill N.J. (2010) Quantitative analysis of immune response and erythropoiesis during rodent malaria infection, *PLoS Computational Biology*, 6(9):e1000946.

This opportunity is only open to UK nationals (or EU students who have been resident in the UK for 3+ years) due to restrictions imposed by the funding body. By 20th July interested individuals should send a pdf - one document of 3 pages which should include their CV (2 pages - include the email addresses of 2 academic referees) and a statement of research interests (1 page) directly to sarah.reece@ed.ac.uk

Dr Sarah Reece Centre for Immunity, Infection & Evolution. Institutes of Evolution, Immunology and Infection Research, School of Biological Sciences, Ashworth Laboratories, University of Edinburgh, Edinburgh EH9 3JT Scotland, UK

Tel +44 131 650 5547 Fax +44 131 650 6564

sarah.reece@ed.ac.uk <http://reece.bio.ed.ac.uk/> - The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

sarah.reece@ed.ac.uk

UEdinburgh NextGenGenomics

http://www.ed.ac.uk/schools-departments/-biology/postgraduate/phdproj?tags=2&cw_xml=-projects.institute.php Genomes from nothing: generating good genomic sequences from minute amounts of DNA

The new generation of sequencing technologies, such as Illumina, have revolutionised genetics and genomics. The cost of sequencing has dropped several thousand-fold, and large-scale sequencing is now an essential part of many biological research programmes. There is a movement to sequence the genomes of a wide range of

species in order to better understand biodiversity, to drive efforts at control or mitigation of parasite, pest and pathogen activity, and to better contextualise the human genome. For many species (for example mammals) obtaining large quantities of material and thus DNA for sequencing is not an issue, or is relatively unproblematic - one small part of a mammal yields sufficient DNA for many genomic sequencing experiments.

However, for most species, the amount of DNA in an individual is tiny (picogrammes) and so many individuals have to be pooled to generate enough for sequencing, raising the issue of sequencing many different variant genomes - not a problem if the target species is colonised or inbred, but hugely problematic if the organisms are taken from the wild. Being able to sequence from miniscule amounts of starting materials will also be of use to forensics, and in genomic epidemiology, as well as in clinical genetics.

This project will investigate and develop best practice methods for the generation of de novo genome sequences from single animals (with small genomes) using Illumina and other technologies. By optimising whole genome amplification methods [1,2] and sequencing library preparation we will take miniscule starting DNA amounts and produce good genome sequence. The whole genome amplification process will introduce its own classes of errors in the data (due to mis-amplification, chimaeric fragment production, and others) and thus the second theme of this project will be the development of optimal bioinformatics routines for the identification of errors and production of highly contiguous assemblies. The target species for this project will be model (*C. elegans*) and new Nematoda, which have genomes of 20-200 Mb, and are easily obtained. These sequences will be verified by comparison to the growing roster of completed nematode genomes generated by both 'last-generation' technology and newer approaches.

Ideal candidate: This project would best suit a biologist interested in both molecular biology and bioinformatics. The informatics component of the project will likely dominate. At the end of the project you will have learnt best practice in genome analysis, programming, use of high-performance computational resources, and developed key technologies for genomics of neglected organisms. You will be based in the Blaxter lab, Institute of Evolutionary Biology, University of Edinburgh, and will work closely with his team of evolutionary geneticists and the GenePool Genomics Facility.

For further information on our research please visit <http://www.nematodes.org> By 20th July interested individuals should send a pdf - one document of 3

pages which should include their CV (2 pages - include the email addresses of 2 academic referees) and a statement of research interests (1 page) directly to mark.blaxter@ed.ac.uk

Professor Mark Blaxter Institute of Evolutionary Biology The University Of Edinburgh Edinburgh EH9 3JT UK

<http://genepool.bio.ed.ac.uk>

[/www.nematodes.org](http://www.nematodes.org)

www.nematodegenomes.org

www.earthworms.org <http://www.tardigrades.org>

mark.blaxter@ed.ac.uk

<http://>

<http://>

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UFZ Halle Germany PopGenetics

Helmholtz Centre for Environmental Research - UFZ

The UFZ is a research institution within the Helmholtz Association in Germany. It provides scientific contributions to the safeguarding of the natural basis of life and of human development potentialities for current and future generations under the challenges of global and climate change. In this way the UFZ contributes towards a sustainable development.

The department of Community Ecology (BZF) has a research focus on patterns and processes of biodiversity; biotic responses to environmental change, invasive species and macroecology.

We are inviting applications for a PhD position, code digit 58/2012

available for 3 years within a DFG (Deutsche Forschungsgemeinschaft) funded project aiming to assess the "Evolutionary potential in functional traits of a wetland macrophyte (*Juncus effusus*) relevant for natural degradation of contaminants".

The successful candidate will have the unique opportunity to establish a molecular and quantitative genetic basis for a wide range of future research in an important wetland plant. Aim of the project is an assessment of European wide distribution of molecular and quantitative genetic diversity related to a critical ecosystem service of wetland ecosystems, namely the natural degradation of contaminants. The work will include (1) a classical experimental approach by assessing quantitative traits in a common garden environment and (2) the implementation of transcriptom data into the framework of molecular population genetics by using SNPs

and microsatellites to describe functional genetic diversity patterns. The ideal candidate has a background in molecular and quantitative population genetics. He/ or she combines organisational skills with strong personal responsibility, has a proven experience in statistics and is fluent in spoken and written English. The desire to engage in collaborative research is essential.

The place of work is the Helmholtz Centre for Environmental Research, Halle (Saale), Germany. Salary will be according to the appropriate civil service level TVÄD 13 (65%). The UFZ is an equal opportunity employer. Women are explicitly encouraged to apply for increase their share in science and research. Physically handicapped persons will be favoured if they are equally qualified. The successful candidates will participate in the Graduate School HIGRADE (<http://www.ufz.de/-index.php?en=11429>). Applicants must hold a Master degree in biology, biochemistry or chemistry.

Scientific information can be provided by Dr. Stefan Michalski, phone: 0049-0345-5585310, E-mail: Stefan.Michalski@ufz.de

Please send your application until 30.08.2012 under code 58/2012 to the Personnel department of the Helmholtz Centre for Environmental Research, PO Box 500136, 04318 Leipzig, Germany, or by email to application@ufz.de.

The Helmholtz Centre for Environmental Research GmbH (UFZ) is the first research institution with EMAS certification. In order to promote sustainability, we ask you to send your application via email.

–

Dr. Stefan G. Michalski Dept.
Biozönoezforschung/Community Ecology

Helmholtz-Zentrum für Umweltforschung GmbH - UFZ
Helmholtz Centre for Environmental Research GmbH
- UFZ Theodor-Lieser-Str. 4 / 06120 Halle (Saale)
/ Germany phone: +49-345-558 5310 fax: +49-345-558-5329 stefan.michalski@ufz.de / www.ufz.de
Sitz der Gesellschaft: Leipzig Registergericht: Amtsgericht Leipzig, Handelsregister Nr. B 4703 Vorsitzender des Aufsichtsrats: MinDirig Wilfried Kraus Wissenschaftlicher Geschäftsführer: Prof. Dr. Georg Teutsch Administrativer Geschäftsführer: Dr. Andreas Schmidt

stefan.michalski@ufz.de

UGeneva EvolutionaryBiol

Graduate position:

PhD Position in Evolutionary Genetics / Adaptive Evolution

The laboratory of Molecular Phylogeny and Evolution in Vertebrates, led by Juan Montoya-Burgos, Department of Genetics and Evolution, University of Geneva, seeks for a PhD candidate with a strong interest in evolutionary biology and advanced knowledge in molecular techniques, gene expression analysis and/or DNA-sequence analyses.

RESEARCH PROJECT:

A significant part of the functional diversity of life on earth is thought to have evolved through multiple bursts of adaptive speciation. The process of adaptive evolution is therefore central in the field of evolutionary biology and the understanding of the genetic mechanisms underlying the evolution of adaptive traits remains a challenging task.

This project is aimed at investigating the evolution of genes that are involved in adaptive responses. The candidate will analyze the transcriptomes established in our laboratory to identify and characterize genes involved in the evolution of adaptive traits and to determine whether particular biological processes are enriched in positively selected genes. The candidate will establish correlations between the emergence of positively selected mutations and particular phenotypes. The role played by lineage-specific positively selected genes will also be assessed, in particular by the analysis of the expression pattern of non-annotated positively selected genes. To these aims, the candidate will participate in the development of new combinations of state-of-the-art techniques to obtain homologous DNA sequences of interest in a large panel of closely related species.

We will use as model organism the Loricariinae catfish subfamily as it is highly diversified in terms of morphology, ecology, behavior, and in number of species.

This project is funded by a Swiss National Science Foundation (SNSF) grant.

The Department of Genetics and Evolution hosts research groups working on regulation of vertebrate development (Denis Duboule), artificial and natural evolu-

tion (Michel Milinkovitch), molecular phylogeny of protists (Jan Pawlowski), developmental and molecular biology of sensory systems in mammals (Ivan Rodriguez), development and regeneration in Hydra (Brigitte Galliot), regulation of development in Drosophila (François Karch), sex determination and early development in Drosophila (Daniel Pauli).

Ideal candidates will have a Ms degree in biology with a specialization in evolution, developmental genetics, or phylogenetics, should be experienced in laboratory techniques (e.g. DNA, RNA extraction, PCR and RT-PCR, DNA sequencing, cDNA library, cloning, In Situ Hybridization), with advanced skills in DNA sequence analysis and in gene expression analysis. The position is initially for three years. The selected candidate will be enrolled in the doctoral program Ecology & Evolution (<http://biologie.cuso.ch/ecologie-evolution/welcome>)

CLOSING DATE: Open until filled, but all application materials, including CV, a summary of research experience, copies of relevant published or in-press papers, and three reference persons should be received by 1st of September 2012 to ensure full consideration. The position will start at the earliest possible date. Candidates should indicate in a cover letter when they could take up the position.

Please send all application material to: Juan Montoya-Burgos, Dept. of Genetics & Evolution, University of Geneva, Sciences III, 30 quai Ernest Ansermet, 1211 Geneva 4, Switzerland; or as e-mail attachments to juan.montoya@unige.ch. For inquiries please contact juan.montoya@unige.ch.

Juan.Montoya@unige.ch

UGöttingen EvolutionMolluscPigments

A PhD position to work on the molecular genetics of a molluscan pigmentation system.

Variation in shell pigmentation patterns of the common garden snail *Cepaea nemoralis* have long served as a model for population geneticists, however very little is known about the molecular mechanisms that generate this morphological diversity. A PhD position to identify and characterise the molecular basis of these mechanisms is available within Daniel Jackson's research group.

This position requires an individual who has expe-

rience with some of the following molecular techniques: RACE-PCR, whole mount in situ hybridization, immuno-cyto chemistry and micro-injection. Familiarity with bioinformatic techniques (scripting in Perl, Python or other common languages and running programs from the command line etc.) are highly desirable.

Candidates should hold an excellent BSc degree in evolution, cell biology, developmental biology, molecular biology, or a related field. In addition to their academic qualifications, candidates should also have excellent communication and team-working skills, be committed to the topic and to working in a dedicated, interdisciplinary research environment. The working language of the group is English, and applicants from abroad are encouraged to apply.

The University of Göttingen seeks to increase the participation of women in areas in which they are currently underrepresented and therefore explicitly urges women to apply. Disabled persons with equivalent aptitude will be favoured.

All applications should be made in English, and must include all of the following 3 items (incomplete applications will not be considered):

1. A full academic CV including any published or unpublished academic work.
2. A 1-2 page letter outlining the candidate's research interests and motivation for applying to this position.
3. Signed letters of reference and the contact details of a minimum of 2 referees (ideally previous supervisors).

Submit your application or any informal enquiries directly to djackso@uni-goettingen.de

The application deadline is August 15, 2012.

For more information about the Jackson group see <http://www.uni-goettingen.de/en/102705.html> "Jackson, Daniel" <djackso@gwdg.de>

UHalle HostParasiteEvolution

PhD position in Host-Parasite Coevolution at the University Halle (Germany)

We are looking for a highly motivated PhD student to work in the field of experimental evolution and QTL mapping of host-parasite systems with the honeybee as model system. The PhD student will contribute to the DFG (Deutsche Forschungsgemeinschaft) funded

project “Host-Parasite-Coevolution: Rapid Reciprocal Adaptations and its Genetic Basis”. The ideal candidate should have experience with standard molecular genetic tools and statistical analysis of genetic data with a strong evolutionary biology background. Experience with honeybees or other eusocial insects would be advantageous. A Diplom or master degree in in Biology or a related field is required. Work place is the Molecular Ecology Work Group (<http://www.mol-ecol.uni-halle.de/>) at the University of Halle-Wittenberg in Halle (Saale) Germany. The position is available for 3 years , annual salary is according to standard German PhD scale TV-L E13 (65%). Please send your application (giving D 141/2012 as reference) in a single pdf file including CV, statement of research interests (maximum 1 page) and contact details of two referees to petra.weber@zoologie.uni-halle.de by 01.08.2012.

Bernhard Kraus <kraus@zoologie.uni-halle.de>

ULausanne EvolutionParthenogenesis

Two PhD positions are available for research on the evolution of parthenogenesis in my newly created group in the Department of Ecology and Evolution at the University of Lausanne.

The general focus of the group is the diversity of reproductive and genetic systems in animals and the proximate and ultimate mechanisms underlying this diversity. Particularly interesting are the factors underlying transitions between genetic systems, and the proposed projects will investigate causes and consequences of transitions from sexual reproduction to (female-producing) parthenogenesis. The students will combine tools from cytology and molecular genetics, experimental evolution and genomics to investigate genetic and genomic implications of transitions between sex and parthenogenesis in one (or both) of two different study systems: orthopteroid insects, mainly stick insects of the genus *Timema*, and thrips. The projects are likely to also involve a combination of field-work and modeling of population dynamics. Successful candidates will have the opportunity and are encouraged to develop their own ideas within the frame-work of the group. For further information and a list of publications, see: <http://www.tanjaschwander.com/> The Department of Ecology and Evolution in Lausanne provides a stimulating research environment, with an active program of

seminars and discussion groups (in English); see <http://www.unil.ch/dee/>. Lausanne is located in the French part of Switzerland, on the shore of Lake Geneva, and is an attractive city with a high quality of life. The city is surrounded by beautiful mountain environments—an excellent area for outdoor activities. See <http://www.lausanne.ch/> Candidates should have a master degree in an appropriate discipline and a keen interest in evolutionary biology. The positions require independent, highly motivated, and scientifically curious individuals with strong interests in the above described central topic. All our projects are highly integrative and require willingness to closely collaborate with researchers of different backgrounds.

Application requirements: Informal enquiries and applications can be sent to Tanja Schwander (tanja.schwander@gmail.com). Formal applications should include: a 1-2 page cover letter (in English) indicating research interests, your CV, and two letters of reference (please include everything in a single pdf file). Full consideration will be given to all applications received by October 25. The PhD candidates would ideally be able to start in February or March, 2013, but the starting date is somewhat flexible.

Tanja Schwander

Current address: Center for Ecological and Evolutionary Studies Evolutionary Genetics, room 06.74 University of Groningen The Netherlands

Phone +31 50 363 2134

Address from February 2013 onwards: Department of Ecology and Evolution Biophore Building University of Lausanne CH-1015 Lausanne Switzerland

t.schwander@rug.nl

ULouvainLaNeuve BehaviourEvol

Biodiversity Research Centre – Earth and Life Institute
Université catholique de Louvain (UCL)

PhD on the plasticity of multimodal communication

*under sexual selection in a butterfly,/Bicyclus anynana/**

PhD Position in Behavioral Ecology (f/m)

Project title

Plasticity of multimodal communication under sexual selection in a butterfly,/Bicyclus anynana/

Available position

A full time four-year PhD position is available at the Biodiversity Research Centre, Earth and Life Institute, University of Louvain-la-Neuve (UCL) in Belgium (<http://www.uclouvain.be/en-bdiv.html>). Description of the project

Individuals often show large phenotypic variation in sexual traits (signals and preferences), which affect their reproductive success. Phenotypic variation may be due to their genotype, to the environment(s) in which their phenotype is present, and to genotype-by-environment interactions (GEIs). The impact of GEIs on sexual selection has only recently drawn the attention of researchers. The project aims at assessing the role of GEIs on the variation observed in sexual traits and tests whether such variation has an adaptive value in mate choice. An integrative approach will allow investigating: 1) multiple phenotypic (visual, olfactory, gustatory) traits to grasp the full phenotype of the organism, forming its “lifestyle”, and 2) the adaptive value of phenotypic plasticity in both sexual signals and preferences in both sexes. More specifically, the project will aim at identifying the extent of plastic and genetic effects in male-female interactions due to signaling and preference for signals. Methods will include behavioral, chemical and statistical analyses to test the extent with which sexual signals and preference depend on individual quality, experience and on environmental conditions (e.g. [1 <#_ENREF_1>, 2 <#_ENREF_2>]). The species under focus is an African tropical butterfly/*Bicyclus anynana*/, in which mutual mate choice and ornamentation has recently been shown [3 <#_ENREF_3>]. This species is a model lab-reared system for studies in phenotypic plasticity, sexual selection and multimodal sexual communication [4 <#_ENREF_4>]. Several sexually selected signals have recently been identified, namely male sex pheromones [5 <#_ENREF_5>, 6 <#_ENREF_6>] and the UV-reflectance of male and female forewing eyespot centres [3 <#_ENREF_3>, 7 <#_ENREF_7>]. We expect the results to contribute significantly to our understanding of the role phenotypic plasticity in sexual traits and other life history traits may play population or species adaptation to reproduce in their environment.

Tasks

The successful applicant will have the opportunity to develop various theoretical and technical skills in an integrative manner while carrying out the scientific research as detailed in the project description. She/he will have the opportunity to develop additional questions related to the main research project. She/he is expected

to produce several manuscripts for publication in international peer-reviewed journals and disseminate this work at international conferences.

Requirements

We are looking for a strongly motivated candidate with a MSc degree in Biology, with advanced courses in Evolutionary and/or Behavioral Biology and Ecology. Experience in behavioral and/or chemical ecology and written and oral communication skills in English are a plus, as is the ability to work efficiently, independently as well as in collaboration. The grant will be delivered upon successful written application (submission deadline: September 3rd 2012) and an oral interview in Brussels (October-November 2012), which can both be done either in English or French. The selected applicant will be supervised throughout the process. The degrees obtained abroad (outside Belgium) or in the Flemish Community will require an equivalence (necessary to provide documentation of passed examinations for 300 credits including a research work of at least six months during master with a scientific report; more information: <http://www.uclouvain.be/356107.html>).

Work environment

The PhD student will work in a highly active and integrated academic environment, in the research team of Prof. Caroline C. Nieberding, including Dr. MJ Holveck and other postdocs and PhD students, and will interact with members of other research teams of the Institute, including Prof. H. Van Dyck. Our University is an Equal Opportunity/Affirmative Action Employer, and is in a French-speaking region, but the language for meetings and scientific interactions is English. For background information about our university, see <http://www.uclouvain.be/en-index.html>. Salary

Salary ranges between 21.349 to 23.659 euros brutto per year (approx.

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UMassey Auckland
YeastSpeciesInteractions

PhD Studentship available in Thomas Pfeiffer’s group at Massey University, Auckland.

I am looking for a highly motivated PhD student to work at the New Zealand Institute for Advanced Study at Massey University, Albany, Auckland. The successful candidate will participate in a research project on species interactions and metabolic strategies of yeasts from natural populations. Research on this project will be conducted in a highly interdisciplinary environment in collaboration with Matthew Goddard (U Auckland) and Paul Rainey (U Massey). Candidates are expected to have experience in microbiology and a strong interest in evolutionary biology. While the main focus of the project is experimental, an interest in theoretical biology and mathematical modeling is of advantage. The Studentship is of three years duration and available immediately. Applications will be accepted until the position is filled.

For informal inquiries and applications please contact Thomas Pfeiffer (T.Pfeiffer@massey.ac.nz). To apply please send a cover letter describing your motivation to apply for this Studentship, your research interests and relevant experiences, a CV and contact information of three referees.

Thomas Pfeiffer NZ Institute for Advanced Study
Massey University Albany Auckland, New Zealand
T.Pfeiffer@massey.ac.nz www.thomaspfeiffer.com
www.nzias.ac.nz pfeiffer.massey@gmail.com

UPolitecnicaMadrid ViralEvolution

A PhD position is available to work on a project aimed at studying the processes by which new viral variants are generated. This is a long-standing goal in the research areas of virology and evolution, as knowledge on this topic is central to understand the emergence of new viral diseases.

The project combines molecular biology techniques and bioinformatic approaches for the analysis of the role of host adaptation, geographic barriers and other ecological factors in the emergence of new viral variants using a plant virus as a model organism. The information gathered will be used to build a predictive model for virus emergence.

The successful candidate will receive a multidisciplinary training, from molecular biology techniques to informatics modelling methods, performing his/her work in a group with a large experience in the study of plant virus evolution.

Period: Four years, starting October 1st 2012.

Conditions: Contract conditions will be equivalent to those of the Spanish "Formacion de Personal Investigador (FPI)" Spanish Programme.

Requisites: Experience in molecular virology or/and bioinformatics are not mandatory, but will be valued. Master degree will be also highly valued.

INTERESTED CANDIDATES PLEASE CONTACT
Dr. ISRAEL PAGAN jesusisrael.pagan@upm.es BEFORE SEPTEMBER 20th 2012

Israel Pagan <jesusisrael.pagan@gmail.com>

UStAndrews ChordateEvolution

Evolution of chordate regeneration mechanisms

The cephalochordate amphioxus is the basal-most chordate, and as such shares many features with vertebrates including a notochord, segmented musculature and a hollow nerve cord. It is therefore ideally placed for understanding the evolution of vertebrate characters from an invertebrate ancestor (Bertrand and Escriva 2011). It is also emerging as a good system for regeneration studies, since it can faithfully regenerate the postanal tail with all its complex morphology (Somorjai et al 2012).

As part of an ongoing project to understand the genetic basis of amphioxus tail regeneration, we have generated transcriptome data of bud-stage blastemas and normal tails (generated by Dr Nori Satoh, OIST, Japan). The first goal of this project will be to analyse commonalities and differences between the two datasets. Interesting candidates will then be analysed for expression during regeneration. A long-term aim of the project is to determine gene function using knock-down techniques. This project will contribute to the regeneration field by developing a new model for regeneration biology that occupies a key position for understanding the evolution of chordate regeneration.

This appointment is a MASTS (Marine Alliance for Science & Technology for Scotland) studentship, and the research will largely be conducted at the University of St Andrews Scottish Oceans Institute (Scotland UK). Applicants must be enthusiastic and ready to accept the challenge of working with a new regeneration model system, ideally with relevant experience in one or more of molecular biology, developmental biology, regenera-

tion research, transgenics/microinjection, cell culture, gene sequence/transcriptome analysis and microscopy (further training will be provided). The project will also involve a significant wet-lab component and field-work. Informal enquiries should be sent to both co-supervisors Dr Ildiko Somorjai (somorjai@cantab.net) and Dr. Dave Ferrier (dekf@st-andrews.ac.uk). Please send a CV and cover letter (max 1 page each) outlining your goals and relevant experience. The deadline for applications is July 31st, 2012.

Recent relevant references:

Bertrand S, Escriva H. 2011. Evolutionary crossroads in developmental biology: amphioxus. *Development*. 138(22):4819-30. Somorjai IML, Somorjai RL, Garcia-Fernandez J, Escriva H. 2012. Vertebrate-like regeneration in the invertebrate chordate amphioxus. *PNAS*. 109(2):517-22.

Dr. Ildiko Somorjai, PhD Cantab. Centre for Organismal Studies (COS) University of Heidelberg Im Neuenheimer Feld 230 69120 Heidelberg Germany

phone: (+49) (0)6221 54 52 56 fax: (+49) (0)6221 54 56 78

Ildiko Somorjai <somorjai@cantab.net>

UStirling 2 MusselOrigins

We are looking for two PhD students to work at the University of Stirling, Scotland:

—
We are looking for a PhD student to work on the genetic origins of *Mytilus* species spat circulating in Scottish mussel farming.

It is A 3-year fully funded PhD studentship at the University of Stirling, (Institute of Aquaculture) in collaboration with Marine Scotland Science, Aberdeen, (Scottish Government) - starting in October 2012. We are looking for someone with an ecology or genetic population background who has good applied computing skills.

More details at <http://tiny.cc/mss2012> Applicants are encouraged to contact Dr. Michaël Bekaert (michael.bekaert@stirl.ac.uk) or Dr Iveta Matejusova (iveta.matejusova@scotland.gsi.gov.uk) for further details of the project.

Complete applications, consisting of a covering letter,

an up-to-date CV and the name and contact details of two referees (at least one academic referee) should be submitted to anda.kilpatrick@stir.ac.uk. Candidates will then be shortlisted and interviewed. Closing date for applications 13th July 2012

—
We are looking for a PhD student to work on Salmonidae lineages, construction of the comprehensive gene duplication, genome history and sexual chromosome re-arrangements.

It is A 3-year fully funded PhD studentship at the University of Stirling, (Institute of Aquaculture) in collaboration with The Marine Alliance for Science & Technology for Scotland (MASTS) - starting in October 2012. We are looking looking for someone with a background in algorithms or sequence analysis who has good applied computing skills. It could suit someone with either a biological or computational/mathematical background.

More details at <http://tiny.cc/uos2012> or <http://www.stir.ac.uk/impact/>

Applicants are encouraged to contact Dr. Michaël Bekaert (michael.bekaert@stirl.ac.uk) or Prof Brendan McAndrew (b.j.mcandrew@stir.ac.uk) for further details of the project.

Complete applications, consisting of a covering letter, an up-to-date CV and the name and contact details of two referees (at least one academic referee) should be submitted to anda.kilpatrick@stir.ac.uk. Candidates will then be shortlisted and interviewed.

—
Michaël

– Dr. Michaël Bekaert Ph: +44 (0)1786 467870 Marine Genomics Institute of Aquaculture University of Stirling Stirling Scotland, FK9 4LA UK

– The University of Stirling is ranked in the top 50 in the world in The Times Higher Education 100 Under 50 table, which ranks the world's best 100 universities under 50 years old. The University of Stirling is a charity registered in Scotland, number SC 011159.

michael.bekaert@stir.ac.uk

UUppsala MolEvol

PhD-student position in Molecular Evolution with specialization in metagenomics: <http://www.uu.se/>-

<http://www.uu.se/-jobb/phd-students/annonsvisning?tarContentId=3D190218&languageId=1> PhD-student position in Molecular Evolution with specialization in genomics and bioinformatics: <http://www.uu.se/-jobb/phd-students/annonsvisning?tarContentId=3D190194&languageId=1> Text of the ads pasted below:

PhD-student position in Molecular Evolution with specialization in metagenomics

at the Department of Cell and Molecular Biology Apply no later than 2012-06-29

Starting date: September 1, 2012.

We study the molecular evolution of genomes from infectious disease causing bacteria as well as symbiotic and free-living bacteria using bioinformatic analyses of next-generation sequencing data (NGS). The knowledge is important to understand the early evolution of life as well as the mechanisms and selective forces that drive adaptations to different environments. Metagenomics is a new area of research in which all DNA present in a particular environment is sequenced and analyzed. With the aid of metagenomics it is possible to identify and study previously unknown microorganisms that have not been cultivated in the laboratory. Another new exciting technology is single cell genomics, which enables the genomes of single cells to be sequenced. By combining metagenomics and single cell genomics, it is possible to perform an in-depth investigation of the microflora, in a way that was not possible with conventional technologies.

The overall aim of this project is to study how bacterial populations evolve using metagenomics and single cell genomics. Samples will be taken from many different environments, such as lakes, fossils, earth, humans and insets. The work will be conducted in silico and consists of bioinformatics, comparative genomics and phylogenetics. Using single cell genomics, the PhD student will reconstruct the genome from individual cells in the environment. Metagenomic reads will be recruited to the reconstructed genomes, with the aim of inferring the natural sequence variation, and more specifically to compare mutation versus recombination frequencies for different species and environments to better understand the evolutionary forces that drive changes and adaptive processes in nature.

The candidate should have a Master of Science degree in Biology or similar qualifications with specialization in bioinformatics, molecular sequence analysis, microbiology or comparative genomics. Knowledge in bioinformatics analyses of sequence data is desirable, as is prior research experience and high grades. The can-

didate should be able to work well as part of a team but also independently, and be proficient in both written and spoken English. In filling this position the university aims to recruit persons who, in the combined evaluation of competence, skills and documented qualifications, are judged most suitable to carry out and develop the work-in-hand and to contribute to the positive development of the department. Departmental work, mostly teaching, will constitute at most 20% of the position. Information about research education can be found at the web site of the Faculty of Science and Technology, <http://www.teknat.uu.se/cms/>. Applicants must be eligible for PhD studies at Uppsala University.

The application should include a letter describing research interests and relevant experiences (maximum one page), CV, copies of grades, exams, master project thesis (or parts thereof) and additional documents. Please provide contact information reference persons and recommendation letters from prior research supervisors.

More information about the position can be obtained from professor Siv Andersson, e-mail: siv.andersson@ebc.uu.se, Phone, +4618-471 64 52 and +4618-471 43 79. Union representatives are Anders Grundström, Saco-rådet, Phone, +4618-471 53 80 och Carin Söderhäll, TCO/ST, Phone, +4618-471 19 96, Stefan Djurström, Seko, Phone, +4618-471 33 15.

You are welcome to submit your application no later than June 29, 2012, UFV-PA 2012/1386. Use the link below to access the application form.

PhD-student position in Molecular Evolution with specialization in genomics and bioinformatics

at the Department of Cell and Molecular Biology. Apply no later than 2012-06-29, UFV-PA 2012/1384

Starting date: September 1, 2012.

We study the molecular evolution of bacterial genomes using bioinformatic analyses of next-generation sequencing data (NGS). The knowledge is important to understand the early evolution of life as well as the mechanisms and selective forces that drive adaptations to different

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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>

UValencia EvolutionaryBiology

Master on 'Integrative Evolutionary Biology'

The 'Cavanilles Institute of Biodiversity and Evolutionary Biology' (ICBiBE, University of Valencia, Spain), offers an official 'Master in Integrative Evolutionary Biology'. This master provides advanced training in Evolutionary Biology, and does so from an integrative perspective. Its main focus is on the ecological and genetic evolutionary analysis of traits and complex systems, and is mainly directed to students who wish to initiate a PhD/Career in Evolutionary Biology. ICBiBE is a modern, leading research institute in Evolutionary Biology and is part of Valencia's International Campus of Excellence. This master also hosts lecturers and professors from several other research institutes within the International Campus of Excellence: IBMCP (Institute of Biomolecular and Cellular Plant Research), COMAV (Institute for the Conservation and Improvement of Valencian Agrodiversity), ai2 (Institute of Automatics and Industrial Informatics), and CIDE (Centre for the Study of Desertification). Subscriptions to this master are now open. More detailed information and subscription at: <http://www.uv.es/biodiver/v/docencia/-index.htm> Please contact Dr. Manuel Serra Cavanilles Institute of Biodiversity and Evolutionary Biology University of Valencia email: Manuel.Serra@uv.es

Dr. Pau Carazo Edward Grey Institute, Dept. of Zoology, University of Oxford, Oxford OX1 3PS email: pau.carazo@uv.es email: pau.carazoferrandis@zoo.ox.ac.uk Phone: (+44) (0)1865 271 258 webpage: <http://paucarazo.com> Pau Carazo <pau.carazo@uv.es>

UZurich EvolutionaryBiology

Position for a PhD student, working with Josh Van Buskirk at the University of Zurich in Switzerland

The project focuses on adaptation across a steep gradient in elevation. We will establish replicate elevational transects from near the southernmost edge of the distribution of the common frog in southern Switzerland to the uppermost edge of its occurrence in the Alps. Fieldwork will involve characterizing amphibian life history

variation in nature and surveying environmental conditions that define the gradient. Experimental work will be aimed at understanding genetic, demographic, and selective factors affecting adaptation to climate extremes. The position will be especially suitable for you if you are interested in controls on the distributions of species, limits to adaptation, and the importance of evolutionary responses to climate change.

The project is funded by the Swiss National Science Foundation for a period of three years. You will participate in the graduate program in Evolutionary Biology (<http://www.evobio.uzh.ch/research.html>) and will be a member of a large and interactive group of evolutionary ecologists working on conservation, population genetics, and demography in a variety of organisms.

Qualifications: Equivalent of a masters degree in biology, and strong professional interests in evolutionary biology, molecular ecology, conservation, or landscape ecology. Experience with molecular methods is an asset.

Application: Please send to the address listed below (i) a letter describing your interest in this position and your previous research experience (masters, RA positions, etc.), (ii) your CV, and (iii) names and contact information of two references. If possible, please email your application as a single PDF document. I will begin screening candidates right away, and the position could begin in fall or winter.

Josh Van Buskirk Evolutionary Biology & Environmental Studies University of Zurich CH-8057 Zurich, Switzerland josh.vanbuskirk@ieu.uzh.ch <http://www.ieu.uzh.ch/staff/leaders/vanbuskirk.html> J Van Buskirk <josh.vanbuskirk@ieu.uzh.ch>

UmeaU ForestPopulationGenomics

Umeå Plant Science Centre is looking to fill a PhD student position in the population genomics of forest trees. The project involves the assessment of diversity and connectivity of spruce stands, pristine and managed, exotic and native, through Genotyping By Sequencing (GBS) and other high-throughput approaches. The chosen candidate will be co-advised by Stacey Lee Thompson and Nathaniel Street, and will collaborate broadly with numerous research groups at UPSC (e.g. Pär Ingvarsson, Stefan Jansson, Rosario García-Gil), Skogforsk and our industrial partner Bergvik Skog. This project utilizes the resources generated by The

Spruce Genome Project, ongoing here in Umeå (<http://www.congenie.org/>).

How do different reforestation methods impact genomic variation within spruce stands? Clear-cut and continuous cover forestry are contrasting natural resource management practices that have been broadly employed through Sweden for hundreds of years. Although each practice has different theoretical expectations for resulting diversity (e.g. allelic richness, relatedness, age structure, spatial dynamics), little is known about realized patterns within the reforested spruce stands of Sweden. This project will fill this knowledge-gap by using high-throughput genotyping and next generation sequencing to profile genomic diversity within forest stands under contrasting management and silvicultural practices, including the use of exotic provenances. Comparisons will be made with pristine forest sites, as well as with island populations of different ages and sizes that have recently uplifted from the Baltic and been colonized by spruce. Site selection will be done in collaboration with our industrial partner, Bergvik Skog, with additional contributions from Skogforsk.

The chosen candidate will perform top-tier research and be exceptionally mentored as a member of the Industrial Research School in Forest Genetics, Biotechnology and Breeding. <http://www.upsc.se/News/Open-Positions/upsc-seeks-eight-industrial-graduate-students-that-will-provide-the-future-competence-of-the-forest.html> UPSC is a centre of Excellence for Plant and Forest Biology and Biotechnology, located in northern Sweden. Our ca. 200 employees (including about 40 faculty members) perform world-leading research and have access to outstanding infrastructure with many shared resources and platforms, including advanced facilities for growing, transforming and manipulating our main model systems. UPSC has been ranked as one of the top places in the world

for doctoral studies. About half of our staff are non-Swedes, and the composition of employed staff and students at UPSC is highly dynamic, representing on average 36 nationalities.

Knowledge of population genetics, evolutionary analyses, molecular methods and bioinformatics is highly desirable. Experience with fieldwork is an asset, but not a requirement. The successful applicant should possess creativity, autonomy and a dedicated team spirit. The working language of UPSC is English and thus high competencies are required.

A full application consists of cover letter, your CV, certificates from higher education, copies of Bachelors/Masters thesis, a written description of your research interests, a written statement about why you are interested in the project, and contact information for three referees. The “official” application instructions should be up on the Umeå University website on 8 August (after staff holidays), with an application deadline of 31 August. Your complete application, marked with reference number 313-663-12, should be sent to jobb@umu.se (state the reference number as subject) or to the Registrar, Umeå University, SE-901 87 Umeå, Sweden to arrive August 31, 2012 at the latest.

For more information about the position, contact Stacey Lee Thompson stacey.thompson@emg.umu.se or Nathaniel Street nathaniel.street@plantphys.umu.se

Cheerio,

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– Stacey Lee Thompson Assistant Professor, Evolutionary and Environmental Genomics Umeå Plant Science Centre Department of Ecology and Environmental Science Linneaus väg 6 Umeå University, SE-901 87 Umeå, Sweden office: +46 (0)90 786 6637

stacey.thompson@emg.umu.se

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AmericanMuseumNatHist LabSupervisor

Job: Laboratory Supervisor Institution: American Museum of Natural History Location: New York City Start Date: August 6, 2012

The American Museum of Natural History is looking for a Laboratory Supervisor to work with a group of researchers on a broad variety of evolutionary and systematic problems.

Responsibilities and Duties: Extract and Sequence DNA. Sequence editing (maintaining database) responsible for ensuring lab supplies are on hand, maintain lab equipment, training other laboratory users such as graduate students and postdoctoral fellows.

Qualifications: BS required, familiar with lab procedures for DNA extraction, PCR amplification, cloning, and sequencing. A plus if experienced in DNA analyzing equipment (3730 DNA analyzer and BIO Mech robot), High-throughput, Basic computer skills, experience with Lab related software (sequence editing software), and sequence databases.

Interested applicants should send a cover letter detailing their experience and interests and a CV in PDF, along with the names and contact information of 3 references to Ward Wheeler at wheeler@amnh.org. Subject line MUST include reference to Lab Supervisor Position.

The position is open now.
crowley@amnh.org

BielefeldU PlantMolEvol

The Faculty of Biology of Bielefeld University, Germany, plans to establish a tenure track position for a

Professorship (W 2) in Molecular Ecology

through the Heisenberg professorship program of the Deutsche Forschungsgemeinschaft, the Lichtenberg program of the Volkswagenstiftung or similar programs. The tenure option is provided by Bielefeld University after successful evaluation of the candidate after a period of five years.

We are seeking a person with a strong background in the study of molecular ecology, preferably of plants. The research should combine ecological with genetic approaches. The successful candidate is expected to develop an internationally competitive research program, supervise research students, and contribute to undergraduate and graduate teaching. We encourage highly qualified candidates willing to compete for such a professorship to submit their applications and research proposals. Research proposals should develop concepts of potential cooperation within the Faculty of Biology. Subsequent to the university selection process proposals including a letter of support from the university will have to be submitted by the applicant to the granting agency of the respective tenure-track professorship program.

Candidates must have a university and a qualified PhD degree in a pertinent field, strong scientific achievements and an outstanding research record.

We welcome applications from severely handicapped people. We particularly welcome applications from

women. Given equal suitability, qualification and professional achievement, women will be given preference, unless particular circumstances pertaining to a male applicant predominate.

Applicants are asked to send their documents no later than August 31, 2012 to the Dean's Office, Faculty of Biology, Bielefeld University, POB 100131, 33501 Bielefeld, Germany, Email: dekanat.biologie@uni-bielefeld.de.

The following documents are requested in PDF format: curriculum vitae, publication list, statements of research and teaching experience and interests, documentation of successful third-party funding, names and addresses of four references.

For more information you could contact caroline.mueller@uni-bielefeld.de

Prof. Dr. Caroline Müller Department of Chemical Ecology W1-142 Faculty of Biology Bielefeld University Universitätsstraße 25 D-33615 Bielefeld GERMANY Phone: +49 (0) 521 106 5524 Fax: +49 (0) 521 106 2963 <http://www.uni-bielefeld.de/biologie/-ChemOekologie/English/index.html> Caroline Mueller <caroline.mueller@uni-bielefeld.de>

Denmark 2 QuantGenetics

Vacant positions: Two quantitative geneticists specialising in genetic improvement programmes

Center for Quantitative Genetics & Genomics (QGG) at Department of Molecular Biology and Genetics, Aarhus University, Denmark, wishes to recruit 2 researchers with a strong theoretical background in quantitative and/or population genetics to join our centre at AU Foulum.

QGG wishes to strengthen its research in design and evaluation of breeding plans, and management and evaluation of the long-term consequences of selection in livestock, agricultural crops and model organisms. The scientists will join our team working on sustainable breeding, which has a close collaboration with the industry and is involved in many collaborative projects. The main activities are currently focused on the implementation of genomic selection in dairy cattle and pig breeding. The successful candidates will contribute to the development of sustainable genetic improvement programmes employing new technologies and developments in statistical, quantitative, population, and

molecular genetics.

QGG was established January 1st 2012 and employs 20 senior level scientists and more than 30 PhD students, post doctoral fellows and visiting scientists from all over the world. It is one of the largest and most wide-ranging research groups within the field of livestock improvement programmes in Europe. Research in QGG ranges from basic research into the genetic basis of complex traits in animals, plants, humans and model organisms, to applied research into sustainable genetic improvement programs for livestock and agricultural crops. We are focused on developing and implementing new methods for analysing the massive amounts of genomic and phenotypic data becoming available and applying these methods to practical problems related to animal and plant breeding.

We offer a progressive and informal working environment with a project- and team-oriented working culture and excellent opportunities for collaboration and project initiation. The ideal candidates are therefore visionary, enthusiastic team players, pro-active, and committed to meeting common goals and deadlines.

Senior researcher/associate professor in sustainable animal breeding The senior researcher will be responsible for maintaining and developing research related to optimisation of breeding programs including development of decision theory, modelling of genetic changes at molecular and population level, along with design and evaluation breeding programmes. Accordingly, the candidate has a strong background in theoretical, computational, and applied approaches to optimising genetic improvement programmes.

The successful candidate will join ongoing projects in genomic selection programmes and is expected to develop his/her own research agenda within the context of the team and take a leading role in attracting funding. Responsibilities will include supervising post doctoral fellows and PhD students, establishing and maintaining collaborations both nationally and internationally and, possibly, teaching at master and PhD level. The successful candidate has the following qualifications: * Documented strong theoretical background in quantitative and/or population genetics with emphasis on consequences of selection * Preferably a strong background in definition of breeding goals and decision theory * Substantial experience in scientific publication * Excellent communication skills and documented teaching experience * Excellent supervision skills and documented experience * Good managerial skills and documented experience in project management * Proven ability to attract external funding

Post doc in sustainable animal breeding The post doc

will join ongoing projects in genomic selection programmes and feed efficiency in dairy cattle and pigs. The main responsibilities will be in designing and evaluating breeding programmes by means of deterministic and stochastic simulation including use of the simulation software ADAM. Other responsibilities include co-supervising PhD students, contributing to grant applications, as well as teaching animal breeding and quantitative genetics at undergraduate and Master level.

The successful candidate has the following qualifications: * Documented postgraduate qualification in animal breeding, quantitative or population genetics * Documented statistics and computing skills (ideally including programming experience) * Preferably experience with computer simulations * Substantial experience in scientific publication * Excellent verbal and written communication skills in English

Both positions are limited to 4 years but may be extended depending on future funding. The positions are located at AU Foulum, Tjele, Denmark.

For more information on the positions and QGG, please contact: Mogens Sandø Lund (Mogens.Lund@agrsci.dk, +45

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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>

DurhamU ArchaeologicalTech

Durham University

Department of Archaeology

Durham University's Department of Archaeology is seeking to appoint an Archaeological Science Technician.

The Technician will assist in the management and day-to-day operation of three Archaeological Science laboratories: Ancient and modern DNA, Isotope Chemistry and Luminescence Dating, all of which have both research and teaching functions. The post holder will play a key role in the development of cutting-edge research and support teaching in the Department. The primary purpose of the job is to provide the technical support needed to maintain full operational capability of these laboratories. In addition, the post holder will

contribute to health and safety management in the Department.

* Archaeological Science Technician

Salary: Â£30,122 - Â£35,938 pa (Ref: 1798: Department of Archaeology)

The post holder will be a member of the technical support group for Archaeological Science and will be required to work within a team structure. As a key member of the support group, he/she will be required to maintain the operational capability of the three laboratories, meet deadlines and contribute to problem solving by working independently and quickly and communicating outcomes to relevant staff.

Interested candidates should contact Greger Larson at greger.larson@durham.ac.uk

Closing date: 07 August 2012 Ref: 1798

Further details of the positions and an application form are available on our website (<http://www.dur.ac.uk/-jobs/>) or telephone 0191 334 6499; fax 0191 334 6504.

Kind Regards

Holly Walton

Recruitment Assistant (Faculty of Social Sciences & Health, Durham Business School & Sport) Human Resources Department University Office Old Elvet Durham DH1 3HP

Telephone: + 44 (0) 191 334 6498 Fax: + 44 (0) 191 334 6504 Email: holly.walton@durham.ac.uk

“Walton, Holly” <holly.walton@durham.ac.uk>

DurhamU PlantEvolutionaryBiol

Research Fellowships in Plant Science at Durham University, UK

Applications are invited for Research Fellowships in Plant Science within the School of Biological and Biomedical Sciences (SBBS), this position is available for 5 years.

The successful applicants will have expertise in any aspect of plant sciences e.g. evolutionary biology, ecology, cell biology, etc at any scale e.g. from molecules to landscapes and have an internationally competitive, and fundable, 5 year research programme plan.

It would be expected that the proposed research

programme would also foster collaboration with one or more of Durham University's Institutes and Centres which have interests in plant science i.e. The Durham Centre for Crop Improvement Technology (DCCIT: <http://www.dur.ac.uk/dccit>), the Biophysical Sciences Institute (BSI: <http://www.dur.ac.uk/-bsi>), The Durham Energy Institute (DEI: <http://www.dur.ac.uk/dei/>) and Institute of Hazard, Risk and Resilience (IHRR: <http://www.dur.ac.uk/ihrr/>).

Appointed Fellows may be offered a non-fixed term academic position at the end of their Fellowship (offer is subject to performance and funding availability).

For further details see: <http://tinyurl.com/casq65a>
Contact for informal enquiries: Professor Marc Knight (m.r.knight@durham.ac.uk)

Application deadline is 8 August 2012 (apply at <http://tinyurl.com/casq65a>)

"HOELZEL A.R." <a.r.hoelzel@durham.ac.uk>

Finland AgricultureBioinformatics

Open position in bioinformatics

A permanent position for carrying out research in the field of bioinformatics applied to farm animals and plants is available at MTT Agrifood Research Finland in Jokioinen.

MTT Agrifood Research Finland is a leading research institute in Finland developing sustainability and competitiveness of the food system (<http://www.mtt.fi/-english>). Operating under the Ministry of Agriculture and Forestry, MTT employs around 750 people at 15 locations across Finland. Our head office is situated at Jokioinen, a 1.5-hour drive from Helsinki.

The bioinformatician will join the Biotechnology and Food Research Unit, genetics group and work mainly in collaboration with researchers in the farm animal and plant genomics teams. The main research focus of the teams is on using genomics tools in animal and plant breeding, nutrigenomics, and systemsbiology of fertility.

The researcher will be responsible of using methods of bioinformatics in carrying out research on animal and plant genomics. The person should especially implement new methods for analyzing large amounts of sequence data, be involved in writing scientific articles and assist other researchers in the use of bioinformatic

tools.

The successful candidate should have a PhD or Masters degree in bioinformatics, statistics, computer science, molecular biology, population genetics or appropriate related discipline. Good knowledge and experience in working with large data sets and sequence data, good programming skills and good knowledge in genomics and biology are essential. We require good language skills in written and oral English.

We offer a flexible working environment and a good opportunity to get involved in many different research projects in the field of genomics.

The salary will be based on the job grade levels 12 to 13 and personal work performance, where the base salary will be from 2.635,82 to 2916,76 and the additional personal amount at most 46 % of the base salary.

The starting date for the job is on September 1st 2012 or as agreed.

Applications, including CV and references should be addressed to director Eeva-Liisa Ryhanen, MTT Biotechnology and Food Research and sent by mail to MTT/kirjaamo, Humppilantie 14, 31600 Jokioinen, Finland or by email in a single pdf-file to the Registry Office of MTT kirjaamo@mtt.fi no later than the 31st of July 2012, 3PM Finnish time. Please, add the code 400-142-12 to your application.

For more information about the position, please contact professor Johanna Vilkki, phone +358 29 5317900, johanna.vilkki@mtt.fi or the director of Biotechnology and Food Research Unit of MTT, Dr. Eeva-Liisa Ryhanen, phone +358 29 531 7692, eeva-liisa.ryhanen@mtt.fi or team leader Maria Tuiskula-Haavisto, phone +358 29 5317831, maria.tuiskula-haavisto@mtt.fi. Please notice that applications sent to the personal e-mail addresses are not accepted.

Nina Schulman <nina.schulman@mtt.fi>

ImperialCollege London EvolutionTeaching

Opportunity Part-time Teaching Fellow/Senior Teaching Fellow: NS 2012 141 JT

Job Title Part-time Teaching Fellow/Senior Teaching Fellow Department/Division/Faculty Division of Ecology and Evolution, Faculty of Natural Sciences

Teaching Fellow - Salary: Â£32,130 - Â£39,920 per annum (pro rata) or Senior Teaching Fellow - Salary: Â£41,030 per annum (pro rata)

Silwood Park Campus

The Department of Life Sciences is currently seeking to recruit a Teaching Fellow/Senior Teaching Fellow in the area of evolutionary biology and/or biodiversity to be in post by 1 October 2012.

The post is to cover the teaching commitments of Professor Timothy Barraclough during a sabbatical fellowship. The main duties will include administration of the MSc and MRes in Ecology, Evolution and Conservation, teaching and supervising research projects of postgraduate students, teaching a two-week evolution course or its equivalent for undergraduate students, and acting as a tutor and examiner for the undergraduate Biology course. The post-holder will be able to offer Masters projects on their own research as well as supervising students conducting projects at external organisations.

For appointment to Teaching Fellow, you must hold a degree (or equivalent professional qualifications and/or experience) in a relevant subject, and have, or be working towards, a recognised teaching qualification. You must also have specialist knowledge in the relevant discipline and of teaching methods and techniques within your own area, and be able to teach effectively at undergraduate level. You must also be familiar with a variety of strategies to promote and assess teaching

For appointment to Senior Teaching Fellow, you must have a degree and PhD (or equivalent professional qualifications and/or experience) in a relevant discipline and a recognised qualification in Higher Education learning and teaching (or nearing completion). You must also have an excellent track record in a research in a relevant discipline, illustrated by a record of publications in good journals. You must also have experience of teaching at undergraduate and postgraduate level, and of supervising student research projects.

You will be based within the Division of Ecology and Evolution at the Silwood Park Campus. This is a part-time (15 hours per week), fixed-term position available for up to 2 years.

For more information and to apply, follow this link: https://www4.ad.ic.ac.uk/OA_HTML/OA.jsp?akRegionCode=-IRC_VIS_VAC_DISPLAY_PAGE&akRegionApplicationId=800&transactionid=1823754726&retainAM=-Y&addBreadCrumb=S&p_svid=37058&p_spid=-1582196&oapc=7&oas=5hpqTl-501pqHKHVZN0DQQ

For an informal discussion about the post please contact Professor Tim Barraclough by email:

t.barraclough@imperial.ac.uk or telephone +44 (0)207 594 2245.

Prof. Timothy G. Barraclough, Professor of Evolutionary Biology

Division of Biology, Imperial College London, Silwood Park Campus, Ascot, Berkshire, SL5 7PY, UK E-mail: t.barraclough@imperial.ac.uk Telephone: +44 (0)207 594 2247 Fax: +44 (0)207 594 2339 Web-page: www.imperial.ac.uk/people/t.barraclough ** MSc course in Ecology, Evolution and Conservation ** www3.imperial.ac.uk/naturalsciences/courses/pg/ls/ecology

Timothy Barraclough <t.barraclough@imperial.ac.uk>

JamesCookU EvolutionaryBiol

Lecturer/Senior Lecturer - Zoology/Ecology

James Cook University, School of Marine & Tropical Biology

Ref. No. 12237 - Cairns

The appointee must have demonstrated a strong interest in teaching and research in biology in the tropics and will have an established and successful profile in tertiary teaching, graduate student supervision and research. The appointee will teach in general and specific areas of expertise and will be expected to become an active partner in the running of the Discipline. The appointee must also have an outstanding research track record and be expected to develop and maintain an internationally recognised research program on the basis of successful competitive grant applications. Preference may be given to applicants with interests in one or more of the following areas: plant-animal interactions, ecosystem services, biological control, invertebrate biology and/or entomology.

Employment Type: Appointment will be full-time on a continuing basis.

Salary: Lecturer - Academic Level B - \$79,837 - \$94,203 per annum; Senior Lecturer - Academic Level C - \$97,075 - \$111,440 per annum. Level of appointment and commencing salary will be in accordance with qualifications and experience. Benefits include 5 weeks annual leave, generous employer superannuation contribution and attractive options for salary packaging.

Applications close on 17 August 2012.

For more information go to www.jcu.edu.au/jobs, en-

ter 12237 in the reference field and follow the links.

simon.robson@jcu.edu.au

Kalahari 3 FieldRes Sparrows

FIELD RESEARCHERS NEEDED

The Evolution of Cooperation in Sparrow Weaver Societies Kalahari desert, South Africa

3 positions: approx 1st Oct 2012 V 30th April 2013

We are seeking three enthusiastic research assistants to join our team studying white-browed sparrow weavers in the Kalahari desert, South Africa. The project is investigating the social dynamics of cooperative breeding, by asking evolutionary and mechanistic questions about parenting, cooperation and dispersal. The project is led by Andy Young, University of Exeter, and is based in Tswalu Kalahari Reserve where we have been studying 30+ groups for the past 3 years. For more information on the sparrow weaver project see www.animalsocieties.org The positions are for the duration of the peak breeding season (1st Oct V 30th Apr; though dates are somewhat flexible). The fieldwork will involve the collection of key behavioural and life-history data from eggs, chicks and birds, and the capture and processing of adult birds. Applicants should be enthusiastic, hardworking and physically fit and hold a driving licence. Previous field experience (particularly any bird handling/ringing experience) is desirable, but not essential V training in all field skills will be provided. Food and accommodation expenses will be covered while in the field and a contribution can also be made towards travel costs.

Please email a CV & covering letter ASAP to Andy Young (but by 30th July latest) a.j.young@exeter.ac.uk www.animalsocieties.org Andrew Young BBSRC Research Fellow Centre for Ecology and Conservation University of Exeter Cornwall Campus Tremough, Cornwall TR10 9EZ

Tel: +44 1326 254241 www.animalsocieties.org
 "Young, Andrew" <A.J.Young@exeter.ac.uk>

Krakow Poland LifeHistoryEvolution

Life History Evolution Group, Institute of Environmental Sciences, Faculty of Biology and Earth Sciences, Jagiellonian University, Krakow, Poland

Led by Professor Jan Kozłowski a prestigious project Maestro (National Science Center) will be supported by two research posts in evolutionary biology and physiological ecology at the Assistant level. The 3-year positions will be available for candidates with a MSc or PhD degree and strong record of research accomplishment. The search for explanation of mass-scaling of metabolism and temperature-dependence of life histories (low temperatures retard ectotherms growth but often increase adult size) is one of the central issues of physiological and evolutionary ecology. The project explores the role of cell size and oxygen conditions in the origin of these two phenomena and involves experimental research conducted on ectothermic invertebrates and vertebrates.

For further information how apply please visit: <http://www.nauka.gov.pl/ministry/job-vacancies-in-poland/> Informal enquiries should be addressed to: Prof. Jan Kozłowski: jan.kozlowski@uj.edu.pl

marcin.czarnoleski@uj.edu.pl

NESCent Informatics

Three developer positions at NESCent

Are you as passionate as we are about open-source, open data, open science? Do you love coding for science? Or do you have a talent for designing interfaces that users love, not loathe? Want to be part of a great team that's always on the pulse of how to use technology for enabling more and better science? We're hiring for several developer positions in NESCent Informatics! Developers will be working on NESCent core software development (nescent.org), the Dryad data repository (datadryad.org) and Open Tree of Life (opentreeoflife.org). Open positions:

* scientific software architect * scientific software developer * UI / UX designer for scientific applications

Detailed information here:

<http://nescent.org/about/employment.php> or contact Karen Cranston (karen.cranston@nescent.org)

karen.cranston@gmail.com

Portugal HumanEvolution

CIBIO(<http://cibio.up.pt>) is a young and highly dynamic Research Centre located close to Porto, in the north of Portugal, which aims to be an international Centre of Excellence in the fields of Biodiversity and Evolution, offering great opportunities for multidisciplinary and stimulating research. The Centre occupies recently-built facilities, and has more than 100 researchers holding a PhD degree, as well as more than 100 MSc and PhD students, and people from many different countries. Researchers are organized in 17 research groups. The working atmosphere is vibrant and enthusiastic, and CIBIO is regularly visited by many scientists from abroad. Porto is a world-heritage town, capital of Port wine, and the Northern region of Portugal provides rich cultural and outdoor activities. The Centre has fully equipped molecular laboratories (multiple PCR rooms, automated sequencers, real-time PCR machines, etc), as well as technicians and administrative staff, and the necessary equipment for fieldwork. Research projects are performed at a global scale. We are now advertising two 30-months full research contracts (www.eracareers.pt) primarily funded by a FP7 CAPACITIES program and expect to recruit enthusiastic and highly motivated researchers in the areas indicated below. The positions are expected to start by September 1st.

1. Plant Biology

A 30-months research position is available at CIBIO (<http://cibio.up.pt>), University of Porto, Portugal, in the area of plant metal homeostasis and hyperaccumulation. The candidate should have a solid research background in the analysis of physiological and molecular mechanisms underlying metal homeostasis and accumulation in plants, and it is desirable experience with both an hyperaccumulator and non-hyperaccumulator plant model species.

The candidate should master molecular biology techniques allowing forward and reverse genetic approaches

for identification and analysis of genes of interest. Additionally experience with genetic approaches, development of molecular markers and use of natural variation in traits of interest (metal accumulation) will be valued. Within this research, the candidate will also study the regulatory and evolutionary mechanisms of the metal/micronutrient homeostasis network, thus previous work in this area will be considered an advantage.

It is appreciated if he/she already started to build a worldwide network of collaborators for future research in plant metal homeostasis and hyperaccumulation. The candidate should have a PhD in biology, plant sciences or related fields, a minimum of 3 years as Postdoc and a Curriculum vitae proving solid knowledge in plant metal homeostasis and hyperaccumulation. The candidate should additionally have a significant publication record in SCI journals for the above-mentioned topics and supervised or co-supervised academic theses (both MSc and PhD theses). Experience in teaching in this field will also be considered valuable. The candidate is expected to build his/her own research group, establish solid international collaborations, and be able to attract national and international funding. The candidate should be a good communicator and speak and write fluent English, and will be invited to participate in teaching at the MSc and PhD levels. The ranking of candidates will result from a global appreciation of the Curriculum vitae followed by a job interview. Salary will correspond approximately to a gross annual income of 50.000 EUR (before taxes).

2. Human Evolutionary Genetics

A 30-month research position in the field of human evolutionary genetics is available at CIBIO (<http://cibio.up.pt>), University of Porto, in the research group headed by Professor Jorge Rocha. The work will cover different research topics related to the evolutionary history of human genes and populations. A strong focus will be devoted to the demographic history of African populations and to the origins and spread of adaptive variation. A particular emphasis will be given to the analysis of spatial patterns of genetic variation. The candidate is expected to have an interdisciplinary attitude, more oriented towards research topics and data analysis than to lab techniques and data generation. Accordingly, he/she is expected to have a sound knowledge of population genetics theory and master different kinds of data analysis software currently available to interpret human population genetic data. Additional computer programming skills will be considered an advantage. Applicants should have a PhD degree, a minimum of 3 years postdoctoral experience, and a significant publication record in SCI journals. Fluency in

English speaking and writing is additionally required. As the candidate will be invited to participate in teaching at the MSc and PhD

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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>

RowanU 1year EvolBiol

Position: Instructor/Assistant Professor, Biological Sciences - 3/4- Time Temporary

Department: Biological Sciences Description: The Department of Biological Sciences invites applications for a one- year, 3/4-time Instructor / Assistant Professor position available beginning Sept. 1, 2012. The successful candidate will teach a total of four courses and 18 instructor credits across the fall and spring semesters.

Courses taught will include major-level introductory courses in 1) adaptation, diversity and evolution; 2) ecology; 3) as available, upper level courses within the candidate's areas of expertise. The successful candidate will contribute appropriate service to the department, and will have the opportunity to pursue research or participate in collaborative research programs within our department and the University.

Qualifications: A Ph.D. or equivalent degree in some field of biology is required, but ABD will be considered. Applicants should have expertise in evolution, organismal diversity or ecology. A strong commitment to excellence in undergraduate education is expected, and previous success and experience in college teaching is strongly preferred.

Starting Date: September 1, 2012 Salary: Competitive General Info: The department serves 650 biology majors with 12 full-time faculty members and 2 full-time laboratory technicians. We have 10 fully equipped, technology supported classrooms as well as research labs supporting the major fields of biology. Current objectives for the department include development of programs in bioinformatics and in environmental studies, contributing to the success of the School of Biomedical Sciences, and contributing to the success of the Cooper Medical School at Rowan University. For information on the Department of Biological Sciences, please refer to the department's website at <http://www.rowan.edu/>

biology. Rowan University values diversity and is committed to equal opportunity in employment.

All positions are contingent upon budget appropriations.

Contact: Send cover letter, CV, a statement of teaching philosophy, a statement of research interests and unofficial undergraduate and graduate transcripts. Applicants should also arrange for delivery of at least two letters of reference. Two letters of reference must attest to the candidate's teaching abilities. Review of applications begins July 9th and will continue until the search is completed.

Applicants should submit materials by e-mail to both obrien@rowan.edu and joslin@rowan.edu

Postal mail (not preferred) may be sent to: Faculty Search Committee Dept. of Biological Sciences Rowan University 201 Mullica Hill Road Glassboro, NJ 08028

Inquiries may be addressed to Dr. Terry O'Brien (obrien@rowan.edu).

Srinivasan@rowan.edu

UCIrvine LabTech DrosmiRNAs

UCIrvine.LabTechDrosmiRNAs

Applications are invited for a specialist position in the laboratory of Dr. José M. Ranz at University of California, Irvine. The position is available starting in October 2012 for one and a half years. The candidate will join different active research lines and contribute to the up-and-running of the laboratory. A strong background in Drosophila genetics and common molecular techniques (extraction of total RNA and genomic DNA; PCR; in situ hybridization on embryos) is required and some experience in bioinformatics is desired. Applicants with prior experience in microRNA research are particularly encouraged. Salary commensurate with experience. Applications should include a covering letter describing previous experience and fit to the position, full CV, and the name and address of two references. The deadline for applications is September 7th, 2012. Applications should be sent to the email address below: msaplala@uci.edu

The University of California, Irvine has an active career partner program, is an equal opportunity employer committed to excellence through diversity, and has a National Science Foundation Advance Gender Equity

Program.

Jose M. Ranz, Ph.D. Assistant Professor Department of Ecology and Evolutionary Biology 465 Steinhaus Hall University of California, Irvine Irvine, CA 92697 USA

E-mail: jranz@uci.edu Telf: +1 949 824 9071 Fax: +1 949 824 2181

jranz@uci.edu

UCaliforniaDavis EvolutionaryGenetics

The UC Davis Canid Diversity and Conservation Unit is seeking a highly motivated person to fill a position as a molecular genetics specialist (university title: Junior Specialist) to assist with research in Ben Sacks's laboratory. Research in the Sacks lab focuses on evolution, ecology, phylogeography, and conservation genetics of mammalian carnivores, domestic dogs, and other vertebrates. We use both molecular-genetic and field-based approaches in our research. Laboratory facilities include modern and ancient DNA units. Additional details about ongoing projects can be found on the lab website (<http://www.vgl.ucdavis.edu/cdcg/home.php>)

The Junior Specialist will assist principal investigator, post-doctoral scholars, and graduate students in ongoing research projects by conducting basic molecular genetics lab work and will help recruit, train, and supervise undergraduate interns. Laboratory activities include DNA extractions, PCR, gel electrophoresis, microsatellite genotyping, sequencing, cloning, database entry and management, maintaining laboratory supplies/ equipment, ensuring compliance with laboratory safety regulations, and training students and interns.

Minimum Qualifications: Bachelor's or Master's Degree in an appropriate

field such as Molecular Biology, Genetics, or Wildlife Biology, along with

1-2 years research experience that included performing DNA extractions

and PCR, and routine use of basic computer software. Experience with microsatellite genotyping and/or DNA sequencing is required. Preference will be given to applicants with a Master's degree or demonstrated experience in the field, especially those with an interest in ecological or evolutionary biology. This is a full time

1-yr position with possibility of renewal.

Qualified candidates should submit (via email) a letter of application

describing qualifications for the position and reason for interest,

CV, and letters from three references detailing level of experience with DNA sequencing and/or genotyping, and overall capabilities working in a laboratory setting to bnsacks@ucdavis.edu

Salary: Will be determined by experience and qualifications.

Starting Date: September 1-15, 2012.

Closing date: For full consideration, all application materials must be submitted by Aug 15, 2012. Interviews may be conducted before the closing date; however, no hiring decision will be made until after that date.

Ben Sacks Canid Diversity and Conservation Lab Dept. Population Health and Reproduction Veterinary Genetics Laboratory University of California, Davis One Shields Avenue/Old Davis Rd. Davis, California 95616-8744 USA

Phone: 530-754-9088

bnsacks@ucdavis.edu

The University of California, Davis is an equal opportunity/affirmative action employer.

bnsacks@ucdavis.edu

UGeorgia Genomics

The Georgia Genomics Facility (GGF, dna.uga.edu) at the University of Georgia (UGA) invites applications for a Non-Tenure Track Assistant Research Scientist with a PhD in the Life Sciences and postdoctoral experience. We are seeking an outstanding scientist with research expertise and skills in some of the following areas: experimental design for genomics research, next-generation sequencing, high throughput genotyping and computational analysis of next-generation DNA sequencing data for a variety of applications including SNP and genome annotation, gene expression analysis, genome and transcriptome assembly, metagenomics, and pathway analysis.

The Georgia Genomics Facility is a core sequencing and genotyping laboratory providing a wide range of library

preparation, sequencing, genotyping and related services. We are looking for a dynamic Research Scientist to help UGA faculty, postdocs, students and off-campus customers use these services to address their specific questions relating a diverse array of research areas including community ecology, population and association genetics, functional genomics, and agricultural and biomedical applications. In addition, the successful applicant will join the GGF leadership team to develop new services and infrastructure to advance genomics and related research at UGA and throughout Georgia.

The responsibilities of the successful candidate will include 75 % administration and service, 15% research, and 10% teaching (e.g. workshops, guest lectures, student mentoring). Non-tenure track Research Scientist positions at UGA are affiliated with academic home departments. The Institute of Bioinformatics (<http://www.bioinformatics.uga.edu/>) is a likely home for this position, but the successful candidate could negotiate membership within alternative departments. More information on non-tenure track research appointments at UGA is available at: www.ovpr.uga.edu/docs/policies/research/-research-scientist-appointment-promotion .

Applicants should send a single PDF containing: 1) a curriculum vitae, 2) a brief statement of research interests including descriptions of experience in genomics and project management, and 3) names of three references to Dr. Jim Leebens-Mack (jleebensmack@plantbio.uga.edu). Application material should be received by July 28th for full consideration but the search will remain open until a suitable candidate is identified. While we hope to fill the position by September 1, 2012, the start date is negotiable. Candidates with experience appropriate for appointment at the Associate or Full Research Scientist level will also be considered. The University of Georgia is an Affirmative Action/Equal Opportunity Employer and strongly encourages applications of women and members of minority groups.

Jim Leebens-Mack Department of Plant Biology University of Georgia Athens, GA 30602-7271

Phone: 706-583-5573 Fax: 706-542-1805 email: jleebensmack@plantbio.uga.edu url: <http://www.plantbio.uga.edu/~jleebensmack/JLMmain.html>

jleebensmack@plantbio.uga.edu

ULouvainLaNeuve Tech Biodiversity

Biodiversity Research Centre – Earth and Life Institute - Université catholique de Louvain (UCL)

Position for a LABORATORY TECHNICIAN in Molecular Ecology

A full time two-year position for a technician in the field of molecular ecology is available at the Earth and Life Institute (Section Biodiversity), University of Louvain-la-Neuve (UCL) in Belgium (<http://www.uclouvain.be/en-bdiv.html>).

The technician will work within the framework of a large collaborative research project over several years between 3 active research groups at UCL (Profs. Hans Van Dyck (Spokesman), Nicolas Schtickzelle and Caroline Nieberding and their international network. The general framework of this project aims for a better understanding of the role and mechanisms of plasticity for present and future adaptation and survival in changing environments in a series of model organisms including butterflies, protists and spider mites.

The technician will be in charge of collecting data using various molecular techniques in development in the field of Molecular Ecology including RNA and DNA extractions, quantification and estimation of RNA and DNA quality, PCR, quantitative and real time PCR, cloning, sequencing and basic bioinformatics work. The technician will work in close collaboration with a postdoc with related expertise hired for the same period of time, and with Prof. C. Nieberding. International collaborations will provide the opportunity to discover and learn techniques in other laboratories (e. g. Dr. P. Beldade, Gulbenkian Institute of Science, Portugal) and develop communication skills in English and French. This position thus offers the opportunity to work in an international, multidisciplinary and stimulating scientific environment.

The following elements are requested: - Diploma of a technical school or equivalent (non university) in biotechnology, molecular biology or equivalent. - Know-how knowledge in some or most of the following molecular techniques : RNA and DNA extractions, quantification and estimation of RNA and DNA quality, PCR, quantitative and real time PCR, cloning, designing primers, sequencing and use of internet applications such as Genbank, Pubmed, Gene Ontology. - Ability

and interest in reading and communication in scientific English - Creativity, personal initiative and ability to identify relevant new protocols and learn new techniques - Ability and interest in working as a team player

For practical information concerning salaries, benefits, insurances and conditions of eligibility please contact Mrs. D. Socquet at UCL (dominique.socquet@uclouvain.be; +32 (0) 10 47 2720). Applications will be reviewed directly until position is filled. Anticipated start date is September-October 2012 (to be negotiated). Our University is an Equal Opportunity/Affirmative Action Employer, and is in a French-speaking region, but the language for meetings and scientific interactions is English. For background information about our university, see <http://www.uclouvain.be/en-index.html> Application should be sent to Caroline Nieberding (caroline.nieberding@uclouvain.be) and include the following: (1) a cover letter describing your research interests and qualifications, (2) a full CV, (3) contact information (email, phone number) of minimum 2 referees. Please include « Technician application » in the subject line of the e-mail. Informal inquiries are welcome.

– Caroline.

Caroline Nieberding Evolutionary Ecology and Genetics Group BDIV Research Centre Earth and Life Institute Académie Louvain (UCL) Carnoy building, office b112 Belgium phone: +32 (0)10 47 34 88 website: <http://www.uclouvain.be/en-273362.html> Parcel and mail deliveries at the secretary's office :

Earth and Life Institute Université catholique de Louvain Secrétaire ELIB SST/ELI/ELIB Carnoy (local B193) Croix du sud 4-5, bte L7.07.04 1348 Louvain-la-Neuve

phone: +32 (0) 10 47 34 98 fax: +32 (0) 10 47 34 90

Caroline Nieberding <caroline.nieberding@uclouvain.be>

UMinnesota TheoreticalBiol

The College of Biological Sciences at the University of Minnesota announces two nine month, tenure-track positions, one at open rank and one Assistant Professor. Individuals in these positions will be the nucleus of a cluster in quantitative, theoretical biology, conducting research to address questions of broad biological import. We welcome applicants working in any area of

theoretical biology, with focal areas of interest in evolution and ecology at levels of biology ranging from molecules to ecosystems.

Duties and Responsibilities:

Each successful candidate will develop a strong, extramurally funded and* * collaborative research program, pursue a scholarly, innovative, and collaborative teaching program, advise undergraduate, graduate and post-doctoral students, and participate in professional service. This position provides numerous opportunities for collaboration in diverse areas of biology, mathematics, and computer science and access to students in multiple graduate programs.

Required Qualifications:

-

Ph.D. or foreign equivalent in ecology, evolution, mathematics, or a related discipline -

Strong record of publication of research relevant to the position -

Potential to initiate and sustain strong research program -

Ability to communicate effectively with multiple audiences -

Record of interacting creatively, collaboratively, and productively with other scientists -

Evidence of commitment to teaching and student learning

Materials Required:

-

Letter of application/intent -

CV -

digital copies of three publications of broadest significance -

Names/Contact information for three professional references (letters of recommendation can be requested after the pool has been narrowed) -

Statement of Research (Additional Document 1) -

Statement of Teaching (Additional Document 2)

Environment:

Founded in 1851, the University of Minnesota, with its five campuses and 67,932 students, is one of the largest, most comprehensive universities in the United States, and ranks among the most prestigious research universities in the world. It is both a major research institution, with scholars of national and international reputation,

and a state land-grant university, with a strong tradition of education and public engagement.

Program Unit/Description:

The College of Biological Sciences at The University of Minnesota-Twin Cities campus has extensive research facilities, including laboratories, greenhouses, field research stations, museum and herbarium collections, high performance computing, and genomics. The campus is located in the heart of the Minneapolis-Saint Paul metropolitan area, which is rich in cultural and natural attractions.

The University of Minnesota provides equal access to and opportunity in its programs, facilities, and employment without regard to race, color, creed, religion, national origin, gender, age, marital status, disability, public assistance status, veteran status, sexual orientation, gender identity, or gender expression.

For more details about this and other positions in the "Cluster Hire Initiative" visit: <http://www.cbs.umn.edu/facres/cluster-hiring-cbs/> Inquiries can be made to Eric Seabloom (seabloom@umn.edu) or Ruth Shaw (shawx016@umn.edu) who cochair the search committee.

shawx016@umn.edu

UOklahoma CuratorHerpetology

NOTICE OF HERPETOLOGY POSITION

POSITION AVAILABLE: Tenure-track Assistant Curator of Herpetology and Assistant Professor of Biology, Sam Noble Museum and Department of Biology, the University of Oklahoma, Norman, Oklahoma.

SALARY: Negotiable (12-month appointment).
NOTE: 1.00 FTE of the salary line item will be in the museum and tenure will be in the Department of Biology.

BEGINNING DATE: (1 July 2013)

RESPONSIBILITIES: The curators responsibilities include four areas: (1) developing and maintaining a program of externally funded scholarly research in herpetology; (2) overseeing care and obtaining support for a collection of more than 50,000 specimens; (3) exhibit development and support, including obtaining or collaborating to obtain external funds to assist with exhibits; and (4) museum-related outreach activities (service). Curators and professors engage in original

funded research in their discipline and make research results available to the scientific community and public through publications in quality journals and participation at annual society meetings or symposia. Curators assure adequate care of the collection, including preservation and conservation, maintaining records, identifying and cataloging specimens, supervising preparators and assistants, expanding the collections, and developing long-range plans for collection maintenance and development. A full-time collection manager is funded in this collection, and a rotating graduate assistant appointment is assigned to the collection. Faculty curators interpret their discipline to students and the public through displays, public programs, and academic activities as graduate student supervisors and instructors of one course per year (one-half the department teaching load). Ph.D., teaching experience, and field and museum research experience in herpetology are required. Research must have a collection base, although diverse fields of study are acceptable (e.g., systematics, biogeography, evolutionary biology, coevolution). We seek a person who in time will become a leading authority in their field of study.

GENERAL INFORMATION: The Sam Noble Museum is an organized research unit of the University of Oklahoma. The present facility is one of the finest university museums in the world. The museum has an outstanding curatorial, collections, exhibits, and support staff that serves the museums mission from research to preservation to education at all levels. The Department of Biology is a leading academic department in the university. Both units seek an individual to complement or expand upon programs in organismal biology and evolutionary biology.

APPLICATIONS: Send cover letter, curriculum vitae, summary of experience and goals, representative pdf reprint examples, and names, addresses, and telephone numbers of references to (electronic applications preferred): Dr. Michael A. Mares, Director, mmares@ou.edu. Attn. Herpetology Search Committee. [Street address] Sam Noble Museum, 2401 Chautauqua Ave., Norman, Oklahoma, 73072-7029. Visit us at <http://snomnh.ou.edu> . **CLOSING DATE:** Screening of candidates will begin 1 October 2012 and continue until the position is filled.

"Wall, Salina E." <salinawall@ou.edu>

UOxford FieldAssist

Dear colleagues,

The aphid lab in the Department of Zoology at the University of Oxford (England) needs a field assistant for a project to study aphid trophic webs in the field. We will establish and maintain aphid colonies on potted bean plants and collect parasitized individuals at regular intervals. Work will also involve rearing parasitized aphids in the laboratory. Work is required for two days a week from July the 9th to August the 13th. Driving license would be preferred. Hour based salary plus travel and field expenses will be covered.

If interested or know of someone that might be please contact Enric.frago@zoo.ox.ac.uk

More information about the group can be found here:

<https://sites.google.com/site/enricfrago/> <http://www.zoo.ox.ac.uk/group/godfray/> – Enric Frago University of Oxford Department of Zoology The Timbergen Building, South Parks Road Oxford, OX1 3PS enric.frago@zoo.ox.ac.uk +44(0)1865281079 <https://sites.google.com/site/enricfrago/>

enric.frago@zoo.ox.ac.uk

UPortsmouth 2 Evolution

Two lecturer (=assistant professor) positions in evolution, ecology, and/or conservation ecology are being advertised at the School of Biological Sciences, University of Portsmouth, UK (<http://www.port.ac.uk/departments/academic/biology/> (<http://www.port.ac.uk>)). We are particularly interested in people working on the evolutionary ecology of species interactions, but related areas will be considered. Additional details and instructions for applying are at: <http://www.port.ac.uk/vacancies/academic/vacancytitle,157625,en.html> and <http://www.port.ac.uk/vacancies/academic/vacancytitle,157624,en.html>. Note that one position requires expertise in plant biology, whereas the second position is open with respect to organisms studied.

Portsmouth is a compact, small city on the south coast of England, with relatively warm, sunny weather (by UK standards). Nearby living situations range from seaside urban to rural, with London and main airports readily accessible by (reasonably) fast trains. Portsmouth lies at the mouth of the Solent/Spithead waterway, which is famous for sailing and ferry connections to the scenic Isle of Wight (which is commutably

close).

Note that the positions close very soon; application materials must be submitted electronically by 6 July, 12 noon British Summer Time. (No letters of reference are needed until after the first cut.)

Informal inquiries can be directed to Prof Scott Armbruster (scott.armbruster@port.ac.uk) or Prof Matt Guille, Head of School (matt.guille@port.ac.uk).

Scott Armbruster <Scott.Armbruster@port.ac.uk>

USheffield DataAnalyst

Postdoctoral Researcher (Data Analyst) University of Sheffield - Department of Animal & Plant Sciences

Job Reference Number: UOS004864 Contract Type: Fixed-term Faculty: Faculty of Science Salary: Grade 7, 28,401 UK pounds per annum Closing Date: 9th August 2012

Summary: An exciting opportunity exists for a researcher with experience in population genetic analyses, with relevant bioinformatic skills to join the NERC Biomolecular Analysis Facility (NBAF) node in Sheffield. The appointee will assist Facility users with study design, data analysis and training, and contribute to the node's research and development activities.

You will have a PhD or equivalent in molecular ecology or evolutionary genetics, including genetic analyses (for example, population structure, mating systems, linkage mapping or phylogeny) and possess excellent analytical skills, preferably including experience of bioinformatic programming tools. Experience in bio-informatic analyses, such as those involving Next-Generation sequencing would also be an advantage.

The post is fixed-term with an immediate start date, for one year in the first instance.

For additional information about the job (and university) please click on "Apply online" on the following webpage

<http://www.jobs.ac.uk/job/AEU543/data-analyst/>

Informal enquiries can be made to Professor Terry Burke (T.A.Burke@Sheffield.ac.uk) or Dr Deborah Dawson (D.A.Dawson@Sheffield.ac.uk).

d.a.dawson@sheffield.ac.uk

UVirginia ResTech EvolutionaryGenetics

The Blackman Laboratory in the Department of Biology is seeking a Laboratory and Research Specialist I to assist with research in evolutionary and ecological developmental genetics using sunflower and monkeyflower as study systems. Research in the lab focuses on how and why plant developmental responses to environmental cues evolve during domestication, adaptation, and speciation.

The position will involve a combination of research and lab management responsibilities. Research duties will include plant care and phenotyping, molecular and biochemical work (e.g. DNA/RNA extraction, genotyping, qRT-PCR, sequencing library construction), and coordination of large field/greenhouse experiments. Initial projects will be closely supervised with increased independence possible as experience and expertise are developed. Lab management duties will include data and germplasm collection management, oversight of lab organization, ordering supplies and equipment, and supervision and training of undergraduate researchers.

A Bachelor's degree in Biology or a related discipline is required. Strong organizational, computer, and communication skills are essential, and demonstrated experience with basic molecular biology techniques and plant care is desirable.

Review of applications will begin July 19, 2012. However, the position will remain open until filled. Ideal start date is September 2012. This is a one-year appointment; however, the appointment may be renewed for an additional one-year, contingent upon available funding and satisfactory performance. To apply, please submit a candidate profile through Jobs@UVA (<https://jobs.virginia.edu>) and electronically attach: curriculum vitae with list of publications, a cover letter that summarizes research interests and professional goals, and contact information for three (3) references; search on posting number 0610348.

Questions regarding this position should be directed to: Dr. Benjamin Blackman bkb2f@virginia.edu

Questions regarding the Candidate Profile process or Jobs@UVA should be directed to: Mary Liberman ml5ac@virginia.edu

The University of Virginia is an Equal Opportu-

nity/Affirmative Action Employer. Women, minorities, veterans, and persons with disabilities are encouraged to apply.

bkb7@duke.edu

UdelosAndes EvoDevo

UNIVERSIDAD DE LOS ANDES

Developmental Biology

The Department of Biological Sciences at the Universidad de los Andes in Bogotá, Colombia, seeks to fill a full-time position in Developmental Biology at the Assistant or Associate Professor level. The successful applicant must possess a Ph.D., preferably with post-doctoral experience and a successful track record of scientific productivity. We especially encourage applications from candidates with knowledge and research interests in evolutionary developmental biology (evo-devo) and/or using research tools in genetics, genomics, molecular biology or bioinformatics.

The successful candidate will be expected to teach an undergraduate course in developmental biology and introductory cell biology, along with possible graduate courses in his or her area of expertise. He or she will advise undergraduate, masters and doctoral students in the Department of Biological Sciences. Teaching load will be 4-6 courses per year (2-3 during the first year).

The Biological Sciences Department at the Universidad de los Andes is among the top biology programs in Latin America, and hosts 27 full-time professors. Internationally recognized research programs include evolutionary genetics, microbial genomics, phylogeography, bioinformatics, evolutionary ecology, human genetics, and molecular systematics. The candidate will have his or her own lab space as well as access to a centralized DNA sequencing facility and confocal microscope and SEM. The Biology faculty is relatively young, dynamic and growing rapidly, and the University offers diverse sources of financing for professors and graduate student research. For more information visit: <http://dcb.uniandes.edu.co/> Interested candidates should send a curriculum vitae, a description of her or his research program, and a teaching statement (preferably as a single PDF) to the following email address: ccontbio@uniandes.edu.co

Deadline for receipt of material is September 15, 2012. Preferred candidates will then be asked to submit let-

ters of recommendation and copies of recent publications.

For additional information, please contact:

Adriana Bernal Profesora Asociada Departamento de Ciencias Biológicas Universidad de los Andes Tel. +57 1 339-4949 x2619 Email: abernal@uniandes.edu.co

Carlos Daniel Cadena Ordoñez
<ccadena@uniandes.edu.co>

vienna.at schlotc@gmail.com

Vienna Bioinformatics

The Vetmeduni Vienna invites applications for a full-time, tenure-track bioinformatician, preferentially with PhD and postdoctoral experience.

We are looking for a dynamic and communicative bioinformatician, who will collaborate with researchers of the Vetmeduni Vienna campus on the study design and analysis of NGS data. The projects, which include RNA-Seq, Chip-Seq, and Pool-Seq data require experience in working with large data sets and sequence data. Good programming skills and familiarity with the available analysis tools are essential.

The responsibilities of the successful candidate include 70% collaborative research, 10% teaching (workshops, student mentoring, etc), and 20% independent research (e.g.: methods development). The institute of Population Genetics will be the home for the position.

The position is available from October 2012, but the starting date is negotiable. The salary will commensurate with experience (minimum: 45000euro/year for candidates holding a PhD). Applicants should send a single PDF containing 1) curriculum vitae, 2) brief statement of research interests including descriptions of past experience with bioinformatics projects, and 3) names of three references to Prof. Dr. Christian Schlötterer (christian.schloetterer@vetmeduni.ac.at). While the search will continue until the position is filled, applications should be received by September, 15 to ensure full consideration.

Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390
<http://i122server.vu-wien.ac.at/pop> Vienna Graduate School of Population Genetics [---

Vienna HeadMolGenetics](http://www.popgen-</p></div><div data-bbox=)

Head of Molecular Genetics Laboratory

Department of Integrative Biology and Evolution
University of Veterinary Medicine, Vienna, Austria

We seek an interactive, motivated scientist capable of managing a genetics laboratory. Independent research is necessary though the main emphasis is to collaborate and support scientists in our department. A PhD in life sciences and a strong background in molecular genetics (e.g., DNA capillary sequencing, microsatellite typing, fragment analysis, SSCP, DGGE, Southern blotting, Western blotting, real-time PCR) are required. Experience with MHC-analyses, RNA-analyses, and diverse genomic techniques (next-generation sequencing) are an advantage. Post-doc experience is preferred.

Our department has a well-equipped genetics laboratory, technicians, and animal facilities. Vienna is generally ranked as one of the top cities in the world to live. The department operates bilingually, but German is useful.

The position is permanent, salary depends upon experience. To apply, please send (preferably via email) (1) CV, (2) publications, (3) a brief statement of research interests, (4) names of 3 people who can be contacted for letters of reference.

Please submit applications until *August 24th 2012* quoting the reference number 2012/0803 via e-mail (preferably) to *bewerbungen@vetmeduni.ac.at <mailto:bewerbungen@vetmeduni.ac.at>* or by post to the Personnel Department of the University of Veterinary Medicine, Veterinärplatz 1, A-1210 Vienna, Austria. Please do not forget to include the reference number or we shall be unable to relate your application to the correct vacancy announcement.

Prof. Dr. Walter Arnold Savoyenstr. 1, A-1160 Vienna Research Institute of Wildlife Ecology Phone +43/1/4890915-100, Fax-333 University of Veterinary Medicine <http://www.fwi.at>

Walter Arnold <Walter.Arnold@fwi.at>

WashingtonU AnthropologicalPopGeneticist

Please post to Evoldir the following faculty-job announcement:

Anthropological population geneticist Department of Anthropology Washington University Saint Louis, MO

We invite applications for a tenure-track appointment in physical anthropology at the level of Assistant Professor to begin in fall 2013. We seek an anthropologist with a research specialization in Anthropological Population Genetics. The successful candidate will be an individual with expertise that involves using genetic/genomic data and analytical techniques to address anthropological research questions among human and/or non-human primate populations. The individual should have appropriate training and skills in the field of human/primate population genetics (including current appropriate biomolecular techniques) and be engaged in an ongoing research program that involves both laboratory and (especially) field research. The successful candidate is expected to work with graduate students in developing research projects and have a strong commitment to undergraduate and graduate teaching. Duties include teaching courses, advising students, conducting sponsored research and writing for publication, and university service.

Applications should consist of a curriculum vitae and a cover letter describing current research and teaching interests, and names of three referees. Applicants must have a Ph.D. in hand by time of appointment. All materials should be sent as MSWord files or PDFs via e-mail with \$B!H(BPhysical Anthropology Search\$B!I(B in the subject line to: Melanie McDowell (melanie@artsci.wustl.edu) .

Priority will be given to applications received on or before November 1, 2012, but the search will continue until the position is filled.

Washington University is an equal opportunity/affirmative action employer. Applications from women and other members of under-represented groups are especially encouraged. This employer prohibits discrimination on the basis of sexual orientation/preference and gender identity/expression. Employment eligibility verification required upon hire.

Allan Larson <larson@wustl.edu>

YaleU PlantEvolution

Faculty Position in Plant Ecology

The Department of Ecology and Evolutionary Biology at Yale University invites applications for a tenure-track assistant professor position in plant ecology, including interactions between plants and other organisms and biogeochemical cycles. We seek applicants that use creative approaches to address fundamental questions in ecology. We are particularly interested in applicants that have or would develop a strong field research program. A record of outstanding achievement and a promising research program are more important than the specific research area.

Interested candidates should submit a CV, three relevant reprints or manuscripts, brief research and teaching statements, and names and addresses of three potential evaluators online at <https://academicjobsonline.org/ajo/Yale/EEB>. The search will remain open until the position is filled. The review of applications will begin 1 September 2012.

Yale University is an Equal Opportunity/Affirmative Action Employer. Yale values diversity among its students, staff, and faculty and strongly welcomes applications from women and underrepresented minorities.

David Vasseur Assistant Professor Yale University Department of Ecology and Evolutionary Biology New Haven CT Yale University

David Vasseur <david.vasseur@yale.edu>

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AgeGuess CitizenScienceProject

Dear EvolDir community,

We are happy to announce the launch of AgeGuess, a new citizen

science project investigating properties and biomarkers of ageing.

The scientific questions we aim at are directly relevant for our understanding of the evolution of aging, such as variance in the rate of aging among individuals, or heritabilities of aging biomarkers. Further we aim at outreaching to the public by informing about aging research and its foundation in evolutionary theory.

Please help us by spreading the word, and visit the website at www.ageguess.org Thank you for your interest!

Uli Steiner and Dusan Misevic

Uli Steiner <ulrich.steiner@inserm.fr>

Bacterial AncestralSequence Reconstruction

Hello,

I have a genome based tree of 48 bacterial taxa using a concatenation of 52 putatively orthologous genes. Quite a few gene tree topology differs from the genome tree.

Now I want to reconstruct the ancestral sequences for each of the orthologs. It needs an input of tree topology

and branch length. Since many gene tree topology are different from genome tree topology, how can I choose the topology for ancestral reconstruction?

There are two strategies here. (1) I would use the gene tree topology and associated branch length. (2) I would use the genome tree topology and re-estimate the branch length for each ortholog. Which one should I use?

Thanks!

Haiwei Luo University of Georgia

hluo2006@gmail.com

Current Zoology

Dear Colleague,

The journal CURRENT ZOOLOGY is planning two special columns for the 1st issue of 2013. One special column is Conservation Genomics/Genetics of Amphibians, and the other is Evolutionary Genomics. The guest editors for the first column are Dr Menghua Li (menghua.li@ioz.ac.cn) at the Institute of Zoology, Chinese Academy of Sciences and Dr. Juha Meril at University of Helsinki, the guest editor for the other column is Dr. Wen WANG (wwang@mail.kiz.ac.cn) at the Kunming Institute of Zoology, Chinese Academy of Sciences. We am now inviting active scientists to contribute to these special columns, and am wondering if you, either independently, or in conjunction with your students or colleagues, would consider contributing an article to this upcoming special column.

The journal CURRENT ZOOLOGY (formerly Acta Zool Sinica, founded in 1935, changed to be an English journal and covered by SCOPUS in 2009, covered by

SCI and Current Contents, BIOSIS Preview beginning from 2010, indexed by Zoological Records and Biological Abstracts for dozens of years), is an international journal focused on ecology, evolution and behavior. CURRENT ZOOLOGY seeks to publish research that explores the interface between zoological disciplines, and is truly integrative by illuminating the greater picture. Submissions in the research fields of ecology, behavioral biology, biogeography, conservation biology, evolutionary biology and ecological/evolutionary genomics are especially welcome. International contributors accounted for 83% of the annual total authorship in 2010 and 76% in 2011.

It is a longstanding commitment for the journal to publish Special Columns. A special column typically include three to eight peer-reviewed papers on the same theme. We encourage proposals for Special Columns on topics that reflect the current trends and hot studies in related research fields. All the manuscripts submitted to special columns are subject to peer review. Authors are not charged for paper handling and publication including color pages; the papers will be put online immediately after the papers have been accepted. Published papers can be read and downloaded free of charge. Previous special columns/issues and their links are attached below.

I'll await your reply as to whether you see yourself contributing a paper. Below is the time schedule for the special columns:

Deadline for manuscript submission: Oct 20, 2012; End of manuscript reviewing and revision: Dec. 20, 2012; Dec 21-Jan 10, 2013: paper finalizing Jan. 11-Feb. 20: typesetting, proof reading and correction, paper online; Feb. 20, 2013: paper printing.

You may send your manuscript now or by deadline. Manuscripts should be submitted to the special column via ScholarOne Manuscripts™ <http://www.currentzoology.org/newsdetail.asp?id=1283>, or <http://mc03.manuscriptcentral.com/currentzoology>. Manuscripts received after the deadline will be considered as submissions for regular issues.

If you do not have appropriate papers for THESE special columns, you are welcome to submit your studies to regular issues.

Whether you accept my invitation to contribute or not, I wish you every success and happiness in 2012! I look forward to your reply.

Sincerely,

Dr Zhi-Yun JIA Executive Editor Current Zoology
<http://www.currentzoology.org>

The published special columns:

Speciation and Sexual Selection: 2012, 58(3), <http://www.currentzoology.org/currentissue.asp>, Maria SERVEDIO, Department of Biology, University of North Carolina; Animal Culture: 2012, 58(2), http://www.currentzoology.org/issuedetail.asp?volume=58&number=2&issue_id=525, guest editors: Alex BENTLEY, University of Bristol, UK; Michael O'BRIEN, University of Missouri, USA; Animal Social Networks: 2012, 58(2), http://www.currentzoology.org/issuedetail.asp?volume=58&number=2&issue_id=525, guest editor: Daniel W. FRANKS, University of York, UK; Aquatic Invasive Species Science: 2011, Vol 57(6), http://www.currentzoology.org/issuedetail.asp?volume=57&number=6&issue_id=525, guest editor: Gerard van der Velde, Rob S.E.W. Leuven, Radboud University Nijmegen, The Netherlands

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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>

Distance between protein sequences

Dear Evoldir Members,

I would like to calculate distances (distance matrix) between protein sequences using my own predefined amino acid substitution matrix. Do you know a software that allows this? The phylib protdist may allow it but I was not able to find a description about the format of the substitution matrix.

Thanks for the suggestions!

Eszter Ari

– Ari, Eszter assistant lecturer Eotvos L. Univ., Dep. of Genetics arieszter@gmail.com +3613722500/8691

Ari Eszter <arieszter@gmail.com>

Drosophila transpositions

Dear Evo-Devo community,

I am working with *Drosophila melanogaster* and I would like to have an easy read-out for transposition events in the germline.

I was thinking about using a line that has a transposon inserted in the gene *white* so that frequency of transposition is $>$ or $=$ to frequency of red eyed flies in the next generation. For this purpose I was planning to use the wDZL stock but it had lost the transposon.

Can anyone help me with a stock or an idea to solve the problem?!

Thank you very much in advance!

All the very best

Marta Marialva

mmarialva@igc.gulbenkian.pt

EvoMedicinePublicHealth journal

For immediate release

*Oxford University Press launches *Evolution, Medicine, and Public Health*/*

Oxford University Press (OUP) and the Evolution, Medicine, and Public Health Foundation are pleased to announce the launch of the open access journal *Evolution, Medicine, and Public Health* (EMPH).

EMPH publishes original, rigorous applications of evolutionary biology to problems in medicine and public health, and research that advances basic evolutionary biology by studying issues that arise in the medical sciences. Knowledge will flow in both directions, with emphasis on work with the potential to reduce suffering and save lives. Because evolutionary biology is a basic science that reaches across many disciplines, EMPH is open to contributions on a broad range of topics.

The President of the Foundation, Randolph Nesse, <<http://nesse.us>> said: “Evolutionary biology is a sci-

ence whose applications in medicine and public health are finally being recognized. Articles published in EMPH will bring new recognition to these applications and to studies of disease that advance basic science. The Foundation is grateful to the distinguished evolutionary biologist Professor Stephen Stearns <<http://www.yale.edu/eeb/stearns/>> of Yale University for agreeing to lead the journal as Editor-in Chief. He has recruited eighty-nine of the most respected scholars in their fields to serve as Associate Editors; they include, as Senior Editors, David Haig (Harvard University), Carlo Maley (University of California, San Francisco), Angela McLean (University of Oxford), Andrew Read (Pennsylvania State University), and Gregory Wray (Duke University). The Foundation looks forward to working with Oxford University Press and appreciates its willingness to make EMPH fully open access and to provide for publication by authors with limited funding. The launch of EMPH marks the coming of age of evolutionary medicine. Its content will transform our understanding of the body and disease in ways that improve human health.”

Cathy Kennedy, Senior Publisher, Life Sciences, at OUP said: “We are extremely proud and excited to announce the EMPH launch. We see the new journal as a great tool to promote dialogue between the disciplines of evolutionary biology and medicine, acting as a catalyst for research that will make a serious impact on humankind. Professor Stearns has gathered together a first-class team of editors who will help to ensure that the new journal is of the very highest quality.”

Evolution, Medicine, and Public Health will be published by OUP in late 2012. The journal is now open for contributions on a broad range of topics and is designed to be of interest and accessible across a broad spectrum of biological and medical disciplines. No author’s fees will apply in the first year, and arrangements are in place for on-going publication of articles by authors with limited funding. Visit the website for more information, submission guidelines, and to sign up to receive tables of contents by email or RSS: www.emph.oxfordjournals.org

For more information contact:

Lizzie Shannon-Little Brand & Communications Assistant Manager Oxford University Press
lizzie.shannonlittle@oup.com +44 (0)1865 353043

Notes to editors Oxford University Press <<http://global.oup.com/>> is a department of the University of Oxford. It furthers the University’s objective of excellence in research, scholarship, and education by publishing worldwide. OUP is the world’s largest university press with the widest global presence. It cur-

rently publishes more than 6,000 new publications a year, has offices in around fifty countries, and employs more than 5,500 people worldwide. It has become familiar to millions through a diverse publishing programme that includes scholarly works in all academic disciplines, bibles, music, school and college textbooks, business books, dictionaries and reference books, and academic journals.

The Evolution, Medicine, and Public Health Foundation < <http://evolutionarymedicine.org/> > is a non-profit organization registered in Connecticut, USA. Its officers are Randolph Nesse < <http://nesse.us> > (Ann Arbor, Michigan), President; Peter Gluckman < <http://www.liggins.auckland.ac.nz/uoahome/about/ourpeople/professorsirpetergluckman> > (Auckland, New Zealand), Secretary; and Cynthia Beall < <http://www.case.edu/artsci/anth/beall.html> > (Cleveland, Ohio), Treasurer. In addition to the journal, the Foundation supports other

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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>

Free software gene environment data

Dear members

I am doing some analysis to find out relationship between environmental and genetic data; I want to do (specifically) stepwise canonical correspondence analysis as well as trend surface analysis but stuck since could not find any free software for these! can anyone suggest me one? Thank you in advance

AVIK RAY National Centre of Biological Sciences
Bangalore-65, India

AVIK Ray <avik.ray.kol@gmail.com>

FreeSoftware Phylogenetics

Hello all,

I have a couple of undergraduate students in my fish biology class this summer working on the systematics of a genus of marine cottid fishes and they are looking for advice on the best free and user friendly software for tree building using morphological data. Any thoughts are most appreciated.

Matt Knope

Matthew Leo Knope <knope@stanford.edu>

Genome amplification kits

I am looking for a whole genome amplification kit to basically “make more” DNA from quantities extracted from small amounts of starting material (small insect legs and butterfly wing fragments). I am using the DNA for genotyping purposes and have had issues of running out of template before I can amplify all of my microsat loci (which happens even with extensive multiplexing).

Commercial kits have recently gone up in price (the illustra GenomiPhi V2 kit now costs \$491 USD for 100 rxns). Does anyone have a less expensive alternative or have protocols down-scaling commercial kits? Experience with 96-well plates would be especially helpful.

Please respond to esaarin@umd.umich.edu

Thanks, Dr. Emily Saarinen Assistant Professor Department of Natural Sciences University of Michigan - Dearborn 4901 Evergreen Road Dearborn, MI 48128

(313)593-5027 esaarin@umd.umich.edu

Emily Saarinen <esaarin@umd.umich.edu>

Human sexual selection survey

Do nice guys finish first, or are looks deceiving?

I am an evolutionary biologist at the Institute of Evolutionary Biology and Environmental Studies at the University of Zurich, with an interest in the evolution and genetics of life, love and death in humans and other animals. For more information on my research or to contact me, please visit my website at <http://www.ieu.uzh.ch/staff/leaders/postma.html>. I would greatly appreciate it if you would participate in a study

investigating the relationship between looks and performance. You will be presented with the portraits of professional cyclists that have taken part in the 2012 Tour de France. You will judge how attractive, masculine and likeable you find each one of them, based on their looks alone. Note that both women and men may participate!

Completing this questionnaire will take about 10-15 minutes. In return, if you leave your email address (facultative), you will receive a summary of the findings. Furthermore, I am giving away a 100 Euro Amazon gift voucher to a randomly selected participant! Note that your e-mail address is stored separately, which ensures anonymity of your answers.

To start the questionnaire, go to <http://fluidsurveys.com/s/tdf2012> Many thanks in advance!

Erik Postma

P.S. Forward this to any colleagues, friends or family who you think might like to participate, and consider posting the link on Facebook, Google+, Twitter, etc.!

– Erik Postma

Institute of Evolutionary Biology and Environmental Studies University of Zürich-Irchel Winterthurerstrasse 190 CH-8057 Zürich Switzerland

Phone: +41 (0)44 635 49 73 Fax: +41 (0)44 635 68 18 Skype: erik_postma

e-mail: erik.postma@ieu.uzh.ch

website: www.erikpostma.net

erik.postma@ieu.uzh.ch

Maptime visualisingDeepTime

We would like to announce that MapTime, a new web application that can be used to visualise timelines with Google Maps for teaching deep time, is now available at www.maptime.co.uk. The program allows teachers and students to easily construct appropriately scaled time lines as describe in Parker, J. D. 2011. "Using Google Earth to Teach the Magnitude of Deep Time." *Journal of College Science Teaching* 40(5):23-27 (summary: http://www.joelparcoeur.com/pdfs/-Parker_Science%202011.pdf). Instructions and more information can be found at the MapTime blog (<http://maptimeblog.blogspot.co.uk/2012/07/how-to-use-maptime.html>).

Although functional, this is only the first version and we are actively developing the site to allow users to add and edit their own time points etc. More details can be found (and will appear) on the blog. Currently, we are looking for willing volunteers who will help to test the site and can also advise on appropriate Time Points for the default Timelines on the site. Any comments or suggestions would be gratefully received.

The MapTime team

Joel Parker (Department of Biological Sciences, SUNY Plattsburgh, USA) <joel.parker@plattsburgh.edu>

Rich Edwards (Centre for Biological Sciences, U. Southampton, UK) <r.edwards@southampton.ac.uk>

Nicola Asamoah & David Milliard (Electronic and Computing School, U. Southampton, UK)

R.Edwards@soton.ac.uk

MarineConservation volunteers

Volunteer Divers wanted -Marine Protected Areas (Philippines), for Sept/Oct or March/April

Project Seahorse and its NGO partner in the Philippines are seeking volunteer, certified SCUBA divers (minimum 15 logged dives) who are interested in participating in a long-term monitoring program for marine protected areas (MPAs) in northern Bohol, Philippines.

The surveys are conducted biannually, one in the dry season (March/April) and one in the wet season (Sept/Oct). An eight-week commitment is required comprising approximately two weeks of training and six weeks of survey work. Surveys are easily influenced by weather and other unpredictable events, so the duration of the fieldwork may vary. If completed quickly, volunteers will be asked to assist with other conservation work, such as data encoding or assisting with other biological field programs.

For applications visit the following - note the deadline for Sept/Oct has been extended to July 15th:

<http://seahorse.fisheries.ubc.ca/node/315> ADDITIONAL INFO:

Diving Survey Work

In the dry season, sites are surveyed for fish communities and seahorses. In the wet season, benthic communities, coral complexity and seahorses are censused. Diving will involve shallow dives, generally 3-10 m, rarely

to a maximum of 14 m, both during the day (benthic, coral and fish surveys) and during the night (seahorse surveys). Photography is used in the benthic surveys; although beneficial, no prior experience with underwater photography is required. We will select 3-4 international volunteers for each survey.

Requirements for volunteering

The Project Seahorse Foundation requires a donation of \$2700 USD to help cover survey costs, local travel, accommodation, and food. Volunteers must also provide their own SCUBA gear and are responsible for the cost of their return airfare to the Philippines, visa costs, travel/health insurance and appropriate vaccinations, together with providing proof of a current dive medical and dive insurance.

A working knowledge of coral reef fish families and benthic fauna (esp. corals) and flora would be an advantage.

Volunteers will be supervised by the Project Seahorse Foundation Survey Biologist and based in Handumon (Jandayan Island). On arrival in Cebu City, the Project Seahorse Foundation staff will organize a comprehensive orientation on its programs and projects, MPA survey schedule, safety protocols, and community and team living.

Application timeline

Interviews will be conducted in the last week of June 2012 by phone.

Payment of donation: 50% of the required donation should be paid after selected applicants have been notified, and the remaining 50% at start of the programme.

Recommended texts

Indo-Pacific Coral Reef Field Guide by Allen, G. and Steene, R. (1999).

Marine Fishes of the Great Barrier Reef and South East Asia by Allen, G. (1997).

Diving/Scuba equipment (*essential)

Mask & snorkel Fins for booties (not socks) Booties (for walking among mangroves and over coral rubble) Full wetsuit (3 mm, protects against stinging jellyfish and sun) Weight belt (Project Seahorse will provide weights) Knife SCUBA gear Buoyancy compensation device (BCD) Regulator with content gauge and depth gauge

Background information

Long-term monitoring of Marine Protected Areas

In 1998, Project Seahorse initiated the long term monitoring programme for assessing MPA effectiveness in

northern Bohol. The motivation behind the programme is three-fold:

(1) to provide up-to-date monitoring data to inform fishing communities about the status of their reefs, (2) to catalyze community interest in managing and establishing additional MPAs, and (3) to provide scientifically robust data for assessing the impact on MPAs on the recovery of coral reefs.

Trial surveys were conducted in the late 1990s, and the full design of the programme was established in 2001. Over the past decade, over 70 international volunteers have participated in the programme, and it is with their hard work and commitment that we continue to meet our objective of quantifying the response of seahorses, fishes and benthic organisms (e.g. live coral) to protection.

Currently a total of seven MPAs are being monitored, each with a control site situated just outside the MPA. In addition, four more distant control sites have also been selected (see table). The MPAs are located in four municipalities in Bohol.

Lindsay Aylesworth <lindsay.aylesworth@gmail.com>

NERC studentships

Prestigious NERC funded studentship. Genetic pedigrees and individual trait variability: Ecological and evolutionary consequences for wild fish populations.

Recent advances in genetic data analysis have provided the tools so that evolutionary processes in wild populations can be inferred from molecular data. Molecular based pedigrees can be used to estimate reproductive success of individuals or phenotypes and for quantitative genetic analysis. The resulting information on heritability of ecologically significant life history traits or behaviours is crucial in accurately predicting responses to selection and is therefore a key element of evolutionary models. Here we will use sophisticated maximum-likelihood and Bayesian approaches for parentage analysis (e.g. molecular pedigree reconstruction) to produce field based heritability estimates. Important aspects of population structure such as geographic or behavioural barriers to migration to gene flow between subpopulations and the effective population size, can be inferred from these molecular data and as such provide both a framework for understanding micro-evolutionary processes and key information for the validation of evolu-

tionary models.

In this PhD, we will use a riverine pike *Esox lucius* population from the River Frome as a model for our predictions. The River Frome is a chalk stream with a total length of approximately 15km where pike are present. Since no freshwater connections exist to other river catchments it constitutes a closed system regarding non-migratory freshwater fish populations. The core investigation area covers approximately 4km of river length (33% of the available pike habitat) including seven discrete spawning sites. Data on growth, diet and sampling location are available for a large proportion of *E. Lucius*, whose population has been studied on the river since 1976. These data have enabled quantitative measures to be made of population changes in terms of abundance, age structure, mortality, individual growth and diet, but a collection of tissue material also provide the opportunity to obtain genetic data and link them on individual life-history traits, providing an important temporal component for the project.

Application deadline 15th of July

Contact Prof. Rudy Gozlan Prof. Rodolphe Gozlan
FSB Head of Academic Group Conservation Ecology & Environmental Sciences Professor in Conservation Ecology Asst. Editor Journal of Fish Biology Assoc. Editor Aquatic Invasion

School of Applied Sciences Bournemouth University Talbot Campus, Fern Barrow Poole, Dorset BH12 5BB Tel: +44 (0)1202966780 Email: rgozlan@bournemouth.ac.uk

–

Dr. Emilie Hardouin Max-Planck-Institut für Evolutionsbiologie August-Thienemann-Straße 2 24306 Plön Germany

Tel.: +0049 (0)4522/763-274 e-mail: hardouin@evolbio.mpg.de <http://www.evolbio.mpg.de/~hardouin/index.html> Emilie Hardouin <hardouin@evolbio.mpg.de>

Protocols for Illumina

Dear EvoDir Members,

We are currently setting up a protocol for pooled indexed paired-end libraries of genomic DNA (gDNA) for whole genome Illumina DNA sequencing of some iridovirids. We want to multiplex isolates and are inter-

ested in ordering from alternate suppliers rather than Illumina to keep costs down. I was hoping that some of you had previous experience with a similar project and would be prepared to share their protocol with us.

Thanks in advance.

Adrien

Adrien RIEUX Research Associate UCL Genetics Institute Department of Genetics, Evolution & Environment Faculty of Life Sciences LONDON WC1E 6BT a.rieux@ucl.ac.uk

adrien_rieux@hotmail.com

SSB CallProposals Symposia

Call for Proposals.

The Society of Systematic Biologists would like to issue a call for proposals for Symposia to be held at the 2013 Evolution Meeting in Snowbird, UT. The society will sponsor two symposia, each consisting of 4-6 talks to occur over two sessions (i.e., during the morning or afternoon). We are now soliciting proposals. Organizers of proposals should include a short description of the organizing theme of the proposed symposium, a list of speakers with affiliations, and contact information for the organizers. Funds are available to defer travel costs for speakers. Members who are interested in submitting a proposal are encouraged to contact the program chair prior to submission, either in person at the 2012 meeting or electronically. To submit a proposal, please send a pdf of the proposal to Bryan Carstens (carstens.12@osu.edu) by October 1st, 2012.

Bryan C. Carstens Assistant Professor Department of Biological Sciences Louisiana State University cell (734) 474-8527 skype bryan.carstens office (225) 578-0960

www.lsu.edu/faculty/carstens/ mail 202 Life Sciences Building Louisiana State University Baton Rouge, LA 70803, USA

Bryan Carstens <bryan.c.carstens@gmail.com>

Software SBEToolbox

Dear all,

We present SBEToolbox (Systems Biology and Evolution Toolbox), an open-source Matlab toolbox for biological network analysis. It calculates a variety of centralities and topological metrics, clusters nodes into modules, and interactively displays the network using different graph layout algorithms. Efficient lightweight design allows large-scale networks to be handled. Straightforward implementation and the inclusion of high-level functions allow the functionality to be easily extended or tailored. SBEGUI, a menu-driven GUI of SBEToolbox, is highly interactive, enabling easy usage of most network and graph algorithms without prior knowledge of programming. The stand-alone executable SBEGUI, running on all major operating systems, does not require the installation of Matlab system. Availability: Pre-compiled stand-alone executable for all major operating systems and source code are freely available at <http://sbttoolbox.sourceforge.net>. Your comments are always welcome.

James Cai

Veterinary Integrative Biosciences Texas A&M
University College Station, Texas 77843
Email: jcai@tamu.edu <http://genomezoo.net>
JCai@cvm.tamu.edu

Talks Recomb Durham Jul14-16

If you'd like to see (or "see again") the great talks from

this meeting, they're nearly all available from this link: <https://sites.google.com/site/aga2012recomb/> (a few are embargoed but will be online later)

The 2012 annual meeting of the American Genetic Association was held from 14-16 July at the Durham Convention Center in Durham, North Carolina, USA. The conference was entitled "Recombination: Molecular Mechanisms & Evolutionary Consequences".

"Recombination" affects myriad areas of biology in general and evolution in particular, ranging from proper segregation of chromosomes to advantages associated with sexual reproduction to patterns of DNA sequence variation within and between species to processes of species formation. This exciting conference had delightful presenters (see below) and participants from diverse areas of biology.

Distinguished lecture: Brian Charlesworth- University of Edinburgh, UK Talk title: "Background selection and patterns of molecular evolution and variation"

Symposium speakers: Adam Auton- Albert Einstein College of Medicine Justin Blumenstiel- University of Kansas Francesca Cole- Sloan Kettering Greg Coperhaver- University of North Carolina Justin Fay- Washington University (St Louis) Bret Payseur- University of Wisconsin Tom Petes- Duke University Jeff Sekelsky- University of North Carolina Nadia Singh- North Carolina State University and more...

Mohamed A. F. Noor noor@duke.edu Earl D. McLean Professor Tel: 919-613-8156 & Associate Chair Biology Department Lab: 919-613-8193 Box 90338 FAX: 919-660-7293 Duke University Durham, NC 27708 USA <http://sites.google.com/site/noorlabduke/> noor@duke.edu

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BielefeldU EvolutionRecombination

Dear members of evoldir,

The Biomathematics group at the Faculty of Technology, Bielefeld University, has a vacancy for a

Research Associate (postdoc, TVL-E13)

for a period of 3 years, starting in November 2012 or later; extension is possible.

We are looking for an individual with a PhD in Mathematics, Biomathematics, or Mathematical statistical physics, to work on a project in mathematical genetics. The project will investigate the dynamics of recombination processes and so-called ancestral recombination trees. The project is part of the recently-established Priority Programme on 'Probabilistic Structures in Evolution' (DFG-SPP 1590), see http://ekvv.unibielefeld.de/blog/uniaktuell/-entry/professorin_ellen_baake_koordiniert_neuen or http://www.dfg.de/foerderung/info_wissenschaft/-archiv/2011/info_wissenschaft_11_36/index.html, which offers an excellent research environment. The same holds for Bielefeld University, a particular strength being due to close interaction between biomathematics, mathematics, bioinformatics, and biology.

Informal inquiries and applications should be sent to the address below before Aug. 24, 2012. Applications via email are welcome.

Bielefeld University is an equal opportunity employer. Women and members of minority groups including disabled persons are strongly encouraged to apply.

Prof. Ellen Baake, Technische Fakultät, Universität Bielefeld, Postfach 100131, 33501 Bielefeld, Germany phone (+49) 521 106 4896 email: ebaake@techfak.uni-bielefeld.de URL: <http://www.TechFak.Uni-Bielefeld.DE/ags/bm/> ebaake@techfak.uni-bielefeld.de

Bretagne EvolBiol

Dear all

[please forward as appropriate, sorry for cross posting]

Postdoc:

The French regional funding board of Region Bretagne is launching a call for postdoctoral funding for 12 to 24 months - provided that the candidate is foreigner (i.e. 12 months outside France during the last 3 years) and that 25% of the salary is provided from other sources. Please see https://xnet1.region-bretagne.fr/Recherche/fichiers_accueil_extranet/-Reglement_dispo_SAD_2012.pdf for details (in French, regrettably). Internal preinscript is (theoretically) next week, deadline is August 15.

Invited foreign PhDs:

>= 3 months, between (theoretically) January and August 2013; please see >below for details

Invited Docent positions at University Rennes 1:

Calls should appear in autumn, but with usually a very short notice. This is for multiple months stays at Rennes for docents/profs who have a permanent position at their home institution. The only teaching load

that is expected here in Rennes is to give one or a few seminars.

All:

Should you fit the criteria and be interested in research at the interface of ecological coexistence and evolutionary diversification (profiting for instance from exceptional databases or field settings on ecosystem and microevolutionary consequences of macroevolutionary niche conservatism) please feel free to contact me at andreas.prinzing@univ-rennes1.fr. We can then discuss possibilities to demand either of these fundings. Please do so as soon as possible, in particular for the postdoc funding. Obviously you are also free to contact any other lab in Bretagne.

Best regards Andreas Prinzing

Andreas Prinzing, Prof. Ecology of Diversification

Team "Structure and Dynamics of Diversity" Research Unit "Ecobio" : Ecosystems - Biodiversity - Evolution Université Rennes 1 / Centre National de la Recherche Scientifique Campus de Beaulieu, Bâtiment 14 A 35042 Rennes, France
Tel : +33 2 23 23 67 12; fax: +33 2 23 23 50 26
andreas.prinzing@univ-rennes1.fr http://ecobio.univ-rennes1.fr/Fiches_perso/Fiche.asp?pseudo=APrinzing
http://ecobio.univ-rennes1.fr/Fiches_perso/Banque/publi1.APrinzing.doc RENNES METROPOLE MOBILITY GRANTS FOR 'INCOMING' FOREIGN PhD STUDENTS

Call for Proposals For foreign PhD students starting a program in Rennes area between January and August 2013

Objective: Increase the number of foreign PhD students in institutions in the Rennes Urban Area.

Description: Grants of 800 euro per month paid directly to the awardees. An allocation document will give details of the conditions for payment of the grant. The grant may be awarded for up to 6 months per candidate. The Rennes Metropole grant must be used by the PhD student to cover the costs incurred when away from his/her usual place of residence. The grant will be paid to the candidate upon his/her arrival in Rennes. The grant can not be combined with similar awards from other institutions.

Eligibility criteria: - Enrolment on a PhD program in a foreign research institution - Participation in a placement of at least 3 months in a research institution in the Rennes area as part of the thesis. - Holder of a letter of invitation from the welcome team - Arrival to begin placement in Rennes planned between January and August 2013

Supporting documents: Standard file including: - A CV and cover letter A letter from the Rennes welcome team setting out the placement conditions and duration - A partnership agreement, if necessary - A description of relationships between the two institutions - Copy of the candidate's bank details - Summary of exchange project - References from thesis supervisor(s)

The application must be completed in French

To be submitted no later than september 25, 2012 to the Secretariats offices of the Doctoral schools.: VAS, SDLM, MATISSE & SHOS

Applicants will be notified of the decision on November 2012.

Andreas Prinzing <andreas.prinzing@univ-rennes1.fr>

Brigham YoungU InsectEvolution

The Whiting Lab in the Department of Biology at Brigham Young University seeks to fill a postdoc position in insect evolution. Qualified applicants with a PhD, and expertise in evolutionary or organismal biology (including, but not limited to, systematics, evolution, and bioinformatics) are encouraged to apply. Skills in phylogenetics, next-gen sequencing and bioinformatics are a plus, but not necessary. The successful candidate is expected to have solid mentoring skills and mentor an active lab involving both undergraduate and graduate students. The successful candidate will be supplied a small research budget to work on a project of his/her choice as well as be involved in several ongoing projects in insect evolution. There is also the possibility to teach a basic entomology course in the fall of 2012.

The review process will begin immediately and will continue until filled with a potential (and ideal) start date of September 1st. Current funding is for one year, with the possibility of a second year, depending upon successful performance evaluations and additional funding. Salary is competitive, and the position will carry full BYU benefits.

Interested persons should apply by sending a cover letter (1 page max), current CV, statement of research interests and potential project (2 pages max), statement of teaching experience (1 page max), and list of three individuals who could supply letters of recommendation to Dr. Michael Whiting (Michael.Whiting@byu.edu). Informal questions and informal inquiries may be di-

rected to Dr. Michael Whiting.

Provo Utah is an excellent place to live and work. Situated in the heart of Rockies it has endless year round outdoor activities. Additional department and college information is available at website: <http://biology.byu.edu/home>. All faculty, including postdocs, are required to abide by the university's honor code and dress and grooming standards.

Brigham Young University, an equal opportunity employer, does not discriminate on the basis of race, color, gender, age, national origin, veteran status, or against qualified individuals with disabilities.

seth.bybee@gmail.com

The position is funded through the internal grant of the Charles University in Prague. The position is available from 1 January 2013 for up to two years. To apply, please send a CV including the list of publications, research statement and contacts of two previous supervisors/colleagues willing to write a reference. The call will be open until 20 August 2012. Shortlisted candidates will be interviewed during the last August week. The final decision will be made in October.

For more information, e-mail Lukas Kratochvil (lukas.kratochvil@natur.cuni.cz).

Lukas Kratochvil <lukas.kratochvil@natur.cuni.cz>

Martina Pokorná <martina.pokorna@natur.cuni.cz>

CharlesU ReptileSexDetermination

Evolution of sex determination and sex chromosomes in squamate reptiles

Reptiles possess variability in sex determining systems ranging from environmental sex determination, where sex chromosomes are not present, to well-differentiated XY or ZW sex chromosomes. This variability is particularly substantial in squamate reptiles, the group encompassing lizards and snakes. Study of the processes responsible for variability in sex determination in some squamate lineages versus conservatism in others, as well as the possibility of comparison of genome organization in closely related lineages or species with and without sex chromosomes, may allow significant contribution to the evolution of sex determination and differentiation in vertebrates as well as our understanding of sexual development in general. The aim of the project is to test homology of sex chromosomes across major lineages of squamate reptiles to uncover the phylogeny of sex determining modes in this group and to determine rates of sex chromosome differentiation within particular selected groups. The project is based on the techniques of molecular cytogenetics including cell cultivation, FISH, chromosome laser microdissection and flow sorting, and single gene mapping and various kinds of molecular approaches. The work will be done in the laboratories in Prague (Charles University) and Libečov (Czech Academy of Science), Czech Republic. The prospective candidate should have experience in molecular genetics and cytogenetics, evolutionary genetics and genomics. Demonstrated expertise in molecular cytogenetics mastering at least some of the above mentioned techniques is essential.

EmoryU FlagellaEvolution

POSTDOCTORAL FELLOW POSITION, EMORY UNIVERSITY

A postdoctoral fellow position is available in the Wright laboratory at Emory University starting fall/winter 2012 (<http://electronmicroscopy.emory.edu>). Research in the lab is focused on bacterial and viral structural biology, with emphasis on 3-D structure/function relationships between host cells and viruses. Areas of interest include cryo-electron tomography of bacteria, bacteria ' bacteriophage interactions, paramyxoviruses, and HIV-1. Technology development interests are in the areas of correlative microscopy and phase plate cryo-microscopy.

The postdoctoral position is to study the structure of flagella and type IV pili from several bacterial species and correlate the structural information with environmental and biodiversity patterns. The long-term goal of the project is to understand 1) the structural implications of the incorporation of multiple flagellins into the flagellar filament and 2) the structural variation between T4bP and Flp-type pili at the macromolecular level. The main rationale is that the architectural complexity of flagella and pili (critical virulence factors for many bacterial species) is an important indicator of environmental adaptations responsible for bacterial biodiversity.

Candidates should have an interest in structural biology and bacteriology, and should enjoy working as part of an active research team. Background experience in one (or more) of the following fields is desirable, but not required: bacteriology, (cryo-) electron microscopy,

and/or image processing/analysis techniques.

The wet laboratory is within the Division of Pediatric Infectious Diseases and is fully equipped for all aspects of microbiology, molecular biology, molecular virology, and protein biochemistry. The Wright lab has complete access to a JEOL 2200FS 200 kV FEG TEM with an in-column energy filter, Zernike-style phase plates, and high-resolution 4kx4k CCD camera; a JEOL 1400 120 kV TEM with 2kx2k camera; and an FEI Vitrobot and a manual grid plunge freezer. Emory is a vibrant, multidisciplinary campus with strong ties to Georgia Tech and other universities within Georgia. Access to facilities in NMR, Mass Spectrometry, and X-ray crystallography are available.

Applicants should include a cover letter describing research experience and interests, curriculum vitae, and names and contact information for three references.

Dr. Elizabeth R. Wright

Emory University

Department of Pediatrics

2015 Uppergate Drive, NE Room: 548 Atlanta, GA 30322 erwright@emory.edu

Website: <http://electronmicroscopy.emory.edu> Applications will be reviewed as they are received and until the position is filled.

“Wright, Elizabeth R.” <erwright@emory.edu>

Finland

Evolutionary Conservation Genetics

A post-doctoral position is available in Craig Primmer's research group (see <http://users.utu.fi/primmer> for more details) at the University of Turku, Finland.

The successful applicant will be expected to have the skill and enthusiasm to contribute to evolutionary and conservation genetic aspects of a project aimed at identifying the genetic basis of ecologically relevant traits in wild Atlantic salmon populations using approaches including hitch-hiking, association and linkage mapping in wild population pedigrees (see background publications below).

Suitable candidate should have a strong background in evolutionary or conservation genetics (in any species) and a good knowledge of quantitative genetic and genetic mapping methodologies. Experience in analysis

of SNP and next-generation sequencing data is also an advantage.

Informal inquiries and applications (preferably as a single pdf file) should be addressed to Prof. Craig Primmer (craig.primmer@utu.fi). Applications should include a full academic CV, a statement of previous research and supervision experience as well as current research interests and names and contact details of at least two referees. Review of applications will commence on September 3rd with the preferred starting date being January 2013 or earlier. The position is available until the end of 2015. The salary range is 3000 - 4100 EUR per month, depending on the previous post-doctoral experience of the candidate.

Turku, Finland's 5th largest city (178 000 people), is located in the southwestern Finland. It has a rich cultural history and is the gateway to a beautiful archipelago. The University of Turku is one of the major multidisciplinary universities in Finland and is ranked in the top 5% of universities in the world.

Vähä et al. (2011) Temporally stable population-specific differences in run timing of one-sea-winter Atlantic salmon returning to a large river system. *Evolutionary Applications* 4:39-53

McGinnity et al. (2009) Impact of naturally spawning captive-bred Atlantic salmon on wild populations: depressed recruitment and increased risk of climate-mediated extinction. *Proc. R. Soc. Lond. B. Biol. Sci.* 276: 3601 3610

Vähä et al. (2008) Retrospective genetic monitoring of Atlantic salmon populations within a river system over two decades implications for management. *Evolutionary Applications* 1: 137 154.

Vähä et al. (2007) Life-history and habitat features influence the within-river genetic structure of Atlantic salmon. *Molecular Ecology* 16: 2638-2654

craig.primmer@utu.fi

FreeU Berlin Conservation Genetics

Dear EvolDir members,

We are looking for a postdoctoral candidate that wants to apply for a Marie Curie fellowship (deadline: August 16, 2012) in order to join us at the Free University of Berlin to work on conservation genetics of endangered plants in Germany. The project is a collaboration be-

tween the Institute of Botany of the Free University of Berlin and the Botanic Garden and Botanical Museum Berlin-Dahlem, and will be funded by the German Federal Agency for Nature Conservation (BfN - Bundesamt für Naturschutz). It will involve population genetics, phylogeography and conservation genetics of ten endangered plant species (i.a. *Arnica montana*, *Campanula baumgartenii* and *Nymphaea candida*) and make use of next-generation sequencing technology to develop genetic markers in the target species. The ideal candidate obtained his/her Ph.D. in the field of population/conservation genetics, has extensive laboratory and data analysis skills, a good understanding of the German language and an interest in communicating with conservation agencies.

Candidates that are interested in applying for a Marie Curie fellowship with our assistance, please send your CV (including the contact information of two references) and letter of motivation to:

Dr. Ludo Muller Freie Universität Berlin Institut für Biologie - Botanik Altensteinstraße 6 14195 Berlin Germany

E-mail: ludo.muller@fu-berlin.de

Deadline for applying: July 25, 2012

Informal inquiries are welcome!

Best regards,

Ludo Muller.

— 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 E-mail: ludo.muller@fu-berlin.de Homepage: <http://userpage.fu-berlin.de/~ludom/> ludo.muller@fu-berlin.de

IST Austria EvoBiol

ISTFELLOW

IST Austria is looking for POSTDOCTORAL FELLOWS

IST Austria (Institute of Science and Technology Austria) invites applications for postdoctoral fellows in all fields of the natural and mathematical sciences and related disciplines.

The Institute, which is on the outskirts of Vienna, was established by the Austrian government with a focus on

basic research. IST Austria has English as its working language, and its Graduate School awards PhD degrees. It has an international mix of scientists chosen solely on the basis of their individual excellence and potential contribution to research.

The Institute has set up a program for exceptional post-doctoral researchers partially funded by the European Union. Appointments will be for 2-4 years. Applications will be accepted at any time, but fellows will be selected twice a year in October and April.

The deadlines for each selection are the 15th of September and March, respectively. Applicants must have the support of one or more members of the IST Austria faculty who will host them in their research group.

The Institute offers an internationally competitive salary, full social security coverage, and additional benefits.

For further information about the program and the online application process, please refer to the ISTFELLOW website: <http://ist.ac.at/istfellow> IST Austria values diversity and is committed to equality. Female researchers are encouraged to apply.

Johannes.IRSCHIK@ist.ac.at

NewMexicoStateU EvolutionVocalLearning

A postdoc position is available in the Wright Lab at New Mexico State University to study the function and mechanisms of vocal learning in adult budgerigars (parrots). The aims of this NIH-funded project include testing hypothesis for call sharing in social groups of budgerigars, examining the role of corticosterone in vocal learning, and examining learning-related patterns of gene expression in parrot neural centers. It is part of a larger research program to understand the evolution of vocal learning and vocal communication signals. The project is a collaboration with Stephanie White (UCLA) and Dennis Hallford (NMSU).

The postdoc researcher will be involved in all aspects of research and will have scope for designing their own experimental direction. I am looking for a highly-motivated and talented individual with expertise in behavioral observations, sound analysis, avian endocrinology, neurobiology and/or molecular genetics. Strong communication skills, good work ethic, an interest in mentoring and evidence of a productive research career

are all essential. The position is available immediately with an (ideal) start date of September 1 and funding for two years. A PhD in Biology or related field must be completed before hiring. The salary and benefits are commensurate with NIH standards and can be adjusted to reflect experience.

New Mexico State hosts an active and growing group of researchers in evolution, behavior and neurobiology. Opportunities exist to participate in an HHMI-funded Preparing Future Faculty program and for mentoring students through our NIH-funded BRAiN undergrad research program in neurobiology and behavior. NMSU is a Hispanic-serving land grant research university with a diverse student body. Las Cruces is a large and culturally diverse town with a growing arts community and awesome outdoor activities in the surrounding Rio Grande valley, Chihuahu desert. Sacramento and Gila mountains.

To apply please send a single pdf containing 1) A cover letter indicating availability and contact information for two references, 2) a CV, and 3) a brief (1-2 page) summary of professional interests to <wright@nmsu.edu>. Inquiries about the position can be directed to me by email or phone at 575-646-1136. NMSU is an equal opportunity employer and candidates from diverse backgrounds and origins are highly encouraged to apply. Review of applications will begin 20 July, 2012 and continue until the position is filled.

Tim Wright

Associate Professor Department of Biology MSC 3AF New Mexico State University Las Cruces, NM 88003 Phone: 575-646-1136 Office: 375 Foster Hall Behavior lab: 301 Foster Hall, 575-646-4863 Genetics lab: 433 Foster Hall, 575-646-4791 <http://biology-web.nmsu.edu/twright> Timothy Wright <wright@nmsu.edu>

New Zealand Fruit Breeding

Post Doctoral Scientist at Plant & Food Research, NEW ZEALAND Mapping & Markers / Pipfruit & Summerfruit Breeding Fixed term: Up to three years

Palmerston North Research Centre, NEW ZEALAND I Vacancy 6419

As the successful candidate you will join a dynamic research team made up of plant molecular biologists and pipfruit breeders, who are world leaders in the applica-

tion of genomics tools for fruit tree breeding.

Focusing on the genetic control of key fruit quality characters in apples, you will use large marker (SNP array) and phenotype data sets to identify genomic regions associated with fruit flesh colour and physiological disorders and use this information to develop strategies for use in genomic selection.

You will have a PhD in genetics, plant or animal breeding or plant molecular biology together with experience in statistical, quantitative and molecular genetics. Experience in molecular marker development and QTL mapping, phenotyping fruit quality traits and applying genomics tools for breeding would be desirable.

For more information, registration details and to apply for this position please visit www.careers.plantandfood.co.nz Applications close 1 August 2012

Many thanks Regards Nadine

Nadine Andrews Human Resources Coordinator www.careers.plantandfood.co.nz T: +64 9 925 7066 F: +64 9 925 7001 nadine.andrews@plantandfood.co.nz www.plantandfood.co.nz The New Zealand Institute for Plant & Food Research Limited

Postal Address: Plant & Food Research Mt Albert Private Bag 92169, Auckland, 1142, New Zealand Physical Address: Plant & Food Research Mt Albert 120 Mt Albert Road, Sandringham, Auckland, 1025, New Zealand

Follow Plant & Food Research online

Nadine Andrews <Nadine.Andrews@plantandfood.co.nz>

Phenoscape Bioinformatics

Postdoctoral fellow: Bioinformatics, Phenotypes

We are recruiting a postdoc with training in bioinformatics who is interested in studying phenotypic evolution by combining model organism genetic data with comparative anatomical data from throughout the vertebrates.

One of the biggest challenges in systems biology is the inclusion of whole organism phenotypes. In the Phenoscape group, we have developed ontology-based methods for representing phenotypes of diverse species in order to integrate them with model organism developmental and genetic data,. We have collected these

data in a sophisticated Knowledgebase, which has an initial focus on the diversity of phenotypes in ostariophysan fish, including zebrafish (kb.phenoscape.org). We are currently scaling up our approach to the vertebrates as a whole, with a goal of allowing similarities to be identified between phenotypes from sources as diverse as dinosaur fossils and mouse knockout mutants.

We invite postdoctoral applicants to propose an independent project that uses the Phenoscape Knowledgebase as a research platform. In particular, we are interested in projects that will leverage functional genomic data to study the evolution of whole-organism phenotype in nonmodel organisms.

The postdoc will work under the direction of Paula Mabee (University of South Dakota) and Todd Vision (University of North Carolina), as part of a distributed, multidisciplinary team that includes evolutionary biologists, computer scientists, model organism experts, and bioinformaticists. It will be based in South Dakota, with opportunities to travel to other sites, including the National Evolutionary Synthesis Center (NESCent), the University of Chicago, and the California Academy of Sciences.

Starting date: This two year postdoctoral position is available to be filled as early as September 2012.

Required qualifications: Ph.D. degree with strong background in bioinformatics; previous experience with ontologies preferred

* Experience in functional genomics or developmental biology * Demonstrated communication and writing skills, in English * Demonstrated ability to work in a team setting

How to apply:

Please contact Paula Mabee (pmabee@usd.edu) for more information. Applications should include a cover letter, CV, a brief statement detailing your research interests and career goals, and three letters of reference. For more information, please see <https://phenoscape.org> and < <http://kb.phenoscape.org/> >

“Mabee, Paula” <Paula.Mabee@usd.edu>

Roscoff Theory Mating System Transitions

A one-year post-doc position is open at Roscoff’s Biological Station (France), to develop theoretical models

on the evolutionary causes and consequences of mating system transitions. This is part of a collaborative project (ANR TRANS) between five French labs, involving theoretical and genomic studies of mating system transitions in Angiosperms; the post-doc will be able to interact with other theoreticians in Montpellier (Sylvain Glémin), Lille (Sylvain Billiard) and Roscoff (Denis Roze).

Different research axes will be possible, including the dynamics of mating system modifier genes under various modes of selection, effects of population structure and spatial heterogeneity, and consequences of shifts in mating system (for example on the evolution of mutation rates or genome architecture). We are looking for a candidate with a strong background in mathematical and/or computational modeling, and interest in evolutionary genetics. French skills are not required. The post-doc could start in Nov-Dec 2012, or early 2013.

Informal enquiries and applications should be sent to Denis Roze (roze@sb-roscoff.fr). Applications should include a CV, statement of interest and contact information for 2 or 3 references. Applications should be sent before mid-September.

Denis Roze Adaptation et Diversité en Milieu Marin Station Biologique de Roscoff Place Georges Teissier 29670 Roscoff, France Ph: +33 2 98 29 23 20

roze@sb-roscoff.fr

SungkyunkwanU Korea Phylogenomics

Bioinformatic specialist or Post-doctoral position in phylogenomics

Sungkyunkwan University, Suwon, Korea

A full-time post-doctoral or bioinformatics specialist position is available in the lab of Dr. Hwan Su Yoon at Sungkyunkwan University in Suwon, Korea. This position involves participation in a microbial genome sequencing project funded by Rural Development Administration. The successful applicant will work in the development, automation and application of data analysis and visualization tools, including de novo genome assembly, comparative genomics, and population genomics. The applicant is required BS, MS, or PhD in bioinformatics, computer science or related field who has a strong background in next-gen sequencing and common bioinformatics tools. Experience with

Unix/Linux, Perl, Python, and de novo genome assembly would be preferable.

Four recent publications from Yoon Lab;

Yoon et al. 2011. Single cell genomes reveal the dynamic world of uncultured marine protists. *Science* 332: 714-717.

Price et al. 2012. *Cyanophora paradoxa* genome elucidates origin of photosynthesis in algae and plants. *Science*. 335: 843-847.

Chan et al. 2011. Signal of Plantae monophyly and gene sharing found in rich repertoire of red algal genes. *Current Biology* 21: 328-33.

Qiu et al. 2012. Ancient gene paralogy may mislead inference of plastid phylogeny. *Molecular Biology and Evolution*. In press.

Applicants should consist of 1) cover letter describing your interest in the position, (2) the names and contact information for three references, (3) a curriculum vita. Applications should be sent to ecyang17@gmail.com. The search committee will begin reviewing applications on August 18, 2012 and will continue until the position is filled. The position is available immediately.

HwanSu Yoon, Ph.D.

Department of Biological Sciences Sungkyunkwan University Suwon 440-746 Korea

Phone: 82-31-290-5915 Email: hsyoon2011@skku.edu

HwanSu Yoon <hsyoon@bigelow.org>

UBern DemographicInference

Postdoc position: Demographic history of camouflaged deer mouse populations

A 3 years post-doc position will be available this Fall at the University of Berne to develop new methods of demographic inference from next-generation sequencing data and their application to the study of the demographic history of camouflaged deer mouse populations in the Sand Hills region of Nebraska. This research will be done in close collaboration with Prof Hopi Hoekstra (Harvard) and Prof Jeff Jensen (Lausanne) with the aim of discovering the genetic basis of coat colour adaptation (see <http://www.sciencemag.org/content/325/5944/1095.short> for more information on the system). Population genomic data generated in Harvard will be jointly analysed in Lausanne and Berne to look

for signals of adaptation after controlling for complex demography.

We are looking for a highly motivated candidate to join our international team. The ideal candidate will have a strong background in statistical or population genetics and proven abilities to work independently and in team. Previous experience in C++ and R or another high-level programming language is a plus.

The successful candidate is expected to be involved in light teaching and administrative duties at the IEE. Gross salary is in the range of 80K CHF per year and follows the Swiss NSF scale. The CMPG lab offers a very stimulating research environment with access to high performance computation facilities and close connections with the Swiss Institute of Bioinformatics. Berne is ideally located in the middle of Switzerland and Europe, and provides rich cultural and outdoor activities.

Please send before August 10th 2012, an application letter, CV and contact information of two references to laurent.excoffier@iee.unibe.ch. Further information can be requested at the same email address.

Prof. Laurent Excoffier

Laurent Excoffier

Computational and Molecular Population Genetics (CMPG) Institute of Ecology and Evolution, University of Bern 6, Baltzerstrasse, CH-3012 Bern, Switzerland Tel: +41 31 631 30 31 Fax: +41 31 631 48 88 Email: laurent.excoffier@iee.unibe.ch <http://cmpg.iee.unibe.ch> Computational Population Genetics Swiss Institute of Bioinformatics (SIB) http://www.isb-sib.ch/groups/-Computational_Population_Genetics.htm Laurent Excoffier <laurent.excoffier@iee.unibe.ch>

UCSantaCruz Paleogenomics

UC Santa Cruz, Ancient DNA and Evolutionary Genomics

A postdoctoral position is available in new Paleogenomics lab at the University of California Santa Cruz. Our lab combines experimental and computational approaches to studying how species and populations evolve over time, taking advantage of the latest technologies in ancient DNA extraction, sequencing and analysis. The lab is jointly run by Beth Shapiro and

Ed Green.

We are currently seeking a postdoctoral scholar to join our ongoing research project focusing on the dynamics of the fauna and flora of Beringia, a non-glaciated Northern refuge for many species that thrived during the colder intervals of the Pleistocene. Our main research goals are (1) to learn how climate drives the generation and maintenance of genetic diversity over time; (2) to infer how species and populations adapt to changes in the availability and quality of their habitat; and (3) to understand how species and populations interact with each other, and how these interactions influence the demographic patterns that can be learned from genomic data.

MINIMUM QUALIFICATIONS: A Ph.D. in evolutionary biology, genomics, population genetics, bioinformatics, or other relevant fields is required along with relevant laboratory experience and demonstrated record of accomplishment. Knowledge of and experience troubleshooting DNA extraction, PCR amplification, genomic library preparation, and DNA sequencing protocols is essential. Experience with next-generation sequencing and analysis of NGS data, including phylogenetic and population genetic approaches to the statistical analysis of genomic data, is necessary. Other requirements include excellent organizational, verbal communication, and collaboration skills and willingness to travel to field sites and museums.

PREFERRED QUALIFICATIONS: The ideal candidate will have experience working in a clean-room environment, some basic programming skills and familiarity working in UNIX environment. Experience in the analysis and manipulation of large, population genomic data sets is also preferred.

The position is for one year with an option to renew for a second year. Annual salary ranges from \$39,264-\$50,628, commensurate with qualifications and experience. The position will be filled as soon as an ideal candidate is found, with initial review of applications to begin August 15.

To apply, please email a CV, research statement, and cover letter to bashapir[at]ucsc.edu. Please include the names and email addresses for three references in the cover letter.

Please refer to position #T12-50 in all correspondence.

Beth Shapiro Associate Professor Department of Ecology and Evolutionary Biology University of California Santa Cruz

beth.shapiro@gmail.com

UCalifornia Berkeley EvolutionPhosphoregulation

Post doc position available in the Holt lab at UC Berkeley.

<http://mcb.berkeley.edu/labs/holt/> - 2 years. Partial funding - applicant will be required to apply for fellowship funding.

Please send a C.V. the contact information for 3 references and a letter of intent. You should state in some detail what you are interested in working on and why. Feel free to propose other project areas on the website or ideas of your own that you think fit in the lab. We are primarily a molecular cell biology and biochemistry lab. We seek highly motivated individuals with good skills at the bench. Computational skills are also preferred.

The control networks that drive cell division have changed extensively during evolution to adapt to the needs of myriad modern organisms. We aim to understand this process of change.

One important signaling currency is phosphorylation. Protein kinases such as the Cyclin-dependent kinase (Cdk1) coordinate hundreds of cellular processes during cell division by phosphorylating proteins and thereby altering their activity. During evolution, kinases have duplicated and diverged, adding complexity to cell division signaling networks. For example, Cdk1 duplicated about 800 million years ago and the duplicate gene diverged to give rise to a related kinase, Ime2. The addition of the Ime2 kinase enabled the conversion of the single mitotic division to the double meiotic divisions (see Mol. Cell. 2007 < <http://mcb.berkeley.edu/labs/holt/PDFs/holt.2007.pdf> >).

We aim to understand how cellular networks adapt when a new kinase diverges and alters its specificity. This event will incur a large cost, due to toxic phosphorylation events, and therefore must confer great benefits to be selected for and fixed in evolution. Our recent work suggests that this benefit can be readily obtained for the simple reason that mechanisms of phosphoregulation are quite simple and therefore easy to evolve (see Science 2009 < <http://mcb.berkeley.edu/labs/holt/PDFs/holt.2009.pdf> >). However, these ideas have yet to be empirically tested. We aim to use synthetic biology approaches to investigate the evolvability of phos-

phoregulation.

** *Global analysis of Cdk1 substrate phosphorylation sites provides insights into evolution* Holt LJ, Tuch BB, Villén J, Johnson AD, Gygi SP & Morgan DO. *Science*, Sep 25;325(5948):1682-6 (2009) *

Evolution of Ime2 phosphorylation sites on Cdk1 substrates provides a mechanism to limit the effects of the phosphatase Cdc14 in meiosis* Holt LJ, Huttu J, Cantley L, Morgan DO. *Mol Cell*. Mar 9;25(5):689-702 (2007)

– Liam Holt University of California, Berkeley Department of Molecular & Cell Biology 142 Life Sciences Addition # 3200 Berkeley, CA 94720-3200

<http://mcb.berkeley.edu/labs/holt/> Liam Holt
<liamholt@berkeley.edu>

UEdinburgh EvolutionDisease

Two full-time Research Fellowships are available in the Centre for Immunity, Infection and Evolution at the University of Edinburgh, UK.

The Wellcome Trust-funded Centre for Immunity, Infection and Evolution (CIIE; <http://ciie.bio.ed.ac.uk/>) has become a major centre for interdisciplinary research into infectious disease since its inception in 2008. This thriving Centre is now looking to attract dynamic and enthusiastic researchers, eager to operate at the interface between disciplines (e.g. infection biology, immunology, evolutionary biology, ecology, epidemiology and mathematical modelling) to create new research paradigms to tackle infectious diseases.

CIIE is hosted within the Institute for Immunology and Infection Research (<http://www.ed.ac.uk/schools-departments/biology/immunology-infection>) and Institute for Evolutionary Biology (<http://www.ed.ac.uk/schools-departments/biology/evolutionary-biology>), these being part of the 'Edinburgh Infectious Disease' research community, one of the largest groups of infection biologists world-wide.

As part of our development, and with funding support from the Wellcome Trust, we have launched a Fellowship Programme. The 2-year Fellowships will fulfil a unique role in pursuing research projects designed between two complementary laboratories aimed at providing innovation and new insight into major questions in infection, immunity ecology and evolution. An ex-

ample set of proposed projects is available from the Centre (<http://ciie.bio.ed.ac.uk/>), although applicants are encouraged to contact members of the Centre with their own ideas or suggestions for a new project. The projects are designed to provide proof-of-principle to underpin new project grant applications or, ideally, fellowship applications for follow-on funding beyond the Centre's 2-year provision. The Fellows will work between two or more Principal Investigators one of whom will be primarily responsible for providing mentorship as well as research space and facilities required for the Fellow's project, while consumables and other running costs for the project (up to £10,000 per annum) will be met by the Centre itself.

Successful candidates will hold, or expect to hold, a PhD qualification, will have a good publication record and the ability to design and lead an interdisciplinary research programme in collaboration with others.

Please see the list of CIIE members (<http://ciie.bio.ed.ac.uk/people>) to find possible mentors and projects. General questions about the Centre and the fellowships can be addressed to the Centre Director, Professor Keith Matthews (keith.matthews@ed.ac.uk); but we encourage candidates to contact the specific CIIE members that they would be interested in working with to further develop their applications/projects.

The salary range is £30,122 to £35,938; dependent on experience.

Applications will be accepted until July 25, 2012.

For the Research Fellowship (Ref. #: 3015298) application and specific job description, please go to: http://www.jobs.ed.ac.uk/vacancies/index.cfm?fuseaction=vacancies.detail&vacancy_ref=3015901 Amy B. Pedersen, Advanced Fellow Centre for Immunity, Infection and Evolution

Institutes of Evolutionary Biology, Immunology & Infection Research School of Biological Sciences University of Edinburgh Kings Buildings Ashworth Labs, West Mains Road Edinburgh EH9 3JT, UK

amy.pedersen@ed.ac.uk +44(0) 131 650 8674

Ashworth 2 - 4.07 <http://www.biology.ed.ac.uk/-research/groups/apedersen/> – The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

Amy Pedersen <apederse@staffmail.ed.ac.uk>

U**Edinburgh** GEOMAR**Kiel** Diatom**Evolution**

A 1.5 year postdoctoral research position is available with S. Collins (University of Edinburgh) and U. Riebesell (GEOMAR, Kiel). Time will be spent at both institutions. Possibility of a further 2 year extension to project.

In-situ and laboratory evolution of diatoms in response to high light and CO₂ levels.

Because marine phytoplankton have large population sizes and reproduce quickly, they have the potential to evolve over months or years, and there is evidence that both freshwater microalgae, and calcifying marine phytoplankton can evolve in response to CO₂ enrichment. Laboratory studies are done on single genotypes or species in isolation, in an artificial and very simple environment, whereas all species evolving in the wild must do so in the context of a community, which affects evolutionary outcomes. We will use field manipulations and laboratory selection experiments to measure evolutionary responses of diatoms to ocean acidification in their natural communities, and compare this with the evolution of those same diatoms in single-species laboratory cultures. By combining field and laboratory evolutionary ecology studies, we will quantify the evolutionary response of diatoms to ocean enrichment for the first time, as well as describe the relationship between laboratory and in situ evolutionary responses.

The postdoctoral research assistant will follow the winter to summer seasonal succession of natural plankton communities in sea-going mesocosm systems subjected to different levels of CO₂ enrichment as part of the ongoing BIOACID program (Theme 1). <http://www.bioacid.de/> They will participate in the mesocosm enrichment experiment near Kristineberg, Sweden (Feb-July 2013). They will gather data to quantify the evolutionary response of diatoms to elevated CO₂ in situ. If the project is extended, diatoms isolated from the mesocosms will be used for a laboratory selection experiment so that evolution in situ and in single-species microcosms can be compared.

A PhD in marine biology or phytoplankton physiology, with lab experience, is required. Candidates who also have experience with fieldwork will be given preference. A basic understanding of evolutionary biology is helpful, but most can be learned on the job, so long as the

candidate demonstrates a strong interest in the topic along with a willingness to dive in.

For more information, contact Sinéad Collins: s.collins@ed.ac.uk

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

U**Exeter** Parasite**Evolution**

We are looking to hire a postdoctoral research associate on a 3-year project on parasite modulation of metabolism.

An astonishing outcome of the antagonistic coevolutionary dynamics between host and parasite is the evolution of parasite ability to interfere with host physiology. The molecular details of such interference is poorly understood, limiting our ability to decipher parasite virulence and its evolution.

A major component of parasite mediated 'host reprogramming' targets host metabolism and thereby results in improved parasite growth. A particularly striking example of this is the ability of several viruses to increase the rate of glycolysis in infected cells by up to 370%. More elaborate modulations include, for example, the alteration of lipid and GTP biosynthesis. These findings strongly indicate that a full understanding of host-pathogen interaction and pathogen-caused disease states require a holistic view that considers host and the pathogen as a single system.

This project will concentrate on the interaction of *Burkholderia pseudomallei* and *Francisella tularensis* with human macrophages. Utilizing metabolic modeling together with phenotypic profiling and flux measurements, we will achieve a better understanding of how these parasites manipulate their host and cause disease. The ultimate aim is to develop better strategies of combating intracellular parasites and developing robust analysis approaches at the host-parasite systems level.

To apply, please send your CV, covering letter (detailing your motivation) and the details of three referees to Orkun S. Soyer quoting the job reference P43557 in any correspondence.

For more information, see group web site at; <http://osslab.ex.ac.uk/> Orkun S. Soyer, PhD Senior Lecturer in Systems Biology Engineering, Mathematics

and Physical Sciences University of Exeter

URL: <http://osslab.ex.ac.uk/> Tel: +44 (0)1392 723615

“Soyer, Orkun” <O.S.Soyer@exeter.ac.uk>

UHull EvolutionSexualRecombination

A 3-year PDRA position is now available at the University of Hull as part of a large project entitled 'The Evolutionary Genomics of Sexual Recombination'. This ad refers to the 2nd of two postdocs on this project who will carry out the molecular evolutionary analyses. Using modern evolutionary comparative genomics approaches we aim to study the rate and pattern of genome sequence change with and without the action of meiosis, and across different levels of inbreeding. The project will be carried out in a phylogenetic design, on a newly generated nematode multi-genome data set, leading to advances in understanding the role of reproductive mode in shaping the structure and diversity of genomes.

The puzzling predominance of sexual reproduction amongst animals has been repeatedly identified as one of the major outstanding questions in biology and has received an enormous amount of study. Meiotic recombination is one of the fundamental forces of evolution and plays a very significant role in both generating and mixing the genetic diversity present in sexual organisms. Recombination is also suggested to be instrumental in shaping the content of eukaryotic genomes. We are embarking on a three year project to study the role of breeding system and recombination in shaping the content and diversity of animal genomes using an exceptionally powerful natural system - the Root Knot Nematodes (*Meloidogyne* spp.). We will, for the first time, be able to take a comparative genomic view of radically different reproductive modes in a phylogenetic design. Together these studies will give us a novel and powerful understanding of the role sexual reproduction plays in shaping genome content.

This project is a collaboration between Dr Dave Lunt at the University of Hull and Prof Mark Blaxter at the University of Edinburgh. The goals of the project are to generate complete, annotated genome sequences for a set of *Meloidogyne* species (at least 16 genomes), carefully chosen to represent independent evolutionary contrasts in reproductive mode, and then to use these whole genome data to characterise the effect of organis-

mal breeding system on abundance, diversity and distribution of transposable elements between amphimicts, automicts, and apomicts. We will also test for adaptive evolution of genes and gene families using statistical models of gene family evolution, and test sequence based signatures of adaptive evolution, relating these to loci involved in reproduction and plant-parasite interactions.

PDRA2- MOLECULAR EVOLUTIONARY ANALYSIS; UNIVERSITY OF HULL

Applicants with a strong background in evolutionary biology, bioinformatics and population genetics are invited for this PDRA position to analyse the new genome datasets. The post-holder will use modern evolutionary bioinformatic approaches to analyse transposable elements, gene families and the type of mutational patterns found across the phylogeny of nematode genomes being generated in Edinburgh.

The PDRA will be based in the Evolutionary Biology Group at Hull University. The group is a large and interactive community of evolutionary biologists, with excellent facilities, and provides a great environment for investigating questions in genomics and breeding system.

We anticipate the successful candidate will work proactively and flexibly across the research groups to gain most from this enormous data set, address fundamental biological questions, and produce some very substantial publications.

You must have, or shortly obtain, a PhD in evolutionary biology, bioinformatics, population genetics or other directly relevant subject. An excellent understanding of the genetic consequences of sexual reproduction and the bioinformatic skills suitable to analyse large datasets would be advantageous.

Informal enquiries to Dr Dave Lunt: dave.lunt@gmail.com or d.h.lunt@hull.ac.uk

Vacancy Reference: FS0217 Closing Date: 12 August 2012 Salary range: ?25,251 - ?30,122 pa Further Information: <http://davelunt.net/research/openings/> Official info and online application: <http://bit.ly/PYo0QJ>

PDRA1- GENOME ASSEMBLY, ANNOTATION, AND ANALYSIS; UNIV OF EDINBURGH Applications for this position were advertised previously and are now closed.

Dr Dave Lunt Evolutionary Biology Group Department of Biological Sciences University of Hull HU6 7RX UK <http://davelunt.net> +44 (0)1482 465514 d.h.lunt@hull.ac.uk

– Dave Lunt Dave.Lunt@gmail.com <http://->

davelunt.net dave.lunt@gmail.com

UIIdaho EvolutionAntibioticResistance

Postdoctoral Position at the University of Idaho: Evolution of drug resistance plasmid persistence in biofilms

We are seeking a postdoctoral scientist to join an interdisciplinary team of investigators to conduct research on the evolution of antibiotic resistance plasmid persistence in biofilms. The goal of this project is to gain insight into the evolutionary mechanisms by which multi-drug resistance plasmids can improve their persistence in biofilms formed by various Gram-negative bacteria. The successful candidate will: (i) characterize, compare and interpret evolutionary changes that occur during stabilization of plasmid-host pairs in biofilms and well-mixed liquid cultures by comparative genomics studies and the resources available through the Institute for Bioinformatics and Evolutionary Studies (IBEST) Genomic Resources Core and Computational Resources Core, (ii) oversee the research done by a laboratory technician, and (iii) assume primary responsibility for preparing and publishing scientific papers for peer-reviewed journals, and for presenting findings at scientific conferences. The successful candidate will work under the supervision of Dr. Eva Top (Professor of Biological Sciences, evatop@uidaho.edu) and in collaboration with Drs. Larry Forney, Zaid Abdo and Matt Settles. The position offers the opportunity to carry out research in a dynamic research environment with excellent resources. The successful applicant will be a member of the Department of Biological Sciences as well as IBEST (see <http://www.uidaho.edu/research/-ibest>). The project will be funded by a two-year grant from the Department of the Army and the position should be filled as soon as possible.

JOB REQUIREMENTS The candidate should have: a Ph.D. degree and research experience in a biological science, a fundamental understanding of molecular evolution, and oral and written communication skills as demonstrated by publications as first author in English language peer-reviewed journals and oral presentations at national or international meetings. The candidate should be able to work independently and within a group.

Preference will be given to candidates who also have the following qualifications: research experience in the

field of microbiology, experience with basic molecular biology techniques and with statistical analysis of biological data, ability to use bioinformatics tools and software, knowledge of high throughput methods used for DNA sequencing, general knowledge of plasmid biology, and familiarity with evolutionary theory and with experimental evolution studies. Depending on background and experience, the successful candidate will receive a salary in the range \$37- \$42K (U.S.) per calendar year, health and dental insurance, and funds for travel to scientific meetings and conferences. The position is for two years assuming satisfactory progress, with the possibility of extension depending on the availability of funds. Qualified candidates must apply via the Human Resources website (<https://www.sites.uidaho.edu/AppTrack/-Agency/Applicant/CurrentOpenings.asp?category=1>). Applications should include a cover letter, curriculum vitae, and the names of three persons who can serve as references.

For more information, candidates can write to Dr. Eva M. Top, University of Idaho (evatop@uidaho.edu).

The University of Idaho is an equal opportunity/affirmative action employer.

Dr. Eva Top Professor Department of Biological Sciences University of Idaho 258 Life Sciences South Moscow ID 83844-3051 Phone: 1-208-885-5015 Fax: 1-208-885-7905 E-mail: evatop@uidaho.edu <http://people.ibest.uidaho.edu/~etop/> evatop@uidaho.edu

ULouvainLaNeuve MolEvol

Biodiversity Research Centre – Earth and Life Institute - Université catholique de Louvain (UCL)

POSTDOC-position in ADAPTIVE MOLECULAR ECOLOGY

Project on molecular evolution of olfactory communication under sexual selection in a butterfly, *Bicyclus anynana*

A two-year postdoctoral position is available at the Earth and Life Institute, University of Louvain-la-Neuve (UCL) in Belgium (<http://www.uclouvain.be/en-bdiv.html>). The position is part of a collaborative 5-year research project on the role and mechanisms of plasticity for present and future adaptation and survival in changing environments using 4 model organisms (two butterflies *Pararge aegeria* and *Bicy-*

clus anynana, the spider mite *Tetranychus urticae* and the unicellular eukaryotic ciliate *Tetrahymena thermophila*). The research project is a collaboration between 3 dynamic research teams at UCL (Profs. Hans Van Dyck (spokesman), Nicolas Schtickzelle and Caroline Nieberding) and their international partners.

Focus of the advertised Postdoc position will be on the identification of the molecular bases for olfactory communication evolution between males and females in the model butterfly *Bicyclus anynana*. The male sex pheromone has been identified in this species and is under sexual selection (1,2), and large-scale diversification of the *Bicyclus* genus is associated to sexual selection on the male blend (3). Recently, a transcriptome was produced for investigating the molecular bases of male-female olfactory interactions which provides material for candidate genes analyses in an ecologically relevant framework (4). The postdoc will be in charge of the molecular work for candidate gene identification and validation, aiming at unravelling the molecular bases of olfactory communication and of its plasticity in the first butterfly studied to date. Importantly, a molecular technician will be hired for the same period of time and will be partly dedicated to process the lab work for the postdoc. This position is under supervision of Prof. C. Nieberding (UCL) who works in collaboration with Dr. P. Beldade (Gulbenkian Institute of Science, IGC, Portugal). In addition to his/her main research project on *Bicyclus*, the successful applicant will also participate in helping to design other molecular projects (transcriptome analyses) related to Pararge butterflies and *Tetrahymena* ciliates in collaboration with Profs. Van Dyck and Schtickzelle. There are possibilities for extension of the postdoc position on alternative national or international funding in case of shared interest.

We are looking for a strongly motivated candidate with a PhD in the field of Molecular Evolutionary Ecology with successful experience in RNA work, candidate gene searching and quantitative real time PCR. Interest or experience in olfactory communication, sexual selection, phenotypic plasticity and Lepidoptera are a plus. Strong written and oral communication skills are essential.

Salary ranges between 2000-2200 euros net per month plus benefits (health insurance,...) which are included in the Belgian system. The successful applicant must not have stayed in Belgium more than 24 months out of the last three years. For practical information concerning salaries, benefits, insurances and conditions of eligibility please contact Mrs. D. Socquet at UCL (dominique.socquet@uclouvain.be; +32 (0) 10 47 2720). Applications will be reviewed directly until position is filled. Anticipated start date

is September-October 2012 (to be negotiated). Our University is an Equal Opportunity/Affirmative Action Employer, and is in a French-speaking region, but the language for meetings and scientific interactions is English. For background information about our university, see <http://www.uclouvain.be/en-index.html> Application should be sent to Caroline Nieberding (caroline.nieberding@uclouvain.be) and include the following: (1) a cover letter describing your research interests and qualifications, (2) a full CV, (3) contact information (email, phone number) of minimum 2 referees, and (4) pdfs of up to three representative publications. Please include « postdoctoral application » in the subject line of the e-mail. Informal inquiries are welcome.

(1) Nieberding C, Schneider MV, de Vos H, Lassance JM, Estramil N, Andersson J, Bång J, Hedenström E, Löfstedt C, Brakefield P (2008) -PLoS ONE 3(7):e2751. (2) Nieberding C, Fischer K, Saastamoinen M, Allen C, Wallen E, Hedenström E, Brakefield P (2012) Ecology Letters 15: 415–424 (3) Bacquet* P, Brattström* O, Wang H-L, Löfstedt C, Brakefield P, Nieberding CM (in prep) Male sex pheromones, sexual selection and diversification in the *Bicyclus* butterflies genus. (4) Nieberding CM, Noirot C, Klopp C, Beldade P (in prep) Transcriptome

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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>

UMinnesota DiseaseDynamics

Dear Colleagues, Please circulate this advertisement for a post-doctoral position at the University of Minnesota. Apologies for any cross-postings. Thank you, Meggan Craft

**

POSTDOCTORAL POSITION IN DISEASE ECOLOGY

/Department of Veterinary Population Medicine, University of Minnesota Twin Cities/

A postdoctoral position is available to investigate infectious disease dynamics in wild and domestic animal populations. Meggan Craft's research group

uses mathematical and statistical models fit to empirical data from field systems to study the spread and control of disease (<http://www.cvm.umn.edu/vpm/faculty/meggancraft/home.html>). Current field sites are located in Minnesota and in several national parks in East Africa. Through the University of Minnesota's Ecosystem Health Initiative, the position provides an opportunity to interact with a diverse community of epidemiologists, veterinarians, wildlife managers, geographers, ecologists, and public health practitioners.

The successful applicant will have a PhD in ecology, statistics, applied mathematics or a related field, with a strong background in infectious disease modeling and quantitative analysis, a track record of publication, and the ability to work independently as part of a multidisciplinary team. Initial appointment will be for one year, with possible renewal depending on progress. Salary will be commensurate with experience. Review of applications will begin immediately and continue until the position is filled.

Apply online at:

<https://employment.umn.edu/applicants/Central?quickFind=104301>

Applications should include (1) a cover letter explicitly describing the fit with this position and a possible start date, (2) a curriculum vitae, and (3) a statement of research interests and experience (attach as Additional Document 1). PDF attachments of published or in press papers are encouraged but not required. In addition to applying online, please have two letters of recommendation sent via email (preferable as PDF files) to Dr. Meggan Craft at craft@umn.edu.

The Ecosystem Health Initiative of the University of Minnesota's College of Veterinary Medicine is working with an international consortium of partners to improve understanding of the relationship among the environment, biodiversity, and the health of humans, livestock and wildlife. The University of Minnesota is an equal opportunity educator and employer.

– Meggan Craft, PhD Veterinary Population Medicine University of Minnesota 1988 Fitch Ave St Paul, MN 55108 phone: 1(612)625-6242 <http://www.cvm.umn.edu/vpm/faculty/meggancraft/home.html> Meggan Craft <meggan.craft@gmail.com>

Postdoctoral Research Associate V Speciation Genomics, University of Montana

A postdoctoral position focused on the genomics of speciation is available in the laboratory of Jeffrey Good at the University of Montana, Missoula. The position is part of an NIH-funded project to determine the genetic basis of reproductive isolation between species of house mice. The position involves using experimental quantitative genetics and diverse high-throughput genomic approaches to dissect the genetic and developmental causes of hybrid male sterility in mice. The successful candidate will demonstrate a strong background in molecular biology, quantitative genetics, evolution, and genomics. A Ph.D. in biology or a related field is required. Candidates with previous experience collecting and analyzing genomic data are strongly encouraged to apply.

The Good lab is based in the Division of Biological Sciences at the University of Montana. The University of Montana is home to a diverse and highly interactive collection of faculty with expertise in ecology, evolution, genetics, genomics, physiology, and behavior. Missoula is a great college town with an exceptional quality of life and is located in the heart of the Rocky Mountains of western Montana. For further information on this position and our research please visit the Good Lab website (<http://good-lab.dbs.umt.edu/GoodLab/Home.html>) or email Dr. Good directly at jeffrey.good@mso.umt.edu.

To apply, please visit <http://umjobs.silkroad.com> and click the job title for this position under Openings. Candidates must apply online, and will be asked to upload the following application materials: a cover letter describing your research interests and qualifications, a CV, and the names and contact information for three references. Review of applications will begin on August 1 but the position will remain open until filled. The appointment is renewable for up to three years. The position is available immediately but the start date will be flexible contingent on the needs of the preferred candidate.

ADA/EOE/AA/Veteran's Preference Employer

Jeffrey Good <jeffrey.good@mso.umt.edu>

Postdoctoral researcher - Evolutionary models of cancer progression and therapies - Université Montpellier II, France

We are looking for a motivated postdoctoral research to employ mathematical and/or computer models to better understand the evolutionary dynamics of cancer progression and chemotherapeutic treatments. We are especially interested in applications of ecology and population genetics towards more general descriptions and ultimately predictive theories.

The contract is initially for one year, and can be extended annually for up to three years, with a starting date on or before December 1st, 2012. The net salary will be in the range of 2000-2500 euros net per month, depending on previous experience. This contract is part of an initiative by the CNRS to support interdisciplinary research involving the ecological and health sciences. Possibility for researcher to apply for a CNRS position after 1 year of contract.

Requirements: PhD and demonstrated experience in mathematical modeling in the context of cell biology and/or evolutionary biology. Excellent command of scientific English.

Interested candidates should send (1) a letter of motivation, (2) a CV, and (3) the names, institutional addresses, and emails of 3 persons who can be contacted for references, on or before SEPTEMBER 15, 2012 to Michael Hochberg (mhochber@univ-montp2.fr). Information about our research group can be found at <http://www.eec.univ-montp2.fr/people/mike-hochberg/> Michael Hochberg <mhochber@univ-montp2.fr>

UMuenster PDFJobGradStd positions

As of July 2012 we have openings for 3 POSTDOCS, one SCIENTIFIC PROGRAMMER and 3 PhD STUDENTS in the Bornberg-Bauer lab as follows:

* POSTDOCTORAL PROJECT LEADER (TVL13/14) to study subfunctionalisation and substrate promiscuity in protein families with some computational but mostly experimental BACKGROUND IN MOLECULAR BIOLOGY (or similar), work in collaboration with group Hollfelder (University of Cambridge), commencing late 2012 / early 2013.

* POSTDOC to work on MODULAR PROTEIN EVO-

LUTION with a background in molecular evolution and biocomputing, commencing late 2012/early 2013.

* POSTDOC to work on TRANSCRIPTOME and STRUCTURAL GENOME EVOLUTION of nematodes evolved under Bt pathogen attack, with a background in biocomputing and/or molecular biology, commencing early 2013.

* SCIENTIFIC PROGRAMMER to work on projects related to host-parasite co-evolution with experience in web-servers, databases and programming, diploma/MSc from from a University or College (Fachhochschule) with the option to obtain a further degree, commencing late 2012. Tenure may become possible.

* PHD STUDENTS to work on PROTEIN EVOLUTION, STRUCTURAL GENOME EVOLUTION of vertebrates and insects with a background (MSc) in bioinformatics or molecular biology, commencing late 2012 / early 2013.

Details on: <http://ieb.uni-muenster.de/bioinf/positions> ebb@wwu.de Recent publications: <http://www.ncbi.nlm.nih.gov/pubmed?term=bornberg-bauer> "E. Bornberg" <ebb@uni-muenster.de>

UNotreDame EnvironmentalGenomics

POSTDOCTORAL POSITION IN ENVIRONMENTAL GENOMICS University of Notre Dame

A postdoctoral research position in ecometagenetics of freshwater species is available on an externally funded project affiliated with the Notre Dame Environmental Change Initiative (<http://environmentalchange.nd.edu/>) and the Genomics and Bioinformatics Core Facility (<http://nd.edu/~genomics/index.html>). The goal of the project is to refine and apply environmental DNA methods to describe communities of fishes and amphibians in a variety of freshwater habitats. The ideal candidate would have a strong interest in using genomic approaches to study biodiversity in natural communities, experience in marker design, qPCR, nextgen sequencing, and bioinformatics. Experience with aquatic systems is preferred but not required. The Environmental Change Initiative also includes researchers applying similar methods to microbes, invertebrates, and ancient plant DNA. Applicant screening is rolling, but with a desired start in winter 2012-early spring 2013. Salary and ben-

efits will be competitive. The postdoctoral fellow will collaborate with Notre Dame faculty members Michael Pfrender (<http://www.nd.edu/~mpfrende/>), David Lodge (<http://nd.edu/~lodgelab/>), and Christopher Jerde (<http://www.nd.edu/~cjerde/Contact.html>). Applicants should email (in one pdf document) a letter describing prior research experience and current interests, a curriculum vitae, and the names and contact information of three references to David Lodge (dlodge@nd.edu), with a cc to eci@nd.edu. In the email subject line, please put “Environmental Genomics–Lodge.” The University of Notre Dame is an Equal Opportunity/Affirmative Action Employer. Interested candidates who will be at the Ecological Society of America meeting in Portland should contact David Lodge to meet there during Mon-Thurs 6-9 August.

Joanna McNulty <Joanna.L.McNulty.9@nd.edu>

UOxford EvolutionAntibioticResistance

Postdoctoral Research Assistant in Genomics of Antibiotic Resistance Evolution

Fixed term for 3 years

Grade 7: £29,249 - £31,948

A 3 year postdoctoral position is available to study the genomics of antibiotic resistance evolution in bacteria from the genus *Pseudomonas* as part of an ERC-funded project on the experimental evolution of antibiotic resistance led by Dr. Craig MacLean.

The overall goal of this ambitious project is to determine the relative importance of chance, historical contingency, and the strength of selection in shaping the outcome of resistance evolution at a genomic scale. To accomplish this goal, the postholder will determine the genomic basis of resistance evolution in experimental populations of *Pseudomonas* using a combination of whole-genome resequencing, amplicon sequencing, and RNAseq.

The ideal applicant will have experimental and computational experience in bacterial genetics, but the most important qualification is previous experience in analysing NGS data, ideally in the context of experimental evolution. This position is ideal for highly motivated and ambitious researchers who would like to work on a large project that will investigate fundamental

evolutionary problems related to antibiotic resistance. This project is funded at a high level and the postholder will be expected to take an important leadership role in the development of this project.

The post will be based in a dynamic and productive microbial evolution research group within the Department of Zoology that brings together experimentalists and theoreticians with a wide range of interests in evolutionary biology.

Informal enquiries with CV should be sent to Dr. Craig MacLean (craig.maclean@zoo.ox.ac.uk)

Only applications received before midday on Wednesday 15 August 2012 can be considered. You will be required to upload a supporting statement and CV. To apply please go to www.jobs.ox.ac.uk and find job reference 103448

Dr. Craig MacLean Royal Society Research Fellow University of Oxford, Department of Zoology

Phone: 01865 281062 Email: craig.maclean@zoo.ox.ac.uk

Craig Maclean <craig.maclean@zoo.ox.ac.uk>

UOxford EvolutionSexChromosomes

Project Title: Evolution of sex chromosomes in plants

We are looking for a postdoctoral researcher to work on an evolutionary genomic project focused on sex-chromosome evolution in plants. This is part of a collaborative project between Filatov (Oxford, UK) and Pannell (Lausanne, Switzerland) labs. The successful candidate will initially work for about a year in Oxford, with the possibility of continuing for another year in Lausanne afterwards. Funding is available immediately.

The focus of this job will be on data analysis and writing up, as extensive genomic and transcriptomic resources have already been generated for several species with relatively young sex chromosomes. These datasets are also suitable to address questions beyond sex-chromosome evolution (such as adaptation and speciation), and the successful candidate will be encouraged to do so (time permitting). Ideally, the successful candidate will have significant bioinformatics skills and solid background in evolutionary genetics/genomics. Programming (or scripting) skills and familiarity with Linux environment will be quite essential for this

project.

Informal enquiries and applications should be sent to Dmitry Filatov (Dmitry.Filatov@plants.ox.ac.uk). Applications should include a letter of motivation, a clear indication when the candidate would be available to start, a CV, and the names of two people willing to provide a reference. Full consideration will be given to all applications received before 15th July, 2012.

Dmitry A. Filatov, PhD University Lecturer in Evolutionary Genetics Department of Plant Sciences, University of Oxford, South Parks Road, Oxford OX1 3RB United Kingdom

Dmitry Filatov <dmitry.filatov@plants.ox.ac.uk>

UOxford EvolutionSexChromosomes

2

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Dmitry A. Filatov, PhD University Lecturer in Evolutionary Genetics Department of Plant Sciences, University of Oxford, South Parks Road, Oxford OX1 3RB United Kingdom

Dmitry Filatov <dmitry.filatov@plants.ox.ac.uk>

UOxford WTCHG StatisticalGenetics

UNIVERSITY OF OXFORD RESEARCH ASSOCIATE IN STATISTICAL GENETICS THE WELLCOME TRUST CENTRE FOR HUMAN GENETICS, ROOSEVELT DRIVE, HEADINGTON, OXFORD, OX3 7BN

Grade 7: £29,249 - £35,938 with a discretionary range to £39,257p.a.

Now is an extremely exciting time in human genetics with the opportunity to use new large datasets to answer important questions in biology and evolution, which may have an impact on human health and healthcare.

Applications are invited for a Research Associate in Statistical Genetics to join the group of Dr Chris Spencer, to participate in the development and application of methods for the analysis of large-scale human genomics datasets. The research, funded by the Wellcome Trust, will have a particular emphasis on combining data from different populations or phenotypes, and on using population genetic inference to understand biology. You will have the opportunity to work on the analysis of data from collaborations investigating autoimmune disease in large collections of European individuals and malaria susceptibility in studies of individuals across Africa. Dr Spencer's group works closely with other groups in Wellcome Trust Centre for Human Genetics including Professors McVean, Donnelly and Kwiatkowski.

We are looking for an individual with a PhD in a quantitative field (such as statistics or mathematics) ideally with experience of genetic analysis. Individuals with PhDs in other areas of biology are invited to apply if they can demonstrate a strong statistical background. The work will involve a large bioinformatics component, so you will also need to have computer programming experience, ideally with the statistical software R, a scripting and low-level language. You should be able to work alone and collaboratively, and be able to digest

and communicate scientific ideas effectively. The successful applicant will have an aptitude for visualising data, problem solving and careful statistical analysis. The position is available for up to three years in the first instance and is funded by the Wellcome Trust.

To apply for this role and for further details, including a job description and person specification, please click on the link below:

www.recruit.ox.ac.uk/pls/hrsliverecruit/-erq_jobspec_version_4.jobspec?p_id3274

Informal enquires can be made by e-mailing chris.spencer@well.ox.ac.uk

Only applications received before 12:00 midday on Monday 16th July 2012 can be considered. You will be required to upload a CV and supporting statement as part of your online application. Please quote reference 103274 on all correspondence.

Dr Chris Spencer

Wellcome Trust Centre for Human Genetics Roosevelt Drive Oxford OX3 7BN United Kingdom

01865 287722 or 01865 617886 www.well.ox.ac.uk/chris-spencer Chris Spencer <spencer@well.ox.ac.uk>

UProvence EvolutinaryBioinformatics

We have a 15 month post doc position available in our lab see: http://sites.univ-provence.fr/evol/index.php?option=com_content&view=category&layout=blog&id=139&Itemid=225&lang=fr
best regards Pierre Pontarotti

Pierre PONTAROTTI <Pierre.Pontarotti@univ-provence.fr>

USalford SeafoodIdentification

PLEASE NOTE APPLICATION CHANGES FOR THIS PREVIOUSLY ADVERTISED POSITION:

We invite applications for a 2-year post-doctoral position, to work on seafood genetic identification in Dr Mariani's lab at the University of Salford, Manchester.

The project is primarily funded by the EU Interreg Atlantic area and offers the opportunity to interact with collaborators in Spain, Portugal, France, Ireland and Germany.

The ideal candidate will hold a PhD in Evolutionary Biology, Genetics, Ecology, Marine Biology, or other relevant subjects, and will have a proven track-record in publishing in international peer-reviewed journals. He/she will also exhibit strong skills in molecular genetics techniques and bioinformatics, and will have a positive, communicative, dynamic personality, suited to work as part of a team.

Dr Mariani's lab at Salford University - still twinned with its previous base at University College Dublin - contributes to a broad range of investigations in population and conservation genetics and fisheries biology (for details: <http://www.els.salford.ac.uk/staff/-profile.php?staffid=3D151>).

Applications should be submitted through the central electronic system at the link: https://atsv7.wcn.co.uk/-search_engine/jobs.cgi?SID=3DamNvZGU9MTI2MTcwOSZ2dF90ZW1wbGF0ZT05MTkmb3duZlI9NTAzNjMyOCZvd25lcnR5cGU9ZmFpciZicmFuZlF9pZD0wJnZhY3R5cGU9MTI1MCZwb3N0aW5nX2NvZGU9MjIzJnJl
cXNpZz0xMzQxNTA0OTkxLWRjNTE1NjE xN-TkzOWNmMzFjYTFjMzkxNmNkNWY4YmYwNzQ4MWIwYWE Please ensure that your application is submitted by July 19th. Please also be advised that the interviews will take place between the 6th and the 10th of August (exact date yet to be decided).

Start date: September 2012. Gross salary: >28,000 £

Dr Stefano Mariani Reader in Wildlife Biology School of Environment & Life Sciences Peel Building, Room 316 The University of Salford M5 4WT, UK Tel. +44.161.2956913 <http://www.els.salford.ac.uk/staff/-profile.php?staffid=3D151> S.Mariani@salford.ac.uk

USheffield GreatTitEvolution

Postdoctoral Research Associate - University of Sheffield

A postdoctoral position, funded by the European Research Council (ERC), is available in Prof. Jon Slate's research group (<http://www.jon-slate.staff.shef.ac.uk/>) at the University of Sheffield.

This is an outstanding opportunity to apply cutting edge genomics technologies (ultra-high throughput sequencing and SNP genotyping) to study microevolution in a classic long-term, individual-based study system - the great tit population at Wytham Woods Oxford (<http://www.zoo.ox.ac.uk/egi/research/studysites.htm>).

I am looking for somebody with a track record of publishing in leading journals and skills in one or more of the following areas: molecular ecology, evolutionary quantitative genetics, QTL mapping, genomewide association studies, molecular evolution or statistical genetics. The postdoc will work as part of a team of six (with the PI, two independent research fellows, one other postdoc and one PhD student) investigating the genetic basis of adaptive variation in a system which has been the focus of intensive evolutionary ecology and quantitative genetics studies (e.g. Garant *et al**. 2005 *Nature** 433: 60-65; Charmantier *et al** 2008 *Science**320: 800-803) but where genomics resources were, until recently, lacking. In this project we have used high-throughput sequencing (Roche 454) to sequence the great tit transcriptome (Santure *et al** 2011 *BMC Genomics* 12: 283) and mine many thousands of SNPs. We have subsequently developed an ~8k SNP chip (van Bers *et al** 2012 *Mol. Ecol. Resources**. 12: 753-770) which we have been using to build a linkage map and map QTL. Over the next year we intend to dramatically increase marker density and applications from people interested in RAD-Seq, genotyping-by-sequencing or similar approaches are strongly welcomed. For example publications from our laboratory see <http://www.jon-slate.staff.shef.ac.uk/html/publications.html>. The project involves close collaboration with Professor Ben Sheldon (Oxford University) and his research group (<http://www.zoo.ox.ac.uk/egi/index.htm>) as well as a group in the Netherlands working on a similar project.

Professor Slate's group is based within the vibrant Department of Animal & Plant Sciences at the University of Sheffield. In the latest Research Assessment Exercise (RAE 2008), Biological Sciences at Sheffield was ranked joint 3rd in the UK based on average quality score and 3rd in the UK based on the proportion of 'world-leading' (4*) and 'internationally excellent' (3*) research activity (Source: Times Higher Education < <http://www.timeshighereducation.co.uk/story.asp?storycode=3D404786> >) It was recently ranked 7th best Environment/Ecology research institution in the world by Thomson Scientific. Sheffield is a fantastic place to live, situated on the edge of the Peak District National Park (<http://www.visitpeakdistrict.com/>). It is also one of the most

affordable cities in the UK and has a good music, arts and culture scene.

The position is available as soon as possible and is funded until 30th September 2013. I realise this is a relatively short term position, but opportunities for continued employment can be pursued by the PI and successful applicant. For example, I can mentor fellowship applications, or help develop research proposals that build on the work done by the successful applicant. The closing date is 29th August 2012. For further details and online applications see <http://www.sheffield.ac.uk/jobs/index.html>, quoting job reference number UOS004979. The salary is in the range £28,401 - £30,122 per annum.

I welcome informal enquiries (j.slate@sheffield.ac.uk)

j.slate@sheffield.ac.uk j.slate@sheffield.ac.uk

USouthDakota BioinformaticsPhenotypes

Postdoctoral fellow: Bioinformatics, Phenotypes

We are recruiting a postdoc with training in bioinformatics who is interested in studying phenotypic evolution by combining model organism genetic data with comparative anatomical data from throughout the vertebrates.

One of the biggest challenges in systems biology is the inclusion of whole organism phenotypes. In the Phenoscape group, we have developed ontology-based methods for representing phenotypes of diverse species in order to integrate them with model organism developmental and genetic data,. We have collected these data in a sophisticated Knowledgebase, which has an initial focus on the diversity of phenotypes in ostar-iophysan fish, including zebrafish (kb.phenoscape.org). We are currently scaling up our approach to the vertebrates as a whole, with a goal of allowing similarities to be identified between phenotypes from sources as diverse as dinosaur fossils and mouse knockout mutants.

We invite postdoctoral applicants to propose an independent project that uses the Phenoscape Knowledgebase as a research platform. In particular, we are interested in projects that will leverage functional genomic data to study the evolution of whole-organism phenotype in nonmodel organisms.

The postdoc will work under the direction of Paula

Mabee (University of South Dakota) and Todd Vision (University of North Carolina), as part of a distributed, multidisciplinary team that includes evolutionary biologists, computer scientists, model organism experts, and bioinformaticists. It will be based in South Dakota, with opportunities to travel to other sites, including the National Evolutionary Synthesis Center (NESCent), the University of Chicago, and the California Academy of Sciences.

Starting date: This two year postdoctoral position is available to be filled as early as September 2012.

Required qualifications: Ph.D. degree with strong background in bioinformatics; previous experience with ontologies preferred

* Experience in functional genomics or developmental biology * Demonstrated communication and writing skills, in English * Demonstrated ability to work in a team setting

How to apply: Please contact Dr. Mabee (pmabee@usd.edu) for inquiries. Applications should be directed to Dr. Mabee and include a cover letter, CV, a brief statement detailing your research interests and career goals, and three letters of reference.

For more information, please see <https://phenoscape.org> and <http://kb.phenoscape.org/>. "Mabee, Paula" <Paula.Mabee@usd.edu>

Uppsala CompGenomicsEndosymbioticBacteria

Researcher in comparative genomics of endosymbiotic bacteria:

<http://www.uu.se/job/other/-annonsvisning?tarContentId=3D196228&languageId=1> The position is for at least 1 year and will be filled as soon as possible.

The Department of Cell and Molecular Biology is one of the most international, broad and distinguished bio molecular departments in Europe, comprising six research programs with about 125 employed. This position is within the program in Molecular evolution.

Project description: The aim of the project is to identify the genetic components of the endosymbiotic bacterium *Wolbachia* that are responsible for the induction of cytoplasmic incompatibility (CI) using genome sequencing and comparative genome

analyses. More information can be found under: <http://www.icm.uu.se/faculty-research/Molecular-Evolution/People/lisa-klasson/?languageId=1> Requirements: The candidate should have a PhD in bioinformatics, molecular biology or other relevant areas. Previous experience of working with next-generation-sequencing data and bioinformatic analyses, used to working in a Linux/Unix environment and familiarity with a scripting language such as Perl is highly desirable. Basic skills in molecular biology laboratory techniques are also desirable. The candidate needs to be proficient in both written and spoken English.

For inquiries regarding the positions please contact Lisa Klasson (lisa.klasson@icm.uu.se). The application should include a CV, a summary of research interest and contact details for at least 2 references.

You are welcome to submit your application no later than 6:th of July 2012

Dr. Lisa Klasson Molecular Evolution Department of Cell and Molecular Biology Uppsala University Box 596 SE-751 24 Uppsala Sweden phone: +46 (0)18 471 6403 guy.lionel@gmail.com

UVermont EcologicalGenomics

Postdoc in Ecological and Evolutionary Genomics at University of Vermont

We are seeking a post-doctoral associate for an NSF-funded project to investigate molecular mechanisms underlying acclimation and adaptation to climate change in North American ant assemblages. This is a collaborative project with researchers at University of Vermont (Nicholas Gotelli, Sara Helms Cahan and Bryan Ballif), Harvard Forest (Aaron Ellison), University of Tennessee at Knoxville (Nate Sanders) and North Carolina State University (Rob Dunn). The project will involve characterizing the transcriptome of one or more ant species, and then using this resource to investigate short-term gene expression responses to temperature modification in the field and laboratory as well as adaptive divergence in regulation of gene expression across a latitudinal gradient. The post-doctoral associate will have primary responsibility for the generation and analysis of mRNA-seq transcriptome datasets, and will work closely with PIs, students, and technical staff to develop and execute comparative and ex-

perimental studies that intersect with ongoing work on species- and community-level responses to climate change. This position will be a unique opportunity to work at the interface of molecular biology and ecology, linking next-generation techniques with pressing current questions in biogeography, community ecology, and climate change.

The position will be based in Burlington, Vermont, with the opportunity to visit and interact with collaborators at partner institutions. Previous experience in genomics/transcriptomics and bioinformatic analysis of large datasets is essential, as well as an interest in working with non-model systems of ecological importance.

Informal inquiries about the position can be addressed to Sara Helms Cahan (scahan@uvm.edu) or Nicholas Gotelli (ngotelli@uvm.edu). To apply, please send a cover letter detailing your interest and qualifications for the position, a current CV, and the names and e-mail addresses of two potential references to Sara Helms Cahan (scahan@uvm.edu).

Application review will begin September 15, 2012. The anticipated start date is 1 January 2013. The position is funded for 2 years, with a possible extension in the third year. Annual reappointment is contingent on satisfactory annual progress.

To find out more about research in the Helms Cahan lab, go to:

<http://www.uvm.edu/~biology/Faculty/Helms-Helms.html>

To find out more about research in the Gotelli lab, go to:

<http://www.uvm.edu/~ngotelli/homepage.html>

To find out more about research in the Ballif lab, go to:

<http://www.uvm.edu/~bballif/> /The University of Vermont and State Agricultural College is committed to a policy of equal employment opportunity and to a program of affirmative action in order to fulfill that policy. All applicants and employees shall be treated in employment matters without regard to unlawful criteria including race, color, religion, ancestry, national origin, place of birth, sex, sexual orientation, disability, age, positive HIV-related blood test results, genetic information, gender identity or expression, or status as a disabled veteran, recently separated veteran, other protected veteran or Armed Forces service medal veteran, as these terms are defined under applicable law, or any other factor or characteristic protected by law.

– Dr. Sara Helms Cahan Associate Professor Co-Director, BioScience Program Department of Biology University of Vermont Burlington, VT 05405 (802) 656-

2962

Sara Helms Cahan <Sara.Cahan@uvm.edu>

UVirginia Evolutionary Genetics

The Department of Biology at the University of Virginia invites applications for a postdoctoral Research Associate position in the lab of Dr. Benjamin Blackman. The aims of the position will be tailored to the expertise of the successful applicant and complement the Blackman Lab's broader interests in the genetic basis of adaptation and speciation, the ecology and evolution of plant development, and mechanisms of gene-environment interaction. Using sunflower and monkeyflower as study systems, current work is focused on the genetic changes and ecological pressures contributing to clinal variation in developmental plasticity, with an emphasis on responses to circadian and seasonal cues. Additional work concerns sunflower domestication genetics and gene family evolution. The postdoc will work closely with the PI, collaborators, and lab personnel to design and lead research in the lab and field. The position also involves preparing grant proposals and manuscripts, data management and dissemination, and mentoring graduate and undergraduate students.

The ideal candidate will demonstrate the ability to integrate across biological disciplines, identify and troubleshoot promising new methodologies independently, and use the appointment to develop and pursue novel, exciting questions. Demonstrated expertise in evolutionary and molecular genetics is essential. Specific experience with analysis of genomic or transcriptomic datasets, programming for bioinformatics, selection analysis, QTL mapping, transgene construction and plant transformation, and gene expression studies are desirable.

The completion of a Ph.D. degree in Biology or related field by appointment start date is required. Preferred appointment start date is October 2012.

This is a one-year appointment; however, appointment may be renewed for an additional two one-year increments, contingent upon available funding and satisfactory performance.

To apply, please submit a candidate profile through Jobs@UVA (<https://jobs.virginia.edu>) and electronically attach: curriculum vitae with list of publications,

a cover letter that summarizes research interests and professional goals, and contact information for three (3) references; search on posting number 0610172.

Review of applications will begin July 3, 2012; however, the position will remain open until filled.

Questions regarding this position should be directed to: Dr. Benjamin Blackman bkb2f@virginia.edu

Questions regarding the Candidate Profile process or Jobs@UVA should be directed to: Mary Liberman ml5ac@virginia.edu

The University of Virginia is an Equal Opportunity/Affirmative Action Employer. Women, minorities, veterans and persons with disabilities are encouraged to apply.

bkb7@duke.edu

The project goal is to apply new DNA sequencing technologies to resolve rapid radiations and recent speciation events in the tree of life. The research project is focused on a diverse group of lizards (genus *Sceloporus*), although candidates with interests in any taxonomic group are encouraged to apply - no previous research experience with reptiles is required. Training and research activities cross multiple disciplines, including phylogenetics, bioinformatics, comparative genomics, and systematics. More information on the Leache lab is available at <http://faculty.washington.edu/leache/-wordpress/> The ideal candidate will have a strong background in phylogenetics, and experience working with next-generation sequence data. Responsibilities include collecting next-generation sequence data, developing and running bioinformatics pipelines to clean, assemble, and align the data, and conducting phylogenetic analyses using high-performance computing resources. Preferably, the candidate will have experience scripting in either Perl or Python, and be familiar with MySQL. Candidates will be expected to have completed a PhD in Biology or a related field.

Candidates should send a CV and statement of research interests to leache@uw.edu. Review of applications will begin immediately and continue until the position is filled. The position is available immediately and renewable for up to three years.

UW IS AN EQUAL OPPORTUNITY/EQUAL ACCESS EMPLOYER

Adam Leache
leache@uw.edu

UWashington Seattle Phylogenomics

POSTDOCTORAL RESEARCHER

University of Washington, Seattle

Department of Biology

A postdoctoral researcher position is available in the lab of Adam Leache at the University of Washington, Seattle. This position is part of a systematics project funded by the National Science Foundation.

WorkshopsCourses

Barcelona GenomicsBioinformatics 78	Keystone SouthDakota VertebrateEvolution Sep21-24
Basel MicrobiotaEvolution Sep12-14 78	2 80
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Keystone SouthDakota VertebrateEvolution Sep21-24	Portugal TypingMicroorganisms Sep25-28 81
80	Wales EvolutionMedicine Ag14-17 82

Barcelona GenomicsBioinformatics

BARCELONA SUMMER SCHOOL IN GENOMICS AND BIOINFORMATICS

Course: Next Generation Sequencing for Population and Medical Genomics

From September 17th to September 21th 2012, at Universitat Pompeu Fabra, Barcelona.

Aim: Next-generation sequencing technologies have revolutionized genomics research. In this course we aim to familiarize the students with the different NGS technologies and their applications to the study of human genetic variation and disease. The course will cover aspects from technology and informatics to experimental design and data analysis. This course is designed to be of interest for master and PhD students preferentially with a background on human genetics. The course will include theoretical and practical sessions.

Number of participants: 25

Confirmed Speakers: Roderic Guigó (Centre for Genomic Regulation) Ivo Gut (Centre Nacional d'Anàlisi Genòmica) Tomàs Marquès-Bonet (Institute of Evolutionary Biology) Nàgria López-Bigas (Universitat Pompeu Fabra) Chris Tyler-Smith (Wellcome Trust Sanger Institute) Yali Xue (Wellcome Trust Sanger Institute) Luis Pérez Jurado (Universitat Pompeu Fabra) Arcadi Navarro (Institute of Evolutionary Biology) Cedric Notredame (Centre for Genomic Regulation) Stephan Ossowski (Centre for Genomic Regulation)

Program: available at <http://www.ibe.upf-csic.es/ibe-actualitat/ngscourse.html> Coordinator: Ferran Casals (Universitat Pompeu Fabra - Institute of Evolutionary Biology).

Tuition: The registration fee of 500 Euros covers course materials, coffee breaks and lunches. Lodging costs are not included in the registration fee. If needed we can help participants to find economic accommodation in Barcelona.

Pre-registration: Please register at <http://biologiaevolutiva.org/BSSGB/>. Accepted participants will receive the instructions for the payment.

Please contact bcnSSGB@gmail.com for further information.

Ferran Casals ferran.casals@upf.edu

Basel MicrobiotaEvolution Sep12-14

WORKSHOP DEADLINE (for the lecture) HAS BEEN EXTENDED!!!

The Organizing Committee would like to invite you to attend a 3-day international workshop on the "Evolution and Ecology of Host-Associated Microbiota" to be held at the Zoological Institute, University of Basel, Switzerland on September 12- 14, 2012. The major aim of this workshop is to provide a synthesis of the emerging evolutionary and ecological patterns governing the complex interactions of host-microbiota across different biological systems. We have invited leaders in the field of host-associated microbiota and microbial ecology to share their insights on the evolutionary and ecological principles that shape bacterial community structure and host-microbiota interactions.

This workshop is intended for undergraduate students, graduate students, postdoctoral researchers and early career investigators (100 slots available) who wanted to be exposed to the evolutionary and ecological concepts and bioinformatics tools being applied on the study of host-associated microbiota systems and microbial ecology. Together with the lecture, a hands-on tutorial (bioinformatic tools and approaches encompassing microbial ecology, comparative genomics, molecular evolution) will be provided on the analysis of complex sequence data sets derived from next-generation sequencing.

Thanks to the generous funding from ProDoc of the Swiss National Science Foundation and the University of Basel, we are only charging a minimal fee of CHF 150 for registration (includes 3 lunches, 1 social dinner, 2 social mixers and snacks during the entire workshop) or CHF 250 (+ tutorial on the analysis of next-generation sequences; 50 slots available). We also have arranged for a number of rooms around Basel ranging from youth hostel dormitories (CHF 32-79/day) to 3-star hotels (CHF 160- 250/day). Moreover, Basel/Mulhouse Airport is a hub for Easyjet, a budget airline in Europe. Application deadline for the tutorial is May 30 and for the lecture series is July 15, 2012. More information can be found at this website:<http://evolution.unibas.ch/ebert/microbiota/index.htm>

Please direct any questions to the organizing committee: Marilou Sison-Mangus (m.sison@unibas.ch), Samuel Pichon (samuel.pichon@unibas.ch) and Dieter

Ebert (dieter.ebert@unibas.ch)

Confirmed Speakers:

Bioinformatics and Computational Tools

1. KNIGHT, Rob (University of Colorado Boulder, USA) - computational tools for understanding the evolution of microbiota through time and space
2. CAPORASO Greg (Northern Arizona University, USA) - QIIME (Quantitative Insights Into Microbial Ecology) and microbiota dynamics
3. HUSON, Daniel (University of Tübingen, DE) - MEGAN (MetaGenome ANalyzer) and phylogenetic networks

4. QI Weihong (ETH Zürich, CH) - Trends and applications of next- generation sequencing technologies

Microbial Diversity and Symbiosis

5. DUBILIER Nicole (Max Plank Institute, Bremen, DE) - Symbioses of bacteria and hydrothermal vent organisms
6. BRUNE, Andreas (Max Plank Institute, Marburg, DE) - Insect gut microbiology and symbiosis
7. EBERT Dieter (University of Basel, CH) - Daphnia parasites and microbiota

Microbiota Dynamics and Evolution

8. GILBERT Jack (University of Chicago, USA) - Microbial community dynamics and function
9. JANSSON, Janet (LNL, DOE-JGI, USA)- bacterial diversity in the environment
10. LEE Carol Eunmi (University of Wisconsin-Madison, USA) - Copepod microbiota and invasion success
11. Van der MEER Jan (University of Lausanne, CH) - Genetic adaptation and evolution of bacteria in the environment

Genomics of Health- and Nutrition-Associated Microorganisms

12. SVANBORG Catharina (University of Lund, SE) - Host imprints on human-associated bacterial genomes
13. VORHOLT Julia (ETH Zürich, CH) - Physiology of plant-associated microbes (metaproteomics)

Bacteria- host interactions and evolution

14. ROSENBERG Eugene and ZILBER-ROSENBERG, Ilana (University of Tel Aviv, IL) - Coral microbial communities and the hologenome theory
15. POULSEN, Michael (University of Copenhagen,

DK) - Multiple interactions between symbionts and host

16. HENTSCHEL, Ute (University of Würzburg, DE) - Mechanisms of interactions between sponges and their microbial communities

Marilou P. Sison-Mangus, PhD Postdoctoral Researcher Evolutionary Biology, Zoology Institute University of Basel Vesalgasse 1, 4051 Basel Switzerland

Tel no: 061 267 03 72

m.sison@unibas.ch

ColdSpringHarbor ComputationalGenomics Oct31-Nov6

Course announcement - Application deadline, July 15, 2012

Cold Spring Harbor COMPUTATIONAL & COMPARATIVE GENOMICS

Oct 31 - Nov 6, 2011 Application Deadline: July 15, 2012

INSTRUCTORS:

William Pearson, University of Virginia, Charlottesville, VA Lisa Stubbs, University of Illinois, Urbana, IL This course presents a comprehensive overview of the theory and practice of computational methods for the identification and characterization of functional elements from DNA sequence data. The course focuses on approaches for extracting the maximum amount of information from protein and DNA sequence similarity through sequence database searches, statistical analysis, and multiple sequence alignment. Additional topics include:

Alignment and analysis of "Next-Gen" sequencing data
The Galaxy environment for high-throughput analysis
Identification of conserved signals in aligned and unaligned sequences
Regulatory element and motif recognition
Integration of genetic and sequence information in biological databases
The ENSEMBL genome browser and BioMart
Function/phenotype prediction for sequence variants
The course combines lectures with hands-on exercises; students are encouraged to pose challenging sequence analysis problems using their own data. The course is designed for biologists seeking advanced training in biological sequence and genome anal-

ysis, computational biology core resource directors and staff, and for scientists in other disciplines, such as computer science, who wish to survey current research problems in biological sequence analysis. Advanced programming skills are not required.

The lecture/lab schedule for the 2011 course can be found at fasta.bioch.virginia.edu/cshl

Speakers in the 2011 course included: Aaron Mackey, U. of Virginia, Next-Gen analysis pipelines Bert Overduin, European Bioinformatics Institute, UK, ENSEMBL and BioMart Francis Ouellette, Ontario Institute for Cancer Research, Databases for Biological Function William Pearson, U. of Virginia, Similarity Searching, Multiple Alignment Lisa Stubbs, U. of Illinois, Urbana, ChIP, Transcription Factors, and Comparative Genomics James Taylor, Emory, Galaxy and genome analysis pipelines The primary focus of the computational and comparative genomics course is the theory and practice of algorithms used in computational biology, with the goal of using current methods more effectively and evaluating new approaches. Students who wish to learn Perl programming for Bioinformatics are encouraged to apply to the Programming for Biology course. Students who would like in-depth training in the analysis of next-generation sequencing data (e.g., SNP calling and the detection of structural variants) should apply to the course on Advanced Sequencing Technologies & Applications. This Computational and Comparative Genomics course will discuss methods for phenotype prediction from variation data.

To apply to the course, fill out and send in the form at:

http://meetings.cshl.edu/course/-courseapp_instr.shtml William Pearson
<wrp@virginia.edu>

Keystone SouthDakota VertebrateEvolution Sep21-24

WORKSHOP: New Tools for Studying Phenotype Evolution in the Vertebrates

What new research opportunities are opened up by the power to compute over phenotype information from thousands of species of vertebrates, particularly when that information is combined with phenotype and expression information for thousands of genes in multiple model organisms? The Phenoscape project invites you to be among the pioneers in opening up this research.

The first release of the Phenoscape Knowledgebase at kb.phenoscape.org includes over 500K species phenotypes linked to 4,000+ genes from zebrafish, and is currently being extended to capture phenotype data from other vertebrates and linked to phenotype and expression data for other model organisms (including mouse and Xenopus).

We are looking for participants for a small, 3-day workshop, September 21-24, 2012 (to be held in Keystone, SD) who are interested in engaging in creative problem-solving directed at this outstanding problem and initiating collaborations. The ideal outcome would be several collaborative projects whose goals would drive the development of the Phenoscape tool set/interface and would present new and creative ways to deepen understanding of phenotypic evolution. Phenoscape aims to support the initial steps in these activities. We are particularly interested in a broad approach to this problem and welcome interest from scientists with backgrounds in computational and systems biology, mathematics, development, genomics, and evolution.

If you are interested, please contact Paula Mabee (pmabee@usd.edu) or Todd Vision (tjv@unc.edu).

“Mabee, Paula” <Paula.Mabee@usd.edu>

Keystone SouthDakota VertebrateEvolution Sep21-24 2

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If you are interested, please contact Paula Mabee (pmabee@usd.edu) or Todd Vision (tjv@unc.edu).

Paula.Mabee@usd.edu

Munich ProteinEvolution Jul27-29 2

We still have a few places left in our 2-day

Workshop on Protein Evolution in Munich from July 27th-29th. Further information can be found at <http://ieb.uni-muenster.de/protein-evolution-workshop-2012> and inquiries should be made to Dr. Sonja Grath s.grath@wwu.de.

“E. Bornberg” <ebb@uni-muenster.de>

Portugal TypingMicroorganisms Sep25-28

Training course in Oeiras (Portugal)

4 days, 28 hours, Course Fee Euro 320

SBTM12 - SEQUENCE-BASED TYPING METHODS
for MICROORGANISMS

with Keith Jolley, Nick Loman, João Carriço, Mario Ramirez, Nuno Faria and Teresa Conceição

IMPORTANT DATES for SBTM12 Deadline for applications: September 10th 2012 Notification of acceptance dates: EARLY: September 3rd 2012 (on special request, see Application) NORMAL: September 12th 2012 Course date: September 25th - September 28th 2012

Course Description Overview Technological advances in

DNA sequencing have led to the adoption of sequence-based typing methods as the standard techniques for bacterial identification at strain level, specially due to their portability and reproducibility. The widespread use of remotely accessible databases offering different typing data and the development of diverse data analysis techniques show the impact of Bioinformatics in this field, and the need for understanding how to operate with the databases and algorithms. Recently, the capability of sequencing whole bacterial genomes in a few days using Next Generation Sequencing (NGS) methodologies, opened a new door for the development of more sophisticated strain identification tools.

Objectives This training course is directed for the data analysis of sequence based typing methods, from the raw-data to the identification of a strain type by several typing methodologies, and the use of analysis algorithms to create groups of related strains. It will span from Single Locus Sequence Typing methods, such as spa typing or emm typing, to the now established MultiLocus Sequence Typing (MLST) and Multilocus Variable Number of Tandem Repeats Analysis (MLVA) methodologies. The course will also cover methods that apply to whole genome sequence data, and show how NGS data can be analyzed and made sense of, in this context. The course will be essentially hands-on. Short presentations will be interweaved by tutored assisted exercises. The participants are expected to gradually gain user independence by acquiring new analytical skills in using software and online databases for specific typing methods. Special attention will be given to methods that can use NGS datasets.

Target Audience This course is aimed to anyone working in molecular epidemiology, that wants to develop or consolidate skills in the use and analysis of sequence-based typing methods. The course will be illustrated with examples from different bacterial species, but the concepts are applicable to any species and to other sequence-based typing methods, not explicitly referred to in the course.

Course Pre-requisites Basic understanding of molecular biology, namely in microbial typing methodologies and elementary computer interaction skills are expected.

Further details, including application instructions available at <http://gtpb.igc.gulbenkian.pt/bicourses/-SBTM12> thank you for your interest

Pedro Fernandes

Pedro Fernandes <pfern@igc.gulbenkian.pt>

Wales EvolutionMedicine Ag14-17

Dear All,

We are pleased to announce an “Ecology Meets Medicine” retreat on the 14th to 17th of August 2012 at Gregynog Hall in Mid Wales, <http://www.wales.ac.uk/en/UniversityConferenceCentre/-GregynogHall.aspx> The retreat will centre around two key topics, “Evolution” - examining issues relating to drug resistance and parasite / pathogen virulence and “Co-infection” - examining the role of parasite-parasite interaction in driving infection dynamics. The retreat will bring together researchers to identify the current progress in these fields and to facilitate the formation of collaborative research teams to address the “big issues”. We also hope that the retreat will lead on to

review papers led by the participants.

Numbers are restricted to 40 delegates. If you would like to attend please contact Dr. Jo Lello, lelloj@cf.ac.uk with your name and affiliation, career stage, and a few lines explaining why you wish to attend and what your expertise is.

Costs are £215 for faculty member and £100 for fellows, post-docs and students. Costs are subsidised by the British Ecological Society and include accommodation and all meals.

The closing date for registration is the Sunday the 15th July 2012

We look forward to seeing you there.

Dr Joanne Lello School of Biosciences Cardiff University Biomedical Sciences Building Museum Avenue Cardiff CF10 3AX

Tel: 02920 875885

perkinss@Cardiff.ac.uk

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as 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 \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.