
E v o l D i r

March 1, 2011

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

Foreword

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

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

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



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Almada Portugal PrimateDiversity Sep14-17

âDiversity within Primatologyâ

IV CONGRESS OF THE EUROPEAN FEDERATION FOR PRIMATOLOGY

Invitation

You are cordially invited to attend the fourth congress of the European Federation for Primatology (EFP).

This congress will be hosted by the Portuguese Primatological Association (APP), at Almada, from 14th â 17th September 2011.

This meeting will coincide with the 3rd Iberian Primatological Conference, which gathers together the 5th

Portuguese and the 9th Spanish Primatological Conferences.

Diversity will be the main theme of the congress.

By diversity we mean diversity of research topics, diversity of approaches in primatology, diversity of species or diversity between individuals.

This conference aims to build strong scientific bridges between European primatologists facilitating the establishment of network contacts and hopefully engaging European scientists in co-operative research activities.

We are looking forward to see you in Almada!

Date

14th - 17th September 2011 (from Wednesday to Saturday).

The proposed format will allow congress participants to stay over the weekend for sight-seeing and social events.

Venue

The conference will take place in the library building that belongs to the Câmara Municipal de Almada (Almada, Portugal).

Almada is a small city located 15 minutes away from the South of Lisbon (across the bridge over Tagus River).

For more specific information regarding the access to Almada and Almada surroundings please see

<http://www.almadadigital.pt/portal/page/portal/-ACDV2> Conference official language

English is the conference language.

Abstracts for both oral and poster communications must be submitted in English and all presentations must be given in English.

More information will be provided soon!

For more informations, please go to: <http://apprimatologia.com/Actividades/-CEP2011.aspx> Maria Joana Ferreira da Silva <silvamaría.ju@hotmail.com>

Amsterdam InsectEvolution Oct2-5

Conference Announcement

The Sixth International Symposium on Molecular Insect Science October 2-5 2011 Amsterdam, The Netherlands

The Sixth International Symposium on Molecular Insect Science is the first of the series to be held outside of the USA. Previous Symposia, organized by the University of Arizona's Center for Insect Science, have been met with great enthusiasm.

By holding the Symposium in Amsterdam, in collaboration with Elsevier, it is hoped that the meeting will be even more accessible to scientists and their students in Europe, Asia, Australasia, and elsewhere. Abstracts are now being accepted in the following categories: < <http://www.molecularinsectscience.com/-submit-abstract.html> > Genomics and Proteomics Arthropod EvoDevo Neurobiology (Antagonistic and Symbiotic) Interactions Toxicology and Insecticide Resistance Immunity Endocrinology Chemical Ecology and Behaviour Pest Control Biotechnology Disease Models and Drug Discovery Submission deadline: April 8th 2011 To submit your abstract, or for more information, visit: www.molecularinsectscience.com < <http://www.molecularinsectscience.com/index.html> >

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Banff CanSocEcolEvol May12-15

The University of Calgary is pleased to host the 6th annual CSEE meeting from May 12-15 (<http://www.ecoevo.ca/banff2011>) in the beautiful mountain town of Banff, Alberta.

The meeting will be held in the Banff Centre, a globally respected conference facility (<http://www.banffcentre.ca>).

Talks and plenary sessions will feature over 40 invited speakers representing leaders as well as rising stars in the fields of ecology and evolution from over 30 institutions across Canada and internationally. Special symposia themes include systematics and biodiversity, mountain ecology, pollinator biodiversity and pollination services, the genetics of evolution and species isolation, population ecology, and paleobiodiversity. Submissions for contributed talks and posters in all areas of ecology and evolution are welcome. Titles and abstracts for oral presentations and posters can be submitted using the registration links below.

The Canadian Institute of Ecology and Evolution (CIEE) will be hosting three one-day workshops on May 16th for a nominal fee. The workshops (and instructors) include:

- 1) Mathematical Modeling in Ecology and Evolution (Dr. Sarah P. Otto)
- 2) Statistics in R (Dr. Dolph Schluter)
- 3) Phylogenetics in R (Dr. Luke Harmon)

Additionally, there will be a symposium for women entering ecology and evolution today (SWEEET). SWEEET is a symposium intended to address issues that influence the advancement of women from post-graduate degrees into academic, government, and industry positions in Ecology and Evolution.

Optional organized field trips include a visit to the

beautiful Kananaskis valley, “Benn’s Big Game Hike” in Banff, and a fossil field trip.

REGISTRATION REMINDER: If you plan to attend the CSEE meeting this year in Banff and have not yet registered, please register soon at: <http://www.ecoevo.ca/banff2011> MEMBERSHIP RENEWAL: If you haven’t already done so, please renew your membership at <http://www.ecoevo.ca/en/-index.htm> (or you can renew when you pay for the meeting).

The registration deadline for eligible student members interested in receiving one of the 30 travel grants sponsored by the CSEE is FEBRUARY 24.

The deadline for registration at a reduced fee for the 2011 meeting is next week (March 1).

We are looking forward to hosting you in Banff!

Local Organizing Committee: Sean Rogers, Jeff Hutchings, Brian Kopach, Leanna Lachowsky, Heather Proctor, Mary Reid, Kathreen Ruckstuhl, Jessica Theodor, Jana Vamosi

Sean M. Rogers Alberta Ingenuity New Faculty Assistant Professor Department of Biological Sciences University of Calgary 2500 University Drive N.W. Calgary, AB, Canada T2N 1N4 Office Phone: 403-210-8573 Lab Phone: 403-220-7907 Fax (403) 289-9311 www.ucalgary.ca/~srogers srogers@ucalgary.ca

CollegeNewEngland EvolutionaryGenomics Jul10-15

Plan to attend the Gordon Conference on Ecological and Evolutionary Genomics! Date: July 10-15, 2011 GRC Location: College of New England, Biddeford Maine

The 2011 Gordon Conference on Evolutionary & Ecological Genomics will present cutting-edge research on using genomics approaches to study adaptation of organisms to changing environments, genome evolution and population genetics, as well as the evolution of complex phenotypes. In particular, several of the talks this year will highlight evidence for evolution at the molecular and phenotypic levels in response to climate change. A diversity of sessions will highlight recent results from natural as well as experimental populations, and will cover both non-model and model species. There will be an exciting balance between ecologists using genomics

to study adaptation in rapidly evolving systems, as well as genomicists using large-scale sequence, expression and functional assays to study variation among populations and species.

The conveners Loretta Johnson (Kansas State University) and Gretchen Hofmann (UC Santa Barbara) are committed to assembling a diverse conference with a mix of high profile established scientists and as well as post-docs and grad students early in their professional careers. We plan to select some submitted abstracts for invited talks. We are actively applying for funds to allow graduate students and others to attend. Although attendance at Gordon conferences is by application, we intend to admit as many as we can on a first-come-first serve basis. The collegial atmosphere of this Conference, with discussion sessions as well as opportunities for informal gatherings in the afternoons and evenings, provides an avenue for scientists from different disciplines to brainstorm and promotes cross-disciplinary collaborations. We hope to see you there, at the College of New England!

More information and application and registration information can be found at the Gordon Conference web site <http://www.grc.org> Confirmed speakers include:

PLENARY SPEAKER: Thomas Mitchell-Olds: Advances in the emerging field of ecological and evolutionary genomics

GENOMICS OF RAPID EVOLUTIONARY CHANGE

Bill Bradshaw (rapid evolution and genetic changes in timing of life history traits in the pitcher plant mosquito),

Ary Hoffmann (molecular and genomic evolution of thermal clines in *Drosophila*)

Mike Lynch (mechanisms of evolution at the genomic and phenotypic levels, origins of gene-structural complexity)

GENETIC ARCHITECTURE OF LOCAL ADAPTATION IN HETEROGENOUS ENVIRONMENTS

David Lowry (local adaptation in *Mimulus* in response to salt and drought),

Luciano Matzkin (host adaptation in cactophilic *Drosophila*),

Cynthia Weinig (Molecular evolutionary ecology of plant adaptation to heterogeneous settings)

Mark Ungerer (evolutionary genomics of transposable elements in sunflower)

GENOMIC RESPONSES TO STRESS

Dick Roelofs (adaptive variation in response to metals in spring tails)

Ana Caicedo (evolutionary genomics of weedy rice, adaptive variation in wild tomatoes in response to environmental stresses)

MOLECULAR EVOLUTION AND GENOMICS OF SPECIES INTERACTIONS

Jack Werren (Wolbachia genome evolution, host-Wolbachia interactions)

May Berenbaum (ecological genomics of host-plant interactions, genomic ecology of global climate on plant-insect interactions)

Ralf Sommer (genetic studies of species interactions and the ecology of *Pristionchus* nematodes)

Mike Herman (ecological genomics of nematode-bacterial interactions)

GENETIC BASIS OF ADAPTIVE VARIATION

Jim Marden (functional genomics of dispersal and female fecundity in *Melitaea cinxia* butterfly metapopulations,

Hopi Hoekstra (adaptive variation in pigmentation in mice)

PHENOTYPIC PLASTICITY and GENOTYPE x ENVIRONMENT INTERACTIONS

Puni Jeyasingh (Genes and ecological stoichiometry, eutrophication and microevolutionary change in *Daphnia*.

Louis Bernatchez (population and quantitative genetics, functional genomics, fish populations of conservation concern)

–

â Loretta Johnson â Associate Professor â Co-Director Ecological Genomics Institute â <http://ecogen.ksu.edu/> â Division of Biology â Kansas State University â Manhattan KS 66506-4901 â Office: 785-532-6921 â www.ksu.edu/johnsonlab

johnson@k-state.edu

Edinburgh EvolTransposableElements Apr1 2

Meeting on Transposable Elements, Edinburgh, April 2011

A one-day meeting on “Transposable elements: their functional and evolutionary biology” will be held at Surgeons’ Hall, Edinburgh, UK on April, 1, 2011. This is the annual Spring Meeting of the Genetics Society of the UK, and details of meeting arrangements and registration can be found on the Genetics Society website (<http://www.genetics.org.uk/>). Please register by March 17.

Laurence Hurst will give the Genetics Society Medal Lecture for 2010 at this meeting. Other speakers are Mark Batzer, Casey Bergman, Tom Bureau, Hugo Dooner, Tom Eickbush, Adam Eyre-Walker, and Zsuzsanna Izsvak.

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

Edinburgh Immunology Evolution Jun30

Dear all,

We are pleased to invite you to the postponed Centre for Immunity, Infection and Evolution (CIIE) one-day symposium on ‘Wild Immunology’ in Edinburgh on Thursday, June 30th. We have a great list of diverse speakers and it should be an exciting day.

The aim of the symposium is to bring together researchers from diverse disciplines to address a central question in infectious disease biology and immunology: Why should we try to understand infection and immunity in wild systems? Specifically, how does the immune response operate in the wild and how does multiple co-infection and commensalism impact the immune response and host health in natural systems?

We have a broad programme of speakers, ranging from laboratory immunologists to infectious disease ecologists, working on wild birds, wild and laboratory rodents, or wild sheep, and studying questions that range from the dynamics of co-infection, to how commensal organisms affect parasites and immune development. Our goal is to bring speakers of various expertise together to try and find meaningful ways to bring immunological tools to the study of wild populations.

Speakers: â Judi Allen (University of Edinburgh) â Jan Bradley (University of Nottingham) â Mark Viney (University of Bristol) â Jim Kauffman (Cambridge University) â Andrea Graham (Princeton University) â Steve Paterson (University of Liverpool) â Ken Smith (Cambridge University) â Richard Grenis (University

of Manchester) à Kathy McCoy (Bern University) à Peter Turnbaugh (Harvard University):

If you'd like to attend, you need to register using the online registration form on the website <http://ciie.bio.ed.ac.uk/>. There's a registration fee of £10. Lunch will be provided for all registered attendees.

You can contact the organisers by e-mailing ciie@ed.ac.uk

We look forward to welcoming you on 30th June.

Cheers, Amy Pedersen & Simon Babayan

Amy B. Pedersen, Advanced Fellow Centre for Immunity, Infection and Evolution

Institutes of Infection, Immunology Research and Evolutionary Biology 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/> Amy Pedersen
<amy.pedersen@ed.ac.uk>

Estonia Temperature Adaptation Apr28-30

REGISTRATION DEADLINE APPROACHING:

Science meeting

“Evolutionary and plastic responses of animal growth to different temperatures: adaptations and constraints” will be held in Tartu, Estonia from April 28 to April 30, 2011. The meeting is organized by the European Science Foundation research networking programme “Thermal adaptation in ectotherms: Linking life history, physiology, behaviour and genetics”.

Support for students/junior scientists is available.

For further information and registration, see

<http://www.ut.ee/~tiited/thermadapt/> SUMMARY: The symposium aims to bring together evolutionary ecologists and physiologists working on temperature-driven a) plastic and b) evolutionary changes in 1) growth rates and 2) body sizes of various (invertebrate and vertebrate) ectothermic animals. Responses to temperature is a topic in which the interplay of different evolutionary forces (primarily, selection and con-

straints) is particularly obvious. Interdisciplinary efforts in this field are therefore likely to contribute substantially to an improved and more integrated understanding of evolutionary processes. Furthermore, clarifying conceptual and terminological problems would serve the needs of both theoretical and applied research on thermal adaptation, and beyond.

Toomas Tammaru professor of zoology <http://www.ut.ee/~tammarut> Toomas Tammaru
<tammarut@ut.ee>

GhentU Plant Comparative Genomics Apr11-12

Dear,

the first international Conference on *Comparative and Regulatory Genomics in Plants* will be held at VIB - Ghent University (Belgium), 11-12 April 2011.

This conference will give an overview of the most recent developments in plant genomics and will discuss the integration of experimental high-throughput data with computational approaches. Topics include plant next-gen genome sequencing, genome evolution, comparative transcriptomics, systems biology, ChIP profiling and plant regulatory networks.

Contribute? *Abstract submission deadline for contributed talks is February 28th.*

Titles invited speakers:

* Georg Haberer - The *Oryza glaberrima* Genome: Comparative Studies in the Genus *Oryza*. MIPS, Germany * Pat Heslop-Harrison - Diversity, evolution and the banana genome in a comparative context. University of Leicester, UK * Beat Keller - Patching gaps in plant genomes results in gene movement and erosion of colinearity. University of Zürich, Switzerland * Stefan Rensing - Genome-wide phylogenetic comparative analysis of plant transcriptional regulation: a timeline of loss, gain, expansion, and correlation with complexity. Freiburg University, Germany * Nathaniel Street - A cross-species transcriptomics approach to identify genes involved in leaf development. Umea University, Sweden * Staffan Persson - A systems biology approach to cellulose production in higher plants. MPI Potsdam, Germany * Erich Grotewold - Gene-specific and genome-wide ChIP approaches to study plant transcriptional networks. Ohio State University, USA

For more details, check the Conference and Workshop website here < http://bioinformatics.psb.ugent.be/-crg_event/ >.

Best regards,
the scientific committee,

Klaas Vandepoele Yves Van de Peer Rony Swennen
Lieven De Veylder Dirk Inzé

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sity Technologiepark 927, 9052 Gent, Belgium E-mail:
Klaas.Vandepoele@psb.vib-ugent.be Website: [http://-](http://bioinformatics.psb.ugent.be/)
bioinformatics.psb.ugent.be/ Conference& Workshop

Comparative& Regulatory Genomics in Plants

Website:[http://bioinformatics.psb.ugent.be/-](http://bioinformatics.psb.ugent.be/-crg_event/)
[crg_event/](http://bioinformatics.psb.ugent.be/-crg_event/) Klaas Vandepoele
<klaas.vandepoele@psb.vib-ugent.be>

Houston CamelConservation Sep16-18

Second International Conference on Camelid Genetics and Reproductive Technology is being organized by Alpaca Registry, Inc. and the Alpaca Research Foundation. It will be held in Houston, Texas, on September 16-18, 2011. Geneticists and reproductive scientists from around the world including the Middle East, Europe, Australia, South America, and North America will convene in Houston to exchange information on the latest developments in their fields. The conference will be open to alpaca breeders, veterinarians, scientists, and all those interested in genetic improvement. Registration will be limited to 200 on a first come first served basis. State of the Art Lectures targeted at all attendees will be delivered in the morning. The afternoons will be devoted to concurrent breeder and scientist break-out sessions. Poster sessions will also be held where attendees can speak personally with the presenters. Topics to be covered include: Color Genetics, Suri Genetics, Genetics of Infertility, Candidate Genes for Choanal Atresia, Alpaca Genome Mapping, Chromosome Mapping, Genetics of viruses affecting camelids such as Corona virus and BVDV, Embryo Transfer (ET), Artificial Insemination (AI), Cost, benefits, and risks of assisted reproduction, Role of the ARI EPD program in genetic improvement, Mechanisms of induction of ovulation, and Infertility. Visit www.camelidconference.com to view the latest informa-

tion and to register.
warjohns@mail.nih.gov

Irapuato Mexico GenomicsBiodiversity Jul23-25

The 2011 Symposium of the American Genetic Association, to be held from July 23-25 in Irapuato and Guanajuato, Mexico, is devoted to the theme of genomics and biodiversity. The 2011 meeting marks the first time in the AGA's 100+ years history that it has met in Mexico.

This year's theme recognizes the remarkable new Laboratorio Nacional Genomica para la Biodiversidad (LANGEBIO), the National Laboratory of Genomics for Biodiversity, located in Irapuato, Guanajuato, Mexico. The Laboratory's mission is "to bring together interdisciplinary groups to carry out cutting-edge research and to generate genetic knowledge about Mexican biodiversity." The meeting also recognizes that Mexico is ranked 5th in the world in terms of biodiversity, leading all other countries in, for example, the number of reptiles, pines and cacti. What better place to celebrate the role of genomics in generating knowledge of biodiversity than the National Laboratory of Genomics?

The meeting will bring together top scientists from around the world, with particular emphasis on scientists from Mexico, to showcase research highlights of genomics and biodiversity. The talks will span the biota, from microbes to humans, and will combine cutting-edge genomics of model systems with the first generation of genomics studies on non-model systems.

The meeting opens July 23 with a day-long symposium at LANGEBIO where attendees can meet LANGEBIO scientists and see their remarkable research facility. The talks on July 24th and 25th (half day) will be held in the wondrous Spanish colonial town of Guanajuato (about 40 km from Irapuato), a World Heritage site with ample accommodation and restaurants. Attendees can fly into Leon (about three hours north of Mexico City by car) and stay in Guanajuato. The meeting will end with a banquet at the historic Mision Guanajuato on the evening of the 25th and a day-long field trip on the 26th to survey biodiversity in the area and the equally stunning city of San Miguel de Allende. We hope to see you there!

Watch the AGA website – more details coming soon.

Scott V Edwards, President American Genetic Association

agajoh@oregonstate.edu

KansasCity ArthropodGenomics Jun9-12

Arthropod Genomics 2011: Exploring Diversity, Relating Similarity 5th ANNUAL ARTHROPOD GENOMICS SYMPOSIUM June 9-12, 2011, in Kansas City, USA <http://www.k-state.edu/agc/-symposium.shtml>

Please save the dates and plan to attend the 5th Annual Arthropod Genomics Symposium, Exploring Diversity, Relating Similarity, June 9 to 12, 2011, in Kansas City at the Marriott hotel on the beautiful Country Club Plaza. Registration will open in January.

KEYNOTE SPEAKER: Marc A.T. Muskavitch DeLuca Professor of Biology Boston College Advancing vector genetics through the power of vector genomics

FEATURED SPEAKERS: Gregor Bucher Department of Developmental Biology Georg-August University, Göttingen, Germany Beetle: Genome wide RNAi screen for embryonic and metamorphic development in *Tribolium*

Owain Edwards Invertebrate Genomics and Evolution CSIRO Ecosystem Sciences Perth, Australia DNA methylation and phenotypic plasticity in the pea aphid, *Acyrtosiphon pisum*

Cassandra Extavour Dept of Organismic and Evolutionary Biology Harvard University Overcoming the gene discovery bottleneck for arthropod evo-devo: Creating de novo developmental transcriptomes

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

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

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

Pedro L. Oliveira Instituto de Bioquímica MÃ©dica

Programa de Biologia Molecular e Biotecnologia Universidade Federal do Rio de Janeiro and Instituto Nacional de CiÃancia e Tecnologia em Entomologia Molecular Rio de Janeiro, Brazil An insight into the transcriptome of the digestive tract of the blood sucking bug, *Rhodnius prolixus*

Michael Pfrender Biological Sciences University of Notre Dame Genome structure, functional diversification, and Genome X environment interactions in *Daphnia*

Dorith Rotenberg Plant Pathology Kansas State University A genomics-based approach to identify insect molecular components associated with vector competency in *Frankliniella occidentalis*, the primary thrips vector of Tomato spotted wilt virus

HervÃ© Seitz Laboratoire de Biologie MolÃ©culaire Eucaryote – CNRS/UniversitÃ© Paul-Sabatier Toulouse, France Genomics of small RNAs in insects

Alexandra C. Wilson Department of Biology University of Miami Genomic insights into nitrogen upgrading and recycling in the aphid [*Buchnera*] symbiosis

Guojie Zhang Beijing Genome Institute Shenzhen, China BGI's recent activity on insect genomic research

WORKSHOPS A pre-symposium workshop, Genome Project 101, by Scott Cain, OICR, and Dave Clements, Emory University; Thursday afternoon, June 9, 4:00-6:00 p.m.

Comparative genomics with the generic synteny browser (GBrowse_syn): Configuration and display of various co-linearity data types, by Sheldon McKay, iPlant, will be presented Saturday morning, June 11.

ORGANISM MEETINGS Friday afternoon/evening, June 10 Meet with scientists who are also working with your organism of interest during small group gatherings. If you are interested in coordinating topics and leading discussions as a group leader, please e-mail dmerrill@ksu.edu. Additional information will be posted to the conference website as details are finalized.

POSTER SESSIONS: There will be two poster sessions. A few platform presentations will be chosen from submitted poster abstracts. The deadline for submission of poster abstracts is May 18.

TENTATIVE SYMPOSIUM PROGRAM Thursday afternoon, June 9 Pre-Symposium Workshop Thursday evening, June 9 Keynote presentation and welcome reception Friday & Saturday, June 10 and 11 - Platform and Poster sessions Friday afternoon/evening, June 10 Organism meetings Saturday morning GBrowse_syn Workshop Sunday morning, June 12 Roundtable dis-

cussion focusing on I5k with Kevin J. Hackett, USDA, and the ArthropodBase Consortium. All are invited to attend!

Noon, Sunday, June 12 - Activities will conclude.

ROUNDTABLE DISCUSSION: Participate in a roundtable discussion with the ArthropodBase Consortium regarding the generation of integrated arthropod genome databases and tools for genome projects. Discussion will focus on I5k, led by Kevin J. Hackett, USDA. Symposium attendees are encouraged to attend.

PRE-CONFERENCE MEETINGS: -International Tribolium Meeting, 6/8 and 6/9. -International Aphid Genomics Consortium, 6/9.

REGISTRATION: Registration will be open in January. Monitor our website, www.k-state.edu/agc/-symposium.shtml and watch for the next announcement.

— / —

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>

KansasCity ArthropodGenomics Jun9-12 RegistrationOpen

REGISTRATION IS NOW OPEN to attend Arthropod Genomics 2011: Exploring Diversity, Relating Similarity 5th ANNUAL ARTHROPOD GENOMICS SYMPOSIUM June 9 & 12, 2011, in Kansas City, USA <http://www.k-state.edu/agc/symp2011>

Deadline to Register at Early-Bird Rates: Wednesday, March 30, 2011

Other important deadlines: *Poster Abstract Submissions: Wednesday, May 18 *Hotel Reservations: Wednesday, May 18, or until room block is filled

Please plan to attend the 5th Annual Arthropod Genomics Symposium, Exploring Diversity, Relating Similarity, June 9 to 12, 2011, in Kansas City at the Marriott hotel on the beautiful Country Club Plaza. A complete brochure is available at:

<http://www.k-state.edu/agc/symp2011/images/-Brochure-2011.pdf>

REGISTRATION is now open. (Access <http://www.k-state.edu/agc/symp2011/register.html> to

register online.)

VENUE: The symposium will take place at the Kansas City Marriott on the beautiful Country Club Plaza.

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WORKSHOPS June 9: A pre-symposium workshop, Genome Project 101, by Scott Cain, OICR, and Dave Clements, Emory University; Thursday afternoon, June 9, 4:00-6:00 p.m.

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Pedro L. Oliveira Instituto de Bioquímica Médica Programa de Biologia Molecular e Biotecnologia Universidade Federal do Rio de Janeiro and Instituto Nacional de Ciência e Tecnologia em Entomologia Molecular Rio de Janeiro, Brazil An insight into the transcriptome of the digestive tract of the blood sucking bug, Rhodnius prolixus

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Notre Dame âGenome structure, functional diversification, and Genome X environment interactions in *Daphnia*â

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Guojie Zhang Beijing Genome Institute Shenzhen, China âBGIâs recent activity on insect genomic researchâ

ORGANISM MEETINGS Friday afternoon/evening, June 10 Meet with scientists who are also working with your organism of interest during small group gatherings.Â If you are interested in coordinating topics and leading discussions as a group leader, please e-mail dmerrill@ksu.edu .Â Additional information will be posted to the conference website as details are finalized.

POSTER SESSIONS: There will be two poster sessions.Â A few platform presentations will be chosen from submitted poster abstracts.Â

TENTATIVE SYMPOSIUM PROGRAM ÂÂ Thursday afternoon, June 9 â Pre-Symposium Workshop ÂÂ Thursday evening, June 9 â Keynote presentation and welcome reception ÂÂ Friday & Saturday, June 10 and 11 - Platform and Poster sessions

— / —

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>

KualaLumpur DNA Barcoding Jun14-17 DeadlineExtended

CALL FOR ABSTRACTS DNA Barcoding of Pacific Invasive and Pest Species 22nd Pacific Science Congress 14-17 June 2011: Kuala Lumpur, Malaysia

DEADLINE FOR SUBMISSION: EXTENDED TO 1 MARCH 2011

Researchers, institutional officials, and students are invited to submit abstracts for oral and/or poster presentations concerning DNA barcoding for the identification and control of invasive and pest species in the Pacific region.

“DNA barcoding” is a technique proposed by Dr. Paul Hebert (Univ. of Guelph, Canada) in 2003 for identifying species using a short standardized gene sequence. Since making this proposal, barcodes have been determined for more than 1 million specimens from approximately 100,000 species. Barcoding is becoming a widely used tool for:

* Basic taxonomy, * Identifying species in ecological studies and biodiversity monitoring; and * Identifying species of concern to government regulators and others, such as: o Agricultural pests and invasive species, o Endangered and protected species, and o Disease vectors.

iBOL, the International Barcode of Life project, and QBOL, the Quarantine Barcode of Life project) are building DNA barcode reference libraries of invasive and pest species. CBOL, the Consortium for the Barcode of Life, is promoting partnerships and support for the use of DNA barcoding to these and similar problems. This full-day symposium/workshop has three goals:

1. Disseminate information on DNA barcoding and the International Barcode of Life Project;
2. Provide an opportunity for local and international initiatives on the identification and control of invasive species to share information (e.g., QBOL, IPPC); and
3. Identify opportunities and priorities for DNA barcoding activities on invasives in the Pacific.

Guidelines for Submission of Abstracts

All abstracts must be submitted through an online form available at <http://www.dnabarcodes2011.org/-barcodeAbstract.php> . Abstracts can be submitted for:

* Longer oral presentation (15-20 minutes) on major initiatives by regions, countries, networks or other associations to improve scientific collections in the Pacific and their access and use; * Short “lightning presentation” (5 minutes) on specific initiatives to improve collections in an institutions; and/or * Presentations for poster display.

Please be sure to designate the type of presentation you would like to make on the submission form. Abstracts not accepted for oral presentation will automatically be considered for presentation as posters. If you want your abstract considered only for oral presentation and

do not want to be considered for poster presentation, please select "Oral presentation only" under Preference on the submission form.

Review and Selection of Abstracts

All abstracts will be reviewed by a Steering Committee for the relevance and quality of their scientific content. Authors will be notified if their abstract has been accepted by 1 April 2011.

Preparation and Submission of Abstracts

Abstracts should be written in English using the online form (<http://www.dnabarcodes2011.org/-barcodeAbstract.php>). The text you submit will be used by the Technical Program Committee to review your abstract. Some formatting (bold, italics, underlining) will be lost. If your abstract is accepted you will be asked to upload a Word file with the abstract exactly as you would like it to appear in the Conference Program.

We look forward to receiving your abstract and to seeing you at the Pacific Science Congress in Kuala Lumpur in June!

Dr. David Schindel, Consortium for the Barcode of Life
Email: schindeld@si.edu

"Schindel, David" <schindeld@si.edu>

Kyoto SMBE Jul27-30 CallSymposia

February 1st, 2011

Call for symposia and workshops to be held in SMBE 2011 Kyoto

Dear SMBE members, we would like you to submit application for symposia and workshops to be held in SMBE 2011 Kyoto. Please visit its website [<http://SMBE2011.lab.nig.ac.jp>] for detailed information on this conference.

There are seven time slots for symposia and workshops as follows.

Wednesday, July 27th, 2011 27-M: <Morning Session> 9:30-12:00 27-A: <Afternoon Session> 13:30-16:00 27-E: <Evening Session> 16:30-19:00

Thursday, July 28th, 2011 28-M: <Morning Session> 9:30-12:00 28-A: <Afternoon Session> 13:30-16:00 28-E: <Evening Session> 16:30-19:00

Friday, July 30th, 2011 30-M: <Morning Session> 9:30-

12:00

There are two places inside Kyoto University Campus for SMBE 2011 Kyoto Conference. One is Centennial Clock Tower Hall (designated as "C"), and the other is Shiran Kaikan (designated as "S"). It takes about 8-minute walk to go from one place to the other. Available rooms are as follows. This list applies to all time slots.

For Symposia: C-1: Centennial Clock Tower Hall First Floor, Main Auditorium (max. 500 persons) S-1: Shiran Kaikan Inamori Hall (max. 220 persons) S-2: Shiran Kaikan Yamanouchi Hall (max. 190 persons)

For Workshops: C-3: Centennial Clock Tower Hall Second Floor Seminar Room 1 (max. 50 persons) C-4: Centennial Clock Tower Hall Second Floor Seminar Room 2 (max. 50 persons) S-3: Shiran Kaikan Annex Seminar Room 1 (max. 90 persons) S-4: Shiran Kaikan Annex Seminar Room 2 (max. 90 persons)

Therefore, in total, we can have up to 21 symposium sessions and 28 workshop sessions.

<Symposium application> Proposed Symposium title: Proposer's name(s) and affiliation(s): Brief explanation (~200 words): Proposed Time slot (such as 27-M): If you plan a symposium longer than one time slot, please indicate such as 27-A&E. Proposed Room to be used (such as C-1): Expected list of speakers (name and affiliation): Possible financial support: SMBE 2011 Organizing Committee may be able to support travel fee for up to one speaker only. Other speakers should be supported by themselves or other supports. Oral presentation submitters may also be included as non-invited speakers, if their contents are appropriate.

<Workshop application> Proposed Workshop title: Proposer's name(s) and affiliation(s): Brief explanation (~200 words): Proposed Time slot (such as 30-M): If you plan a workshop longer than one time slot, please indicate such as 28-M&A. Proposed Room to be used (such as C-3): Expected list of speakers (name and affiliation): Possible financial support: SMBE 2011 Organizing Committee will not support travel fee for any speaker. All invited speakers should be supported by themselves or other supports. Oral presentation submitters may also be included as non-invited speakers, if their contents are appropriate.

Deadline of application: Monday, February 28th, 2011
Submit to: SMBE2011@lab.nig.ac.jp

SMBE 2011 Kyoto Global Organization Committee
SMBE 2011 Kyoto Domestic Organization Committee

Saitou Naruya Professor, Division of Population Genetics, National Institute of Genetics Professor (con-

current), Department of Genetics, Graduate University for Advanced Studies Professor (concurrent), Department of Biological Sciences, University of Tokyo

Postal mail: Mishima, 411-8540, Japan
 Email: nsaitou@genes.nig.ac.jp Phone/FAX:
 +81-55-981-6790/-6789 Web Home Page:
 sayer.lab.nig.ac.jp/~saitou/index-j.html

Saitou Naruya <nsaitou@genes.nig.ac.jp>

London EcolMarcoevolution Mar9

We warmly invite you to a CEE Symposium on “Integrating Ecology into Macroevolutionary Research” to be held at the Zoological Society of London meeting rooms on 9th March (9am - 6pm).

Our updated schedule of speakers includes: Luke Harmon

University of Idaho

New Frontiers for the Comparative Analysis of Adaptive Radiations

Gavin Thomas

Bristol University

Can models of trait evolution tell us anything about the evolutionary process?

Sam Turvey

Zoological Society London

What can the recent fossil record actually tell us about past and present human-caused extinction?

James Rosindell

Leeds University

Neutral theory and macroevolution

Lynsey McInnes

Imperial College

Evolution and ecology of the species:area relationship in mammals

Bill Baker

Kew Gardens, London

Museum model diversification of palms in the earliest tropical rain forests

Anjali Goswami

University College London

Convergence, competition, and constraints: case studies in carnivore evolution

Andy Purvis

Imperial College

Species ecology and macroevolutionary dynamics of Cenozoic planktonic foraminifera

Helene Morlon

CNRS, Paris

Reconciling molecular phylogenies with the fossil record

Kanchon Dasmahapatra

University College London

Phylogenetic and mimetic relationships in Neotropical butterflies

Tim Barraclough

Imperial College

Are there evolutionarily significant units of diversity above the level of species?

We have one poster slot left, available on a first come first serve basis. Please email us to reserve the slot. To register for the symposium and to receive further updates on the schedule for the day please email lynsey.mcinnnes01@imperial.ac.uk. Attendance will cost £5.00, payable on the day, to cover refreshments.

Best wishes, Lynsey McInnes & Ally Phillimore

Lynsey McInnes PhD Student Imperial College London
 Silwood Park Campus

<http://www.bio.ic.ac.uk/research/apurvis/-lynsey.htm>
<http://www.justgiving.com/-offset-silwood-carbon> ”McInnes, Lynsey“
 <lynsey.mcinnnes01@imperial.ac.uk>

London Macroevolutionary Research Mar9

We warmly invite you to a CEE Symposium on “Integrating Ecology into Macroevolutionary Research” to be held at the Zoological Society of London meeting rooms on 9th March (9am - 6pm).

Talks will include:

Luke Harmon (University of Idaho) New frontiers for

the comparative analysis of adaptive radiations

Gavin Thomas (Bristol University) Can models of trait evolution tell us anything about the evolutionary process?

Sam Turvey (ZSL) What can the recent fossil record actually tell us about past and present human-caused extinction?

James Rosindell (Leeds University) The macroevolutionary predictions of ecological neutral theory

Lynsey McInnes (Imperial College) Evolution and ecology of the species:area relationship in mammals

Anjali Goswami (University College London) TBA

Andy Purvis (Imperial College) Species ecology and macroevolutionary dynamics of Cenozoic planktonic foraminifera

Hélène Morlon (CNRS, Paris) Modelling diversity dynamics using time backwards

Kanchon Dasmahapatra (University College London) Phylogenetic and mimetic relationships in Neotropical butterflies

Tim Barraclough (Imperial College) Are there evolutionarily significant units of diversity above the level of species?

We will have eight poster slots available on a first come first serve basis. Please email us to reserve a slot.

To register for the symposium and to receive further updates on the schedule for the day please email lynsey.mcinnes01@imperial.ac.uk.

Attendance will cost £5.00, payable on the day, to cover refreshments.

Best wishes,

Lynsey McInnes & Ally Phillimore

“McInnes, Lynsey” <lynsey.mcinnes01@imperial.ac.uk>

Lunteren Netherlands Galaxy Community May25-26

2011 Galaxy Community Conference May 25-26 Lunteren, The Netherlands May 25-26 in Lunteren, The Netherlands

We are pleased to announce the 2011 Galaxy Community Conference, being held May 25-26 in Lun-

teren, The Netherlands. The meeting will feature two full days of presentations and discussion on extending Galaxy to use new tools and data sources, deploying Galaxy at your organization, and best practices for using Galaxy to further your own and your community's research. See <http://galaxy.psu.edu/gcc2011/> for complete details.

ABOUT GALAXY: Galaxy is an open, web-based platform for accessible, reproducible, and transparent computational biomedical research.

- Accessibility: Galaxy enables users without programming experience to easily specify parameters and run tools and workflows. - Reproducibility: Galaxy captures all information necessary so that any user can repeat and understand a complete computational analysis. - Transparency: Galaxy enables users to share and publish analyses via the web and create Pages-interactive, web-based documents that describe a complete analysis.

Galaxy is open source for all organizations. The public Galaxy service (<http://usegalaxy.org>) makes analysis tools, genomic data, tutorial demonstrations, persistent workspaces, and publication services available to any scientist that has access to the Internet. Local Galaxy servers can be set up by downloading the Galaxy application and customizing it to meet particular needs.

CONFERENCE OVERVIEW: This event aims to engage a broader community of developers, data producers, tool creators, and core facility and other research hub staff to become an active part of the Galaxy community. We'll cover defining resources in the Galaxy framework, increasing their visibility and making them easier to use and integrate with other resources, how to extend Galaxy to use custom data sources and custom tools, and best practices for using Galaxy in your organization.

Additional topics include, but are not limited to: * Talks submitted by the Galaxy community * Integration of tools (including NGS analysis tools) and distributed job management * Deployment of Galaxy instances on local resources and on the Cloud * Management of large datasets with the Galaxy Library System * Using the Galaxy LIMS functionality at NGS sequencing facilities * Visualizing Data without leaving Galaxy * Performing reproducible research * Performing and sharing complex analyses with Workflows * An “Introduction to Galaxy” session, offered on May 24, for Galaxy newcomers.

REGISTRATION: The conference fee is euro 100 on or before April 24, and euro 120 after that. The meeting is being held at the Conference Centre De

Werelt in Lunteren, The Netherlands, which is also the conference hotel. You are encouraged to register early, as space at the hotel (and at the “Intro to Galaxy” session) is limited and is likely to fill up before the conference itself does. See <http://galaxy.psu.edu/gcc2011/Register.html> ABSTRACT SUBMISSION: Abstracts are now being accepted for short oral presentations. Proposals on any topic of interest to the Galaxy community are welcome and encouraged. The abstract submission deadline is the end of February 28. See <http://galaxy.psu.edu/gcc2011/Abstracts.html> SPONSORS: The 2011 Galaxy Community Conference is co-sponsored by the US National Science Foundation (NSF, <http://www.nsf.gov/>), and the Netherlands Bioinformatics Centre (NBIC, <http://www.nbic.nl/>). NBIC is a collaborative institute of the bioinformatics groups in the Netherlands. Together, these groups perform cutting-edge research, develop novel tools and support platforms, create an e-science infrastructure and educate the next generations of bioinformaticians.

We are looking forward to a great conference and hope to see you in the Netherlands!

The Galaxy and NBIC Teams

– <http://galaxy.psu.edu/gcc2011/> <http://getgalaxy.org>
<http://usegalaxy.org/> clementsgalaxy@gmail.com
 clementsgalaxy@gmail.com

Montpellier EvolutionaryRescue Jun7

Dear all,

An international conference on “Evolutionary rescue” will be held in Montpellier, June 7th 2011, Grand Amphithéâtre du CNRS, France.

Programme and registration on <http://www.evorescu.univ-montp2.fr/> While global change might be causing the 6th major extinction crisis on Earth, we know very little about how evolutionary responses may modulate the response of biodiversity to these changes. Can we make general predictions about situations where evolutionary responses are most likely to occur and to mitigate or aggravate the demographic response of species to global change? Can we identify target species or groups of species for which incorporating evolutionary responses in ecological forecasts is most needed?

The aim of this conference is to synthesize recent ad-

vances improving our understanding of the role of evolutionary mechanisms in species responses to global change and of how these mechanisms may affect biodiversity patterns.

Four topics will be discussed: 1) The race between decline and adaptation 2) The interplay between migration, adaptation and plasticity 3) Evolving communities in changing environments 4) From microevolutionary to macroevolutionary patterns and back

For more information on the programme and registration, see the website <http://www.evorescu.univ-montp2.fr/>. Registration is free but you must register to attend. There is no deadline for registration: registration will be closed when the capacity of the lecture room (165 attendees) is exceeded. So visit our website quickly! Book your hotel room very soon as well (June is a busy time for conferences in Montpellier).

For questions, contact: evorescu@univ-montp2.fr

Hoping to see you in Montpellier, next June,

The organizers: Ophélie Ronce (ISEM, France), Nicolas Mouquet (ISEM, France), Andrew Gonzalez (McGill University, Canada)

Ophelie Ronce Genetique et Environnement cc 65 Institut des Sciences de l’Evolution de Montpellier UMR 5554 Université Montpellier II, Place Eugene Bataillon 34095 Montpellier cedex 5

tel: 33 (0)4 67 14 32 50 fax: 33 (0)4 67 14 36 22

NOTE THE NEW E-MAIL ADDRESS:
ophelie.ronce@univ-montp2.fr

<http://www.isem.cnrs.fr/>

ophelie.ronce@univ-montp2.fr

NESCent Durham GMOD Mar Registration

Registration is now open for the March 2011 GMOD Meeting (http://gmod.oicr.on.ca/wiki/-March_2011_GMOD_Meeting). This meeting is part of GMOD Americas 2011, an event that includes a day of Satellite Meetings, a GMOD Course (already full), and for the first time, an “Introduction to GMOD” session the night before the meeting for GMOD newcomers. GMOD Americas 2011 events are being held at the US National Evolutionary Synthesis Center (NESCent) in Durham, North Carolina, United States.

As with previous GMOD meetings, this meeting will have a mixture of project talks, component talks, and user talks. Our guest speaker is Dr. Eric Stone of North Carolina State University. Dr. Stone will talk about his experience on the “Drosophila Genome Reference Panel,” a project that is sequencing 192 lines. See <http://gmod.oicr.on.ca/wiki/March.2011.GMOD.Meeting#Agenda=A0for> more. The agenda is driven by attendee suggestions, and you are encouraged to add your suggestions now (<http://gmod.oicr.on.ca/wiki/March.2011.GMOD.Meeting#Agenda.Proposals>). For examples of what happens at a GMOD meeting, see the writeup of the September 2010 GMOD Meeting (<http://gmod.oicr.on.ca/wiki/September.2010.GMOD.Meeting>), or any previous meeting. GMOD meetings are an excellent way to meet GMOD developers and users and to learn (and affect) what’s coming in the project.

Registration for the March 2011 GMOD Meeting is \$80 on or before February 18 <<<<=====\$95 after February 18

Please register early, both to save money, and ensure a spot. You are also strongly encouraged to sign up for (or propose) a Satellite Meeting (more details to come). Details on transportation, suggested lodging, and other logistics are on the GMOD Americas 2011 page.

This meeting, and all GMOD Americas 2011 events, are jointly sponsored by NESCent and the Galaxy Project.

Dave Clements Galaxy Project

– http://gmod.org/wiki/GMOD_Americas.2011
<http://nescent.org> <http://usegalaxy.org/> <http://getgalaxy.org> clementsgalaxy@gmail.com

Norman iEvoBio Jun21-22 CallAbstracts

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

Accepted talks will be about 15-20 minutes in length and will be presented during the full talk sessions in the morning of each of the two conference days, following the day’s keynote presentation.

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

Submissions consist of a title and an abstract at most 1 page long. The abstract should provide an overview of the talk’s subject. As the number of program slots for full talks is limited, the abstract should give enough detail so reviewers can decide whether the submission merits a full talk or whether it should be moved to one of the Lightning Talk sessions. If the subject of the talk is a specific software component for use by the research community, the abstract must state the license and give the URL where the source code is available so reviewers can verify that the open-source requirement(*) is met.

The deadline for submission is March 18, 2011. We intend to notify authors of accepted talks before early registration for iEvoBio (and Evolution) ends. Further instructions for submission are at the following URL:

<http://ievobio.org/ocs/index.php/ievobio/2011/-schedConf/cfp> Full talks are 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Lightning talks (5 mins long), 2) Challenge entries, 3) Software bazaar demonstrations, and 4) Birds-of-a-Feather gatherings. The Call for Challenge entries is already open (see <http://ievobio.org/challenge.html>). The calls for contribution to the other 3 sessions will open later, and will remain open until shortly before the conference or until the respective track fills up.

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

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

(*) iEvoBio and its sponsors are dedicated to promoting the practice and philosophy of Open Source software development (see <http://www.opensource.org/>

docs/definition.php) and reuse within the research community. For this reason, if a submitted talk concerns a specific software system for use by the research community, that software must be licensed with a recognized Open Source License (see <http://www.opensource.org/licenses/>), and be available for download, including source code, by a tar/zip file accessed through ftp/http or through a widely used version control system like cvs, Subversion, git, Bazaar, or Mercurial. Authors of full talks who cannot meet this requirement at the time of submission should state their intentions, and are advised that the requirement must be met by June 19, 2011, at the latest.

Robert Guralnick <Robert.Guralnick@colorado.edu>

Norman iEvoBio Jun21-22 RegistrationOpen

Registration is now open for the conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio), at <http://ievobio.org/register.html>. iEvoBio aims to be a forum bringing together biologists working in evolution, systematics, and biodiversity, with software developers and mathematicians. The goal of iEvoBio is both to catalyse the development of new tools, and to increase awareness of the possibilities offered by existing technologies (ranging from standards and reusable toolkits to mega-scale data analysis to rich visualization). The inaugural meeting in 2010 (see <http://ievobio.org/2010>) attracted over 300 participants.

The 2-day meeting will take place June 21-22, 2011, in Norman, OK, jointly with the 2011 Evolution Meetings as a satellite conference. The event will feature traditional elements, including a keynote presentation at the beginning of each day and contributed talks, as well as more dynamic and interactive elements, including a challenge, lightning talk-style sessions, a software bazaar, and Birds-of-a- Feather gatherings.

The topic of this year's challenge is Data Integration. Cash prizes will be awarded for first place (\$1,000) and runner-up entries. The winning entries will be selected by a vote of the iEvoBio meeting participants. More details about the challenge will be provided in a separate announcement.

Attendees can register jointly for Evolution and iEvoBio at a discount, or only for the iEvoBio conference.

For more information about registration, venue, travel, or accommodations please visit the Evolution 2011 website at <http://www.evolution2011.ou.edu/>. More details about the program and guidelines for contributing content are available at <http://ievobio.org>. You can also find continuous updates on the conference's Twitter feed at <http://twitter.com/iEvoBio>, or subscribe to the low-traffic iEvoBio announcements mailing list at <http://groups.google.com/group/ievobio-announce>. iEvoBio is sponsored by the US National Evolutionary Synthesis Center (NESCent) in partnership with the Society for the Study of Evolution (SSE) and the Systematic Biologists (SSB). Additional support has been provided by the Encyclopedia of Life (EOL).

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hlapp@nescent.org

NottinghamU EvolutionaryParasitology Apr12-14

British Society for Parasitology Spring Meeting with Ecology & Evolution Sessions throughout (12th - 14th April 2011), Nottingham University.

Abstract deadline: 11th February 2011 Registration deadline: 18th February 2011 Registration and abstract submission at [http://www.bsp.uk.net/events.php?id\\$](http://www.bsp.uk.net/events.php?id$) Following the great success of the Ecology / Evolutionary theme at last year's British Society for Parasitology Spring Meeting at Cardiff University, the organising committee would like to invite you to join them again at Nottingham for this year's meeting which will again include a full series of sessions entirely devoted to ecological and evolutionary parasitology.

Session Topics:

Wild vertebrates as natural models in immunology Convened by Dr Joseph Jackson (Aberystwyth University) and with invited speaker Dr Andrea Graham (Princeton University, USA). Dr Graham's work ultimately aims to understand how natural selection has shaped strategies for both host defence and parasite transmission.

Parasites and Behaviour Convened by Dr Jo Cable

(Cardiff University) and with invited speaker Prof Janice Moore (Colorado State University, USA). Prof Moore's research focuses on the evolution of host behavioural manipulation by parasites.

Ecological and Evolutionary Impacts of Parasites on Hosts Convened by Dr Andrew MacColl and with invited speaker Prof Armand Kuris (UCSB, USA). Prof Kuris is best known for his work revealing the role of parasites in ecosystem structure and function in marine systems, and the applied consequences of this for fisheries management and biological control.

Medicine Meets Ecology Convened by Dr Jo Lello (Cardiff University). This open session will examine how ecological and evolutionary approaches are currently, or could in the future, help to improve medical practice in dealing with parasites and related issues.

Co-infection Consequences Convened by Dr Jo Lello (Cardiff University). This session will cover both parasite-parasite and pathogen-parasite combinations, looking at how these infections impact upon the host, the parasite dynamics and the evolution of host-parasite relationships.

Modelling Parasites Convenor TBC and with invited speaker Dr Andrew Fenton (Liverpool University). Dr Fenton's work focuses on the use of simple population dynamic theory as a tool for understanding the epidemiology and evolution of parasites with a current focus on the evolution of macroparasite life-history strategies.

Wildlife, Biodiversity and Disease Convenor Dr Sarah Perkins (Cardiff University). This session will explore the effects of wildlife and biodiversity on the emergence and transmission of infectious diseases.

WORKSHOP: Getting the most from your data - using the best statistical methods. Leaders Dr Jo Lello (Cardiff University) & Prof Mike Stear (Glasgow University); Those interested in this session should bring along their laptops where possible and ensure that they have loaded the freeware statistical package R and have a basic understanding of how it works. On request a simple Getting started with R guide can be obtained directly from Dr Lello (lelloj@cf.ac.uk).

Joanne Lello <LelloJ@cardiff.ac.uk>

OhioU Athens Bioinformatics
May2-4

GLBIO 2011 - Call for Abstracts

The 6th Annual Great Lakes Bioinformatics Conference (GLBIO), the newest official conference of the International Society for Computational Biology (ISCB), is pleased to announce the call for abstracts for 2011

GLBIO 2011, formerly known as OCCBIO, will be hosted by Ohio University in Athens, Ohio on May 2-4, 2011

Oral presentations will be selected from the submitted abstracts. To submit your abstract, please go to http://www.ohiobioinformaticsconsortium.org/-glbio/2011/call_for_abstracts.shtml Oral presentations will be selected from the submitted abstracts. To submit your abstract, please click here.

As in past years, this conference will provide an interdisciplinary forum for discussing approaches, research findings, and educational experiences regarding computational investigations of biological problems.

An important goal of the conference continues to be fostering long-term collaborative relationships among informatics and life sciences researchers and educators from academia, government and industry, spanning Ohio and adjacent states.

This meeting is not only for experts in bioinformatics, but also for faculty, students and staff who make substantial use of bioinformatics tools in their work, or would like to expand such use.

Please note the following conference deadlines: Feb. 21, 2011: Deadline for Submission of Abstracts for Oral Presentations March 21, 2011: Authors Notified of Abstract Acceptance March 28, 2011: Deadline for Submission of Abstracts for Poster Presentations April 4, 2011: Early Bird Registration Ends May 2-4, 2011: Conference Begins.

Online registration is now available. Visit glbio.org or click here to register.

Conference Chairs: Lonnie Welch, Ohio University
Terry Lewis, OARnet

Program Chairs: Jundong Liu, Ohio University
Robert Colvin, Ohio University
Jim Cavallari, University of Michigan

Sponsors: ISCB The Ohio University OARnet Ohio Supercomputer Center

Quick Links

GLBIO Website <http://www.ohiobioinformaticsconsortium.org/occbio/-GL2011/>
Call for Abstracts <http://www.ohiobioinformaticsconsortium.org/glbio/2011/>

call_for_abstracts.shtml Sponsor Information <http://www.ohiobioinformaticsconsortium.org/occbio/GL2011/sponsorship.shtml> Registration http://www.iscb.org/cms_addon/conferences/glbio2011/register/index.php Keynote Speakers

Michael Becich, Director of the Center for Pathology Informatics, University of Pittsburgh Medical Center

Elodie Ghedin, Asst. Professor of Computational Biology, University of Pittsburgh

Al Hero, R. Jamison and Betty Williams Professor of Engineering, University of Michigan

Richard Lenski, John Hannah Professor of Microbial Ecology, Michigan State University

GLBIO is also seeking proposals for Invited Sessions, Panel Discussions, and Tutorials - please go to <http://glbio.org> for more information.

Ohio Supercomputer Center | 1224 Kinnear Road | Columbus | OH | 43212

Kathryn Kelley <terry@osc.edu>

Plymouth PlanktonBiodiversity Sep22-23

Plankton 2011: An international symposium on plankton biodiversity and global change in the aquatic systems.

To celebrate the 80th Anniversary of the Continuous Plankton Recorder Survey, The Sir Alister Hardy Foundation for Ocean Science will host Plankton 2011. It will seek to identify causes and consequences of long-term changes in plankton communities in fresh and marine waters. The Symposium will be held on 22nd and 23rd September 2011 in Plymouth Guildhall. For more information and to register your interest please go to www.plankton2011.org Gemma Brice Plankton 2011: Biodiversity & Global Change Plymouth, UK. 22/23 Sept 2011 Abstract submission to www.plankton2011.org Gemma Brice <Gemma.Brice@sahfos.ac.uk>

Roscoff Brittany DiseaseEvolution Jun25-29

Roscoff.Brittany.Emerging_Fungal_Disease&Evolution.June25-29.2011

First Call << New and Emerging Fungal Diseases of Animals and Plants : evolutionary aspects in the context of global changes>>

Registration deadline: 15th March 2011.

The CNRS and Conferences Jaques Monod are hosting a 4-day meeting at the French Marine Biology research station in Roscoff, Brittany on the evolution and dynamics of emerging fungal pathogens. This meeting will focus on the rapidly widening impacts that fungi are having on human, plant and animal health by considering the factors that drive their emergence within an evolutionary context. Specifically, the meeting will consider the extent that anthropogenically-mediated environmental change is facilitating fungal range expansions and genotypes, and to what extent this is predictable. The meeting will bring together leading evolutionary biologists, theoreticians and fungal biologists/ecologists in a beautiful setting at the French National Marine Biology Station, Roscoff, to consider these questions and to formulate new research strategies.

Plenary speakers:

Francois Balloux ; Imperial College London, UK Lynne Boddy ; University of Cardiff, UK Bruno Le Cam ; INRA Angers, France Ignazio Carbone ; North Carolina State University, USA Jean Carlier ; CIRAD Montpellier, France Jean Marie Cornuet ; Centre de Biologie et de Gestion des Populations Christopher Gilligan ; University of Cambridge, UK Francois Delmotte ; INRA Bordeaux, France Marie-Laure Desprez-Loustau ; INRA Bordeaux, France Matthew Fisher ; Imperial College London Sylvain Gandon ; CNRS Centre d'Ecologie Fonctionnelle et Evolutive Montpellier, France Trenton Garner ; Insitute of Zoology, UK Greg Gilbert ; University of California, Santa Cruz Tatiana Giraud ; CNRS - Université d'Orsay, France Michael Hood ; Amherst College, USA Clive Brasier ; Forestry Commission, UK Levente Kiss ; Plant Protection Institute of the Hungarian Academy of Sciences Linda Kohn ; University of Toronto, Canada Marc Henri Lebrun ; INRA BIOGER, France Celeste Linde ; Australian National University David Lodge ; Uni-

versity of Notre Dame, USA Benoit Marcais ; INRA Nancy, France Bruce McDonald ; ETH Zurich, Switzerland Michael Milgroom ; Cornell University, USA Ingrid Parker ; University of California, Santa Cruz Amy Pedersen ; Sheffield University, UK Anne Pringle ; Sheffield, USA Virginie Ravigne ; CIRAD Montpellier, France Eva Stukenbrock ; University of Århus, Denmark John Taylor ; University of California at Berkeley, USA Frank van den Bosch ; BBSRC, Rothamsted Research, UK

Conference website:

<http://www.ese.u-psud.fr/-CJMemergingdiseases2011/> To participate, please contact:

Matthew Fisher <matthew.fisher@imperial.ac.uk> Tatiana Giraud <tatiana.giraud@u-psud.fr>

See you there!

–

Tatiana

Tatiana Giraud

Departement Genetique et Ecologie Evolutives Laboratoire Ecologie, Systématique et Evolution UMR 8079 CNRS-UPS-AgroParisTech Bâtiment 360 Université de Paris-Sud 91405 Orsay cedex France

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English: http://www.ese.u-psud.fr/pages_perso/-spip.php?article21 Français: http://www.ese.u-psud.fr/pages_perso/spip.php?article41
<http://www.ese.u-psud.fr/> tatiana Giraud
 <tatiana.giraud@u-psud.fr>

traditionally a great platform for young Evolutionary Biology graduates to present their work and to meet their peers from all over Europe in a friendly, social environment.

A small selection of senior scientists will be present to provide guidance, give feedback, and of course share their own research in a plenary talk. We are happy to be able to confirm the following speakers:

Madan Babu - Cambridge, UK Bertus Beaumont - Delft, the Netherlands Trine Bilde - Aarhus, Denmark Lounçs Chikhi - Oeiras, Portugal

Tom Tregenza - Exeter, UK Ana Rivero - Montpellier, France Walter Salzburger - Basel, Switzerland Marcelo Sanchez - Zürich, Switzerland Günter Wagner - Yale, USA

Registration will close on April 15th. Because of a limited number of slots, your registration does not equal participation, but we will confirm participation before May 1st. Participation will cost –290. *To register, as well as for more and up to – date information, please check our website :* <http://www.igc.gulbenkian.pt/empseb17> or contact us directly at empseb17@igc.gulbenkian.pt

If you would like to advertise the meeting in your institution, please send us an email with your postal address and we will send you poster and flyers.

We hope to welcome you in Seia this August!

The organizing committee,

Marisa Oliveira (president) Pedro Lima (secretary) Barbara Vreede (treasurer) Rui Castanhinha Marc Gouw Alexandre Leitão Cláudia Mendes
 pedro lima <lima.pt@gmail.com>

Seia Portugal 17th EMPSEB Aug10-15

Registration is now open for the 17th European Meeting of PhD Students in Evolutionary Biology (EMPSEB).

Another great encounter of students in Evolution is in the making! This year's meeting will take place from 10-15 August 2011 in Portugal, in the beautiful village of Seia, located in the Serra de Estrela mountain range.

We encourage all PhD students in evolutionary biology to apply and join us this summer. EMPSEB is

Spain EMBO Comparative Genomics Oct15-20

Comparative genomics of eukaryotic microorganisms: understanding the complexity of diversity

15 - 20 October | 2011 | Sant Feliu de Guixols | Spain Website: <http://events.embo.org/11-comparative-genomics/>
 COMPARATIVE GENOMICS OF EUKARYOTIC MICROORGANISMS: UNDERSTANDING THE COMPLEXITY OF DIVERSITY

We invite you to participate in the upcoming EMBO conference on Comparative Genomics of Eukaryotic Microorganisms to be held in San Feliu de Guixols,

Spain, 15-22 October 2011 (see Website: <http://events.embo.org/11-comparative-genomics/>).

This conference will address the big evolutionary questions of what makes a eukaryote, how multicellularity arose, the evolution of reproduction, pathogenesis, and so on. Lineages of the Eukaryotic Tree of Life (TOL) that until now received only moderate attention, such as the Excavates, Archaeplastids, Amoebozoa and Choanozoa, will be discussed, together with the better studied Chromalveolates and Fungi.

There will be opportunities for participants to present both short talks and posters, which will be conducted interactively with plenty of time reserved for questions and discussions. In addition there will be interactive workshops on 'Do It Yourself' genomics, databases and bioinformatics.

This is the 4th time the meeting will be held at this very nice venue on the Costa Brava, on the Mediterranean near Barcelona. The weather is still generally nice at this time of year and the food is great. There will be free shuttle buses from the Barcelona airport.

There are still spaces available and room for more short talks as well as poster presentations. We hope to see you at what will be an exciting and informative meeting. Please contact Heather Barnett at heather.barnett@nottingham.ac.uk +44-(0)115-823 0354 for details.

Teun Boekhout, Amparo Querol and Ed Louis, conference organisers

Teun Boekhout

CBS Fungal Biodiversity Centre

Uppsalaalaaan 8

3584 CT Utrecht

The Netherlands

t.boekhout@cbs.knaw.nl

Teun Boekhout <t.boekhout@cbs.knaw.nl>

Switzerland EconomicsEvolution Apr17-20

REGISTRATION DEADLINE APPROACHING: 10th FEB

Conference on Social Decision Making: Bridging Economics and Evolutionary Biology

www.evolveingeconomics.com Date 17 April-20 April 2011

Location Monte Verita, Ascona, Switzerland.

Purpose The fields of evolutionary biology and economics have similar foundations, both attempting to explain individual decisions based on the costs and benefits of particular actions. However, the two fields also rely upon very different working assumptions about how and why individuals take the actions that they do. Our conference sets out to create an environment that is conducive to dialogue, mutual learning, and the development of new collaborations between the two fields by focusing on an area of mutual interest: decision-making in social interactions. Sessions will pair leading economists and evolutionary biologists to discuss specific topic so as to explore the common interests between the fields.

Confirmed Speakers Professor Colin Camerer, California Institute of Technology Professor Alan Grafen, Oxford University Professor Arnon Lotem, Tel Aviv University Professor John McNamara, University of Bristol Professor Paul Seabright, Université des Sciences Sociales de Toulouse Professor David W. Stephens, University of Minnesota Professor Stuart A. West, Oxford University Professor Peyton Young, Oxford University

Abstracts We are inviting abstracts for posters or contributed talks. When registering, please indicate whether you wish to present, and include a title and abstract.

Conference fees Conference fees include registration, welcome drink, accommodation for three nights in Monte Verit  and full board (breakfast, lunch and dinner).

Students: 400CHF for sharing a twin room, 440CHF for a single room. Post-docs/researchers: 450CHF for sharing a twin room, 490CHF for a single room. Professors: 500CHF for sharing a twin room, 550CHF for a single room.

Registration Registration deadline: 10th February 2011. Please visit the registration page on the conference website: <http://www.evolveingeconomics.com/> There are only 60 places for delegates to attend this conference.

Further information Web: <http://www.evolveingeconomics.com/> E-mail: info@evolveingeconomics.com

Organising Committee Claire El Mouden, Oxford University Lorenz Goette, University of Lausanne Laurent Lehmann, University of Neuch tel Daniel J. Rankin, University of Z rich Stuart A. West, Oxford University

Claire El Mouden <claire.elmouden@chch.ox.ac.uk>

Tuebingen ESEB 2011 Aug20-25 ParallelEvol CallAbstracts

ESEB 2011 Parallel Evolution Symposium - Call for abstracts We would like to invite you to submit your abstracts for oral or poster presentations to the symposium "Parallel Evolution" at the ESEB meeting 20-25 August 2011 in Tübingen, Germany.

Please find further information on the submission process and the link to abstract submission here: http://www.eseb2011.de/call_for_abstracts.htm DEADLINE: 28TH FEBRUARY.

Symposium:

Parallel evolution is the emergence of the similar phenotypes in independent lineages. The evolution of parallel (or convergent) morphologies can be a response to similar selection pressures. Alternatively, developmental or genetic constraints could lead to convergence. This symposium focuses on the genetic and developmental basis as well as on the ecological circumstances of parallel evolution.

Invited speakers:

Hopi E. Hoekstra (Harvard University) Louis Bernatchez (Laval University)

Organizers:

Walter Salzburger (University of Basel, walter.salzburger@unibas.ch) Moritz Muschick (University of Basel, moritz.muschick@unibas.ch)

Please approach us with any questions you might have regarding the symposium. For further information on the meeting please visit the official website: <http://www.eseb2011.de/index.htm> We are very much looking forward to meeting you in Tübingen in August!

Walter Salzburger and Moritz Muschick
moritz.muschick@unibas.ch

Tuebingen ESEB2011 Aug20-25 RegistrationDeadline

13th Congress of the European Society for Evolutionary Biology Tuebingen, Germany, 20-25 August 2011

DEADLINE COMING UP: Registration and abstract submission CLOSE on 28 February. See www.eseb2011.de for details

Important remarks 1. Registration, abstract submission and booking of accommodation are three separate, independent processes. Make sure you have finished all three. Although there is no deadline for accommodation, space in the small city of Tuebingen is limited. Late bookings will have to take into account that they will be housed in nearby towns.

2. Regular posters will receive exceptional visibility: All posters will be up for the duration of the meeting, lunch will be served in the poster area, three separate poster sessions will highlight one third of the posters each, there will be poster prize(s), free drinks, and several novel activities that will encourage people to see you at your poster. In other words: If your oral submission is not accepted, enjoy the upgrade to a poster! Consider going for one without the detour.

Yours, Nico Michiels

Nico Michiels, Prof. Dr. Animal Evolutionary Ecology Faculty of Biology Auf der Morgenstelle 28 72076 Tuebingen Germany

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nico.michiels@uni-tuebingen.de <http://www.evoeco.uni-tuebingen.de> <http://www.eve.uni-tuebingen.de> Nico Michiels <nico.michiels@uni-tuebingen.de>

Tuebingen ESEB 2011 MacroEvolution Aug20-25 Deadline

Dear all,

The deadline for abstract submission to ESEB 2011 is fast approaching and we invite abstract submissions for oral and poster presentations in the symposium on "Predicting macroevolution from microevolution".

ESEB 2011 Meeting (European Society for Evolutionary Biology meeting, Tuebingen, Germany 20-25 August 2011).

ABSTRACTS submission is now open at: http://www.eseb2011.de/call_for_abstracts.htm DEADLINE

for abstract submission is the 28TH OF FEBRUARY 2011.

Symposium description

Most current quantitative macroevolutionary models are divorced from the ecological and microevolutionary processes that underpin broad-scale evolutionary trends. This symposium will explore how theory, empirical data and methodological approaches from diverse fields including community ecology and evolutionary genetics can reveal the processes that underpin macroevolutionary patterns.

Invited speakers: Oliver Pybus (Oxford University), Emma Goldberg (University of Illinois),

Organizers: Gavin Thomas, Bristol, gavin.thomas@bristol.ac.uk Rob Freckleton, Sheffield, r.freckleton@sheffield.ac.uk

Contact us for further information. Conference details are available here < <http://www.eseb2011.de/-index.htm> >.

Dr. Gavin Thomas NERC Postdoctoral Fellow School of Biological Sciences University of Bristol Woodland Rd. Bristol BS8 1UG +44 (0)117 9288041 Gavin.Thomas@bristol.ac.uk <http://seis.bris.ac.uk/~gt0027/index.html> Gavin Thomas <gavin.thomas@bristol.ac.uk>

Tuebingen ESEB ExperimentalEvol Aug20-25 CallAbstracts

Dear all,

We invite abstract submissions for oral and poster presentations in the symposium on "Experimental evolution across the microbe/macrobe divide" at the ESEB 2011 Meeting (European Society for Evolutionary Biology meeting, Tuebingen, Germany 20-25 August 2011).

ABSTRACTS submission is now open at: http://www.eseb2011.de/call_for_abstracts.htm DEADLINE for abstract submission is the 28TH OF FEBRUARY 2011.

Symposium description

Experimental evolution is one of the most powerful approaches available for the study of microevolutionary processes and has been used since the early age of evolutionary biology and genetics. It offers the possibility to study a very broad range of problems from enzyme

efficiency to ecosystem organisation, from adaptation to changing environment to antidrug resistance evolution and from ageing to host-pathogen coevolution. Experimental evolution, as any method, has some favourite experimental models but they represent a great biological diversity: virus, prokaryotes, unicellular eukaryotes and multicellular animals and plants. This biological diversity translates into diversity in generation time and mutation rate, which in turns translate into a diversity of genetic mechanisms underlying the phenotypic changes observed. The goal of the proposed symposia is to bring together scientists using experimental evolution of a variety of organisms and to ask very different biological questions, so as to favour exchange around the commons and potentials of this method. Moreover this symposium will be a great opportunity to highlight how emerging next generation techniques can be combined with EE for greater understanding of the genetic basis of evolution.

Invited speakers:

Graham Bell (McGill University), Richard E. Lenski (Michigan State), Tadeusz Kawecki (University of Lausanne)

Organizers:

Rhonda R. Snook, Sheffield, r.snook@sheffield.ac.uk
Nick Colegrave, Edinburgh, n.colegrave@ed.ac.uk
Thomas U. Berendock, Dresden, thomas.berendonk@tu-dresden.de
Oliver Kaltz, Montpellier, oliver.kaltz@univ-montp2.fr
Stéphanie Bedhomme, València, stebed@upvnet.upv.es
Santiago F. Elena, València, sfelena@ibmcp.upv.es

Contact us for further information. Conference details are available here (<http://www.eseb2011.de/-index.htm>).

Stephanie Bedhomme <stebed@upvnet.upv.es>

Tuebingen ESEB Genomics Aug20-25 CallAbstracts

ESEB 2011 Evolutionary ecological genomics symposium - Call for abstracts We invite abstract submissions for oral and poster presentations in the symposium on Evolutionary ecological genomics at the ESEB meeting 2011 (European Society for Evolutionary Biology meeting, Tuebingen 20-25 August 2011, Germany).

ABSTRACTS submission is open at: http://www.eseb2011.de/call_for_abstracts.htm

/www.eseb2011.de/call_for_abstracts.htm DEADLINE for abstract submission is the 28TH OF FEBRUARY.

The symposium: Progress in ecological genomics is hindered by limited genome information in non-model species and the lack of an ecological context in genetic model species. This symposium will focus on integrating cutting edge molecular biology in model and non model organisms within an evolutionary and ecological context. Our aim is to understand adaptive responses in multidimensional selection pressures in the wild. Our symposium aims to attract contributions from aquatic and terrestrial systems as well as vertebrates and invertebrates to present advances in the field of ecological genomics and promote constructive discussion.

Invited speakers: We are honored to have FOUR invited speakers with expertise in complementary fields of ecological genomics, functional genomics, and evolution. Their research focuses on different model systems including both genetic model and non-model species. Ilkka Hanski, Department of Ecology and Evolutionary Biology, PO Box 65 (Viikinkaari 1) 00014 University of Helsinki

Michael Pfrender (Department of Biological Sciences, University of Notre Dame, 109B Galvin Life Sciences, Notre Dame, IN 46556, PH)**

Hopi Hoekstra (Harvard University, Department of Organismic and Evolutionary Biology, Museum of Comparative Zoology, 26 Oxford Street, Cambridge, MA 02138 USA)

Katie Peichel (Fred Hutchinson Cancer Research Center, 1100 Fairview Ave. N. PO Box 19024 Seattle, USA)

Organizers: Luisa Orsini, Catholic University Leuven, Belgium (luisa.orsini@bio.kuleuven.be) Christophe Eizaguirre, Leibniz Institute for Marine Sciences (IFM-Geomar), Kiel, Germany (ceizaguirre@ifm-geomar.de) For further information on the symposium feel free to contact the organizers. For logistic details on the conference refer to the ESEB webpage (<http://www.eseb2011.de/index.htm>). Do not forget to register before submitting your abstract.

Luisa Orsini & Christophe Eizaguirre

–

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Phone: +32 016323851 Fax: +32 016320771
e-mail luisa.orsini@bio.kuleuven.be website:<http://bio.kuleuven.be/de/dea/people.php> Luisa Orsini
<luisa.orsini@bio.kuleuven.be>

UMichigan DiseaseEvolution Apr16

Dear Colleagues,

We are pleased to announce this year's Early Career Scientist Symposium, to be held Saturday, April 16, 2011 at the Blau Auditorium at the Ross School of Business on the campus of the University of Michigan, Ann Arbor. The theme this year will be "Infectious Disease across Scales". Our outstanding lineup of up-and-coming field leaders will address diverse ecological and evolutionary aspects of host-pathogen and -parasite systems from within individual hosts to the broad community of multiple hosts and pathogens. The keynote address will be given by Prof. Steven Frank of the University of California at Irvine, who will describe "Three unsolved puzzles in infectious disease".

Register to attend and obtain more information by going to <http://sitemaker.umich.edu/ecss2011/home>. Registration is free of charge but we strongly encourage you to register so we may provide adequate food and refreshment. Graduate students from all universities and all disciplines are invited to present their work during a lunchtime poster session. Further information on posters will be forthcoming. Lunch will be provided at the poster session and a dinner reception will follow the symposium.

Looking forward to your participation,

Aaron King

on behalf of the 2011 ECSS organizing committee:
Aaron King, Mercedes Pascual, Pej Rohani, Andres Baeza, Micaela Martinez-Bakker, Gail Kuhnlein

– Aaron A. King, Ph.D. Ecology & Evolutionary Biology Mathematics Center for the Study of Complex Systems University of Michigan GPG Public Key: 0x6E74F51B

kingaa@umich.edu

UOklahoma Evolution 2011 Jun17-21

The Evolution 2011 website is now open for registration

www.evolution2011.ou.edu<
www.evolution2011.ou.edu >

Sincerely,

Larry Weider, Rich Broughton, and Ingo Schlupp
 tri-chairs, Evolution 2011 Organizing Committee
 Department of Zoology

University of Oklahoma

Norman, OK 73019

“Weider, Lawrence J.” <ljweider@ou.edu>

West Virginia Malaria Evolution Aug1-Aug4

FIRST ANNOUNCEMENT

* *

International Workshop on Malaria and
 Related Haemosporidian Parasites of Wildlife
 Monday August 1st V Thursday August 4th, 2011
 National Conservation Training Center, Shepherd-
 stown, West Virginia

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

Dear Colleagues,

The NSF-sponsored Research Coordination Network
 for Haemosporida of Terrestrial Vertebrates (Malari-
 aRCN) is pleased to announce our first annual work-
 shop on the malaria parasites and closely related
 haemosporidians of natural populations of vertebrates.
 The four day workshop will include both field and lab-
 oratory exercises as well as lectures and discussions led
 by RCN members².

Topics to be covered through the workshops exercises
 include vertebrate field capture techniques, blood sam-
 pling and preparation of blood smears, sample vouch-
 ering and cryopreservation, light microscopy for parasite
 species identification and parasite and cell counts, DNA
 extraction and PCR screening of parasites, sequence
 data analysis including phylogenetics, and databas-
 ing. Discussion topics will include, but are not limited
 to, the basic biology, phylogenetics and systematics of
 Haemosporida, community ecology of parasites, coe-
 volution of parasites and hosts, the evolution of virulence,

<http://> and conservation and disease.

The workshop will commence on Monday morning, Au-
 gust 1st, and continue through until the afternoon of
 Thursday, August 4th. The workshop will be followed
 by a three day meeting on the malaria and related
 haemosporidian parasites of wildlife, organized by the
 same RCN group.

All food, lodging and workshop events will take place
 at the US Fish & Wildlife Services National Conserva-
 tion Training Center in Shepherdstown, West Virginia,
 a site easily accessible through Washington, D.C., area
 airports.

The workshop is geared towards graduate students,
 postdoctoral researchers, and other investigators new
 to the field of wildlife haemosporidians. We will be
 accepting applications in early 2011 and encourage in-
 dividuals from outside the United States, particularly
 from developing countries. Funds will be available for
 travel, accommodation, and meals for selected appli-
 cants. Additional information on the workshop in-
 cluding an overview of the four days of events will be
 provided with the Second Workshop Announcement as
 well as on an official workshop website (to be launched
 in early 2011). In the meantime, further information
 can be obtained from the workshop organizers (email:
MalariaRCNWorkshop@gmail.com).

¹ The Research Coordination Network for Haemo-
 sporida of Terrestrial Vertebrates (RCN), sponsored
 by the U. S. National Science Foundation and funded
 through 2015 at the University of Missouri-St. Louis,
 was established to promote communication among re-
 searchers working on the ecology and evolution of
 haemosporidian parasites of vertebrate wildlife popula-
 tions. A website for the network (www.malariarcn.org)
 will be available early in 2011. In the meantime,
 inquiries can be directed to R. E. Ricklefs at ricklefs@umsl.edu.

² Workshop organizers include Ellen Martinsen (Smith-
 sonian Institution), Patricia Parker (University of Mis-
 souri V St. Louis), Staffan Bensch (Lund University),
 and Gediminas Valkiunas (Nature Research Center,
 Vilnius). Other members of this RCN include Robert
 Ricklefs (University of Missouri V St. Louis), Robert
 Fleischer (Smithsonian Institution), Ravinder Sehgal
 (San Francisco State University), Susan Perkins (Ameri-
 can Museum of Natural History), Tom Smith (Uni-
 versity of California, Los Angeles), Carter Atkinson
 (USGS), and Robert Adlard (Queensland Museum).

**The workshop is likely to be of interest to evolution-
 ary biologists as it will center around the systematics
 of a very successful and diverse group of parasites of

natural vertebrate populations and include laboratory exercises involving phylogenetic analysis of parasite lineages and readings and discussions on the evolutionary history of the parasites including cospeciation of hosts and parasites as well as the evolution of virulence.

Ellen Martinsen, Ph.D. | Postdoctoral Fellow Smithsonian Conservation Biology Institute Center for Conser-

vation and Evolutionary Genetics National Zoological Park Mail: P.O. Box 37012, MRC 5503, Washington, DC 20013-7012 Location: 3001 Connecticut Ave., NW, Washington, DC 20008 T 202-633-4119| F 202-673-0040 | Email ellensarah.martinsen@gmail.com

Ellen Martinsen <ellensarah.martinsen@gmail.com>

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Barcelona ClimateAdaptation

PHD OPPORTUNITY IN BARCELONA

A four year PhD studentship is available to study the adaptation of porcine creole breeds to extreme climates using new sequencing technologies. During the thesis, whole genome sequence data from pigs adapted to heat (tropical and subtropical animals) and altitude (Andean altiplano) will be analyzed. This data will be combined with extant and forthcoming data on Illumina SNP data. The project is in cooperation with diverse international groups. The student will work

in a multidisciplinary group with expertises in quantitative, population and molecular genetics. The work will be developed in a new center in Agrigenomics (www.cragenomica.es) within the campus of Universitat Autònoma of Barcelona (www.uab.es). Ample opportunity exist for interaction with other groups and to train in Bioinformatics and in animal breeding and genetics, including the newly founded National Center for Genomic Analysis, which hosts several Illumina sequencers.

The fellowship does not require a MSc title and no restriction on nationality exists, although more paperwork is required for non European students. The fellowship is accompanied by travel allowances to visit foreign labs and medical insurance.

We are looking for highly motivated students with an interest in population and quantitative genetics and bioinformatics as applied to livestock. Interested students please email CV including the transcript of University record with full qualifications, and name and email of two professionals who can provide references at miguel.perez@uab.es .

Miguel Perez-Enciso ICREA professor Dept. Ciencia Animal i dels Aliments Facultat de Veterinaria Universitat Autonoma de Barcelona 08193 Bellaterra, SPAIN Phone: +34 93 581 4225 Fax: +34 93 581 2106 miguel.perez@uab.es <http://www.icrea.cat/-Web/ScientificForm.aspx?key=255> “Sebastian E. Ramos-Onsins” <sebas@ramos.net>

DonanaStation BiologicalInvasions

Prof Andy Green (<http://www.ebd.csic.es/andy>) and Dr. Ciro Rico from the Biological Station of Doñana-CSIC (EBD-CSIC, Sevilla, Spain; <http://www.ebd.csic.es>) are proposing a PhD opportunity, to apply for a 4-year JAE-predoc funding.

Issue: The PhD will focus on key mechanistic processes that enable invasive invertebrate species to establish in the face of novel environmental conditions. We aim to test the roles that propagule pressure, greater physiological tolerance and enemy release play in the successful establishment of invasive species and declines of native species. Studied organisms are two invasive crustaceans (one caridean shrimp and one brine shrimp) with major impacts on their native European and Mediterranean congeners. The candidate must have a strong interest in ecology and evolution, especially in biological invasions. The student will acquire skills in molecular work, especially on gene expression and population genetics. The student will also conduct experiments in aquaria and mesocosms, but also work in the field.

Ideal profile: - Highly motivated student with a Higher degree, Engineer diploma or Masters degree in Ecology, Environmental Sciences, Evolution, Genetics or similar. - Outstanding grades (>2/4); published papers would be a competitive advantage. - Experience in molecular work (gene expression, population genetics or similar) would be greatly appreciated. - Good level of written English. Spoken English or Spanish is essential.

We are looking for candidates with EITHER outstanding grades OR relevant molecular experience. Those

with neither need not apply.

Candidates should send their CV, details of the grades for their degree, and a presentation letter (in English or Spanish) stating their interest and suitability for the position, and the names and contact details of two referees to both Andy Green (ajgreen@ebd.csic.es) and Ciro Rico (ciro@ebd.csic.es).

lejeusne@ebd.csic.es

DurhamU GeneticDiversity

PhD studentship in the School of Biological and Biomedical Sciences, Durham University

Genetic diversity, population connectivity and population dynamics of a top predator species in the context of Holocene environmental change.

The primary objective is to test for a relationship between historical environmental change (especially associated with climate change and deforestation) and the genetic diversity, population structure and population dynamics of an alpha predator species in Europe. The expectation is that habitat change or loss will be reflected in periods of population decline. The initial focus will be on the lynx. During the Holocene native felids suffered the effects of human persecution and landscape modification, and the range of the lynx in Europe is now greatly reduced. There has been interest in the reintroduction of the species to its former range, however their effective re-introduction must be based on understanding the historical pattern of genetic differentiation and distribution. Ancient DNA and coalescent methods will be applied to investigate the population genetics and demographic trends of the species over the course of the Holocene. For further details of this project contact Prof. Rus Hoelzel (a.r.hoelzel@dur.ac.uk), and for reference to a similar study recently completed in Durham see de Bruyn et al. (2009) PLoS Genetics 5: e1000554.

The studentship would be funded through the NERC algorithm, and the full studentship is open only to UK nationals. Applicants should have an undergraduate degree and preferably a master's degree in a relevant subject. Please send a c.v., course records and a cover letter to a.r.hoelzel@dur.ac.uk, have two letters of recommendation sent to the same email address, and submit an application online at the Durham University web site by 4 March 2011.

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

EastCarolinaU PopulationGenetics

GRADUATE STUDENT POSITIONS: POPULATION GENETICS, PHYLOGENOMICS, AND COMPARATIVE GENOMICS OF LEGUMES AT EAST CAROLINA UNIVERSITY

Graduate student (Ph.D. or M.S.) positions are available in the laboratory of Dr. Ashley N. Egan in the Department of Biology, East Carolina University. We seek highly motivated colleagues to study evolutionary genetics and genomics of the plant tribe Phaseoleae (family Leguminosae/Fabaceae) that includes many species of economic importance (soybean, common bean, jicama, etc). Research interests in our lab include bioinformatics, computational biology, molecular systematics, evolutionary and population genetics, and evolutionary comparative genomics.

Research activities can involve fieldwork in the US and abroad, next-generation DNA sequencing, and phylogenetic, phylogenomic, and comparative genomic analyses. Opportunities exist for students to develop independent projects making use of considerable 454 transcriptome data collected from several species across phaseolid legumes. For an outline of current projects and prospective projects in the lab, please go to <http://www.ecu.edu/cs-cas/biology/egan.ashley.cfm> .

Prospective students with a background in genomics, botany, phylogenetics, and/or population genetics are encouraged to apply. Evidence of robust quantitative/analytical skills, strong work ethic, passion for investigating scientific questions, ability to work in both field and laboratory conditions and collaborative skills will all be vital for the success of potential candidates. Students will be supported by a combination of research and teaching assistantships.

Applications should include: cover letter with statement of research interests, CV, transcripts, and GRE scores. The packet must be sent to Dr. Ashley Egan (egana@ecu.edu). In addition, please have three references send letters to the same e-mail address. Also follow the direction for applications to the Department of Biology (www.ecu.edu/biology) at <http://www.ecu.edu/cs-cas/biology/applyingforadmission.cfm> and, for PhD¹s, apply to the Interdisciplinary Doctoral Program in Biological Sciences (www.ecu.edu/idpbs) . Application

review begins immediately for a start date of August 2011.

Ashley N. Egan, Ph.D. Assistant Professor, Department of Biology North Carolina Center for Biodiversity Howell Science Complex ' Mailstop 551 East Carolina University Greenville, NC 27858-4353 Office: N303a/N304 Lab: N304/N305 Phone (252) 328-4244 fax (252) 328-4178 egana@ecu.edu

“Egan, Ashley” <EGANA@ECU.EDU>

FloridaIntlU USDA PopulationGenetics

Dear Brian,

Could you please forward the following for posting to evoldir?

SIX MS RESEARCH ASSISTANTSHIPS IN AGROECOLOGY at Florida International Universitys Earth and Environment Department, Miami, Florida: We have six Research Assistantships at the Masters level funded by the USDA National Needs Fellows (NNF) Program for two years. While enrolled in the Master of Sciences in Environmental Studies degree program, candidates will conduct research in the areas of soil microbiology, soil science, natural resource economics, agroecology and sustainable agriculture, population genetics, land use change and urban ecology, water resources, GIS applications in sustainable agriculture, and/or forest resources. Students are expected to test and analyze research data, prepare research manuscripts, as well as make research presentations at local, regional and national meetings. Students are encouraged to perform studies related to research projects in collaboration with USDA agencies, Students will also participate in general activities relating to our Agroecology Program growth and development. Some of the duties involve mentoring undergraduate USDA-funded Multicultural Scholar students and interns, as campus Organic Garden activities, urban community garden education and service, farmers markets, and agroecology event management. A B.S. degree in soil science, ecology, microbiology, biochemistry, environmental science, or closely related discipline is required. Some of the additional requirements are: US Citizenship or residency, demonstrated excellence in course work, excellent written and oral communication skills, and ability to work independently and as a team

member. Each Fellow receives \$18,500 per year for two years, and in-state and out-of-state tuition waivers. For further details about these positions please contact Dr. Krish Jayachandran, Associate Professor and Co-Director of Agroecology Program, phone 305-348-6553, jayachan@fiu.edu and Dr. Mahadev Bhat, Professor and Co-Director of Agroecology Program, Phone 305-348-1210, bhatm@fiu.edu To apply, please visit Florida International University's University Graduate School (UGS) website (<http://gradschool.fiu.edu/>) and send us a copy of your completed application. The deadline for this National Needs Fellowship screening and acceptance is March 31, 2011.

– Eric Bishop von Wettberg Biological Sciences Florida International University Miami, Fl, USA

Center for Tropical Plant Conservation Fairchild Tropical Botanic Garden Coral Gables, Fl, USA

Eric J Bishop-von Wettberg <ebishopv@fiu.edu>

GoettingenU ComparativeGenomics

The "Geomicrobiology and Symbiosis" research group (<http://www.uni-goettingen.de/en/102704.html>) in the Courant Research Centre (CRC) for Geobiology, University of Göttingen, Germany invites applications for a Ph.D. position funded through the German Research Foundation (DFG).

Topic: A comparative genomics approach will be applied to study the evolution of a host-specific symbiosis between *Niphargus* amphipods and sulfur-oxidizing Thiobacteria. This ectosymbiosis occurs within sulfide-rich limestone caves in Italy (Dattagupta et al., 2009, ISME J 3, 935-943; Flot et al., 2010, BMC Evol Biol 10: 171-184). Genome analyses of the symbionts will be complemented with cultivation-based and biochemical methods to examine the basis for host specificity. The project will involve field collections, lab work, and extensive bioinformatic analyses.

Environment: Göttingen is a quaint German university town with an international student-based community. The CRC Geobiology offers state-of-the-art analytical facilities and an excellent environment for interdisciplinary research. Genome analyses will be done in collaboration with the Göttingen Genomics Laboratory (<http://www.g2l.bio.uni-goettingen.de/>).

Requirements: Candidates should hold a Master's degree in Biology, have a strong background and/or in-

terest in Bioinformatics, and be fluent in English. International applicants and women are encouraged to apply. Disabled persons with equivalent aptitude will be favored.

Employment: A two-year position is offered, with the possibility of extension to three years. Salary is approximately 65% of the German TV-L system, level 13.

Application: Candidates should send a curriculum vitae and a statement of research interest to Dr. Sharmishtha Dattagupta (sdattag@uni-goettingen.de) by March 31, 2011. They should also arrange for letters to be sent by two referees to the above email address.

Sharmishtha Dattagupta <sdattag@uni-goettingen.de>

HumboldtStateU FishConservationGenetics

*Position/Title: MS Graduate Assistantship *

Agency/Location: Humboldt State University Department of Fisheries Biology

*Responsibilities:** Study conservation genetics of the federally endangered tidewater goby in northern California. Project involves use of a time series of collections to evaluate metapopulation dynamics in tidewater goby. *Project will involve field collection and laboratory genetic assays. *Successful candidate will work with major advisor to develop a project. Collaboration with the US Fish and Wildlife Service is also expected.*

*Qualifications:** Applicants should have a BS in fisheries, ecology, or a related field with competitive GPA and GRE scores. Prefer experience with genetics methods and exposure to microsatellite genotyping and analysis.*

*Salary: **Approximately \$11,550/yr plus \$2,600/term towards tuition*

*Closing Date:** until filled*

*Contact:** Submit a letter of interest, resume, unofficial transcripts and GRE scores, and contact information for three references to Andrew Kinziger: Andrew.Kinziger@humboldt.edu. Formal acceptance to the M.S program at Humboldt State University is required.*

*Web link: **<http://www.humboldt.edu/fisheries/>*

Additional Project Background:

The project will be extension of past work recently published in *Molecular Ecology* (McCraney et al., 2010). The main goal will be to determine levels of genetic diversity, genetic structure, and stability in genetic structure through time (2006 to 2010 or 5-6 generations) in the north coast tidewater goby (*Eucyclogobius newberryi*). The interesting conservation genetics question would involve studying metapopulation dynamics focusing on the potential for recolonization of extirpated populations. Previous investigations of the federally endangered tidewater goby showed that artificially fragmented populations within Humboldt Bay exhibited higher genetic differentiation and lower genetic diversity relative to naturally fragmented populations (McCraney et al. 2010). It was unclear whether these patterns were the result of multidecadal isolation and lack of migration among geographically separated populations or if periodic recolonization of fragmented habitats combined with founder effects (e.g., metapopulation dynamics) were responsible. Determining which process is operating can provide insights into the extent of migration between Humboldt Bay tidewater goby populations. Such information is key for management because it would indicate the likelihood of recolonization of extirpated populations.

**

Andrew P. Kinziger, Ph.D. Associate Professor and Curator of Fishes Department of Fisheries Biology Humboldt State University One Harpst Street Arcata CA 95521

707-826-3944

“Andrew P. Kinziger”
<Andrew.Kinziger@humboldt.edu>

IMPRS Berlin EvolutionaryGenomics

Reminder - application deadline in two weeks:

There are funded PhD positions in bioinformatics available at the International Max Planck Research School for Computational Biology and Scientific Computing in Berlin, Germany, for autumn 2011.

This is a structured 3-year PhD program aimed at students holding a master's or comparable degree in bioinformatics, scientific computing, mathematics, physics, computer science, or biology. Students with a degree in mathematics, computer science and physics should

have the relevant biological background, whereas students with a degree in biology are expected to show profound knowledge in mathematics and computer science. Exceptional students with a bachelor's degree and the necessary background in bioinformatics can apply to the preparatory program, which aims to lead the student to a PhD degree after a year of coursework and 3 years of PhD research.

Areas of research include evolutionary genomics, computational systems biology, proteomics, mathematical modeling. For further details please visit our website at www.imprs-cbsc.mpg.de. The IMPRS-CBSC is a joint program between the Max Planck Institute for Molecular Genetics, the Freie Universität Berlin and the CAS-MPG Partner Institute for Computational Biology, Shanghai. The program language is English.

Please apply via our website at www.imprs-cbsc.mpg.de/application.shtml before the 25th of February or contact Kirsten Kelleher (kelleher@molgen.mpg.de) for further information.

—

Kirsten Kelleher IMPRS-CBSC Coordinator Max Planck Institute for Molecular Genetics Ihnestrasse 73 14195 Berlin

Tel: +49 30 8413-1154 Fax: +49 30 8413-1152 Email: kelleher@molgen.mpg.de www.imprs-cbsc.mpg.de

kelleher@molgen.mpg.de

JagiellonianU EvolutionaryGenetics

Institute of Environmental Sciences at the Jagiellonian University, Kraków, Poland

The leading Polish institute in:

Behavioral ecology, Evolutionary genetics and life histories, Physiological and bioenergetics, Ecotoxicology and industrial pollutants, Ecosystem ecology, environmental education and management

Is opening applications for:

• 4-year interdisciplinary doctoral studies programme in ecology in English, with net-scholarships 2200 PLN per month, offering research in Poland and half-year placements in academic centres outside Poland and a choice of 4 out of 8 courses from different scientific disciplines conducted by eminent Polish and foreign specialists

Application deadline: 10 June 2011

Detailed information, containing the description of research projects proposed for PhD students, profile of the applicant and the application instructions are available at:

www.eko.uj.edu.pl/ecology – Launching interdisciplinary doctoral studies programme in ecology in English and increasing the didactic potential of the staff of the Institute of Environmental Sciences at the Jagiellonian University

Project co-financed by the European Union under the European Social Fund

Ecology <ecology@uj.edu.pl>

Liverpool StatGenetics

We are seeking to appoint an outstanding candidate for a PhD studentship position in Medical Entomology/ Statistical Genetics: Liverpool School of Tropical Medicine UK and Wellcome Trust Sanger Institute (UK). Enquiries should be directed toward the supervisors (contact details below) by February 25th.

Genome-wide association studies for insecticide resistance in the malaria vector *Anopheles gambiae*

Project Summary Resistance to the insecticides used for malaria control is widespread in the African malaria vector, *Anopheles gambiae*. The Donnelly group uses microarray and association-mapping technologies to detect genes that are associated with insecticide resistance and develops assays for detecting these resistance associated mutations for use in Africa. The student will be part of a collaboration with Professor Dominic Kwiatkowski of the Wellcome Trust Sanger Institute (www.sanger.ac.uk) to use next-generation sequencing technologies for genome-wide association studies (GWASs) of insecticide resistance in *An. gambiae*. The student will spend time at the LSTM, sites in sub-Saharan Africa and at the Sanger Institute.

Required Skills The student will undertake hypothesis-driven exploration of an existing data set and will thereby acquire a range of skills in bioinformatics and statistics. These skills will then be applied to a genome wide association study of an insecticide resistance phenotype. The only specific skills that the student would require is that they were numerate. All analytical and biological techniques would be acquired during the

project. The project would suit biology graduates in ecology, population genetics or evolutionary biology although graduates in applied mathematics and statistics/biostatistics are also encouraged to apply.

For further information, please contact the supervisors directly: Supervisors Primary supervisor: Dr Martin Donnelly < <http://www.lstmliverpool.ac.uk/research/-academic-groups/staff-profiles/martin-donnelly> > Secondary supervisor(s): Dr David Weetman < <http://www.lstmliverpool.ac.uk/research/academic-groups/staff-profiles/david-weetman> >, Professor Dominic Kwiatkowski < <http://www.sanger.ac.uk/-research/faculty/dkwiatkowski/> > (Wellcome Trust Sanger Institute)

<http://www.lstmliverpool.ac.uk/learning-teaching/-lstm-courses/research-degrees/studentships/-insecticide-resistance-in-anopheles-gambiae> Dr Martin James Donnelly, Reader in Vector Biology, Vector Group, Liverpool School of Tropical Medicine, Pembroke Place, Liverpool, L3 5QA UK Tel +44(0) 151 705 3296 Fax +44(0) 151 705 3369 Email m.j.donnelly@liv.ac.uk Web <http://-donnelly.openwetware.org/Home.html> Skype martin-donnelly

D.Weetman@liverpool.ac.uk

LundU AlgalPopulationDifferentiation

PhD Scholarship in Aquatic ecology

Dispersal barriers in an invasive bloom-forming alga

Job description The aim of the research project is to identify the barriers to dispersal in a microalgal species that forms blooms in freshwater lakes. This research has implications for the understanding of the dispersal of microalgae and microorganisms in general, as well as for predicting the occurrence of new algal blooms. The approach is to determine the importance of physical versus biological dispersal barriers by analyzing the genetic diversity patterns. The current hypothesis is that physical dispersal barriers are important for generating genetic differentiation. Instead, differentiation among microalgal populations might be explained by so called founder effects. Founder effects refer to the dominance of strains or species that arrive first to a new habitat. In laboratory and mesocosm experiments, priority effects and invasion sequence will be investigated

in the algal species *Gonyostomum semen*. The position will be based at the unit of Aquatic Ecology, Department of Biology, Lund University, in southern Sweden. The PhD project is a part of a larger project financed by Formas (The Swedish Research Council for Environment, Agricultural Sciences, and Spatial Planning), and will involve collaboration with other PhD students and a group at Gothenburg University (Ass. Prof. Anna Godhe). The project is suitable for applicants who would like to combine ecology and population genetics with molecular biological tools. The practical work will include PCR-based techniques, analyses of population genetic data, algal culturing, and microscopy. Experimental work will be performed both in the laboratory and in the field. In addition, the PhD student will be able to join the Research School in Genomic Ecology (GENECO) in Lund. This program will give access to a network of other PhD students and researchers in genomic ecology, annual meetings, workshops, travel grants to visit other institutions, as well as a career mentor.

Eligibility/Entry Requirements Requirements for this position are an MSc or comparable degree in ecology preferably with an aquatic and/or molecular ecological specialization. The successful candidate will have very good experience in molecular techniques. A driver's license is required, as is very good knowledge of written and spoken English.

For further information please contact: Karin Rengefors, Professor +46 46 2228427 karin.rengefors@limnol.lu.se

Type of employment: Limit of tenure, 18 months, after that doctoral employment Extent: 100 % Location: Department of Biology (Ecology), Lund First day of employment: 2011-03-01 or as soon as possible Official Records Number: NPA 2011/9

Basis of Assessment Regulations for employment as a postgraduate student can be found in the Swedish Statute Book (SFS 1998:80). Only those admitted to postgraduate studies can be appointed to such a position. When appointing applicants to such a position, first and foremost their ability to benefit from postgraduate studies must be taken into consideration. In addition to pursuing postgraduate studies, the doctoral student may also perform other duties, including research, teaching and administration, according to the specific regulations.

Application Procedure

Last Day of Applying 2011-02-06

Please apply on-line on: <http://admin.lu.se/o.o.i.s?id=22598&Dnr=375341&Type=E> Appointment Proce-

dure

Complete information about the application process can be found here: <http://www.naturvetenskap.lu.se/o.o.i.s/11729> Applications for advertised positions must be received by the date specified in the announcement. Lund University promotes an equal opportunities code. We encourage both men and women to apply for this position.

Applications will be destroyed or returned (upon request) six months after the decision of employment has become final. Applications from the employed and from those who appeal the decision will not be returned.

Karin Rengefors, PhD Professor in Limnology Director of the Graduate School in Genomic Ecology (GENECO) Limnology, Biology Department Lund University Ecology Building 22362 Lund, Sweden

e-mail: karin.rengefors@limnol.lu.se phone: +46462228427 URL: <http://www.limnol.lu.se/> New! International Society for the Study of Harmful Algae (ISSHA) <http://www.issha.org> Karin Rengefors <Karin.Rengefors@limnol.lu.se>

RoyalHollowayU London 2 LearningAdaptation

ROYAL HOLLOWAY

UNIVERSITY OF LONDON

PhD Studentship

School of Biological Sciences

Synergistic effects of parasites and pesticides on behaviour, learning and fitness in two key pollinators

Global declines in pollinators threaten a key ecosystem service and thus the viability of terrestrial ecosystems and agricultural productivity. Ongoing research suggests that single factors are not responsible for these declines, although parasites, pesticides, management practices and habitat loss have all been implicated. This project will combine the expertise of two groups, Dr Mark Brown's and Dr Nigel Raine's, in the School of Biological Science, Royal Holloway University of London, to determine the synergistic impacts of parasites and pesticides on behaviour, learning and fitness in two key pollinators - the bumble bee *Bombus terrestris* and the honey bee *Apis mellifera*.

In a world of agricultural intensification, understanding

how anthropogenic chemicals (pesticides, herbicides, miticides) impact ecosystem service providers is a central question in applied ecology and sustainability studies. Similarly, the emergence of new parasites and diseases, and the disruption of established host-parasite systems through land-use and climate change, makes understanding the impact of parasites on important host systems central to sustainable ecosystem management. However, whilst neither chemicals nor parasites live in a vacuum, almost nothing is known about their potential synergistic effects. The two major agricultural pollinators - *B. terrestris* and *A. mellifera* - are impacted by both parasites and pesticides. Here we will use a series of controlled laboratory and field experiments to determine the synergistic impact of these actors on key aspects of bee biology, including survival, learning, behaviour and fitness.

Applicants should be interested in, and have skills in, some or all of the following areas: animal behaviour, entomology, parasitology, physiology, pollinator biology.

Informal enquiries may be directed to Dr Mark Brown (mark.brown@rhul.ac.uk) and Dr Nigel Raine (nigel.raine@rhul.ac.uk).

For full details, visit <http://www.rhul.ac.uk/Biological-Sciences/Vacancies>. The application form <http://www.rhul.ac.uk/BioSci/Vacancies/SBSPHD2011.doc> should be submitted with a CV to tracey.jeffries@rhul.ac.uk by 17th March.

References

Alaux C et al. 2010 Interactions between *Nosema* microspores and a neonicotinoid weaken honey bees (*Apis mellifera*). *Environmental Microbiology* 12:774-782

Brown MJF et al. 2000 Condition-dependent expression of virulence in a trypanosome infecting bumble bees. *Oikos* 91:421-427

Gegear et al. 2006 Bumble-bee foragers infected by a gut parasite have an impaired ability to utilize floral information. *Proceedings of the Royal Society B* 273:1073-1078

Raine NE, Chittka L. 2008 The correlation of learning speed and natural foraging success in bumble-bees. *Proceedings of the Royal Society B* 275: 803-808

ROYAL HOLLOWAY

UNIVERSITY OF LONDON

PhD Studentship

School of Biological Sciences

The adaptive value of learning in different ecological

contexts

Despite much research into the mechanisms of learning we still know little about how cognitive traits might be adapted to different ecological conditions. Anticipated environmental change is almost certain to affect the structure and dynamics of pollination systems. A more complete understanding of pollinator behaviour means we will be better able to predict how the pollination of crops and wild flowers will be affected by environmental change.

Learning is an important way in which animals can respond to changes in their environment. Many pollinators are faced with a complex food-collecting environment: dozens of flower types which not only vary in colour, shape and scent, but also in the quantity and quality of pollen and nectar available. The rewards on offer can change very rapidly over the course of the day, so learning to modify flower choices could be advantageous. There is a range in learning performance among bee colonies with individuals in some colonies learning much faster than others. So what maintains this variability in cognitive abilities if faster learning performance is at a selective advantage?

This project uses the bumblebee (*Bombus terrestris*) as a model system. In the laboratory several generations of bees can be raised each year and this will form the basis of selection experiment to examine the heritability of learning performance. 'Fast-' and 'slow-' learning bumblebee colonies will be bred, and the foraging performance of these colonies will then be tested in a range of habitats to assess the ecological conditions to which cognitive behavioural phenotypes are best adapted. This project will also examine how variation in learning

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TromsøU Museum Biosystematics

<http://www.jobbnorge.no/job.aspx?jobid=72709> Research Fellow in biosystematics at Tromsø University Museum

Application deadline: 17 March 2011 The following reference number must be quoted in your application:

2011/457

The University of TromsÅ has a research fellow position in biosystematics (botany) vacant from 1st of July 2011 for applicants who would like to complete a PhD degree.

The period of appointment is four years.

For further information, please contact project leaders Inger Greve Alsos, e-mail: inger.g.alsos@uit.no<<mailto:inger.g.alsos@uit.no>> or TorbjÅrn Alm, e-mail: torbjorn.alm@uit.no<<mailto:torbjorn.alm@uit.no>> or head of Department of Natural Sciences: Karl Frafjord, e-mail: karl.frafjord@uit.no<<mailto:karl.frafjord@uit.no>>, phone + 47 77 64 50 00.

The position is connected to the Department of Natural Sciences, TromsÅ University Museum, and the successful applicant will be enrolled in the PhD programme of the Faculty of Biosciences, Fisheries and Economics at the University of TromsÅ. The Department of Natural Sciences presently employs 25 staff members, including 10 permanent scientific positions and 5 PhD students. The department has large scientific collections, documenting more than 130 years of research in North Norway and other northern regions. The research at the department covers both taxonomy and ecology, and our molecular laboratory is used for studies in taxonomy, phylogeography, and conservation genetics of various organisms including fungi, plants and animals.

The PhD position is within the field of conservation genetics and taxonomy of vascular plant species. Potential research topics are taxonomy of poorly separated sister species or complicated species complexes, genetic and morphological distinctiveness of disjunct populations, conservation genetics of rare or disjunct species, and correlation between levels of genetic variation and viability of populations. The research group has long experience in taxonomy and ecology of vascular plant species growing in northern Norway and Svalbard, and thus the PhD study should focus on species occurring within these areas. Examples are the rare *Stellaria hebecalyx* and *S. pojoenis*, or the extremely disjunct *Lysiella oligantha* and *Trisetum alpestre*.

The successful applicant must document knowledge in botany at Master's level. Furthermore, the successful applicant must fulfill the requirements for admission to the faculty's PhD programme, cf. Å§6 of Regulations for the degree of Philosophiae Doctor (PhD) at The University of TromsÅ, English translation and the faculty's supplementary regulations.

Applicants must have a good command of English and

preferable also Norwegian. Skills in Russian are of advantage as part of the field work may take place in Russia.

The normal period of appointment is four years. The PhD study is standardized to three years. The fourth year consists of teaching or other duties for the university, organized according to a distribution formula of 25 % per year in agreement with the Head of Department of Natural Sciences, TromsÅ Museum, cf. Directive for duties for research fellows (in Norwegian only)

A shorter period of appointment may be given if the research fellow has already completed parts of his/her researcher's education, or when previous appointments to educational positions (research fellow, research assistant or equivalent) are counted as part of the duration of the research fellowship, so that the combined duration of the researcher's education is three years.

The remuneration is in accordance with the State wage scale code 1017. A compulsory contribution of 2 % is made to the Norwegian State Pension Fund.

For applications for appointment, an application for admission to the PhD study must be enclosed; application form in English.

A two pages description outlining the academic basis of the doctoral degree project must be included with the application.

Within three months after commencement at the latest a final plan for the researcher education must be approved and regulated by contract. The plan shall also state who is responsible for providing academic supervision. Admission to the doctoral degree programme is a prerequisite for commencement as a research fellow. If an admission contract has not been signed within the deadline, as stated in the work contract, the employer may cancel the work contract, cf. Å§1-3 (8) in Regulations concerning terms and conditions of employment for the posts of postdoktor (post-doctoral research fellow), stipendiat (research fellow), vitenskapelig assistent (research assistant) and spesialistkandidat (resident) - (in Norwegian): <http://www.lovddata.no/for-sf/kd/kd-20060131-0102.html> TromsÅ Museum is the oldest scientific institution in northern Norway,

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UCanterbury EvolutionBirdOdours

Scholarships for Graduate Studies at School of Biological Sciences, University of Canterbury, Christchurch, New Zealand

Topic: Predation risk and the evolution of odours in island birds

Two fully funded Ph.D. scholarships are available to study the evolution of odours in island birds and role these may play in increasing predation risk from introduced mammalian predators.

Background to project: Some New Zealand birds appear to have strong odours. For example, even to the insensitive human nose, kiwi smell like ammonia, while the odour of the kakapo has been likened to a dusty violin case. Strong odours are unusual in birds, but common in mammals, which use odours for communication and locating food. Preliminary work has revealed that strong odours may be widespread among New Zealand birds, and that these odours arise from the preen waxes produced in the uropygial gland. Preen waxes function to maintain feathers, but may also attract predators that use olfaction to locate prey. The first objective of this project is to determine if there are differences in the composition of preen waxes between island and continental birds and if these are the result of their differing evolutionary histories with predatory mammals. The New Zealand area provides an ideal system for studying odours and predation risk as the preen wax composition can be compared across a number of island birds that evolved without mammalian predators and their close phylogenetic relatives that co-evolved with predators in continental Australia. The second objective of this project is to then test whether differences in odours now put island birds at greater risk from introduced mammalian predators. This study will not only increase our understanding of the evolution and function of odours in birds, but also determine whether these odours are now playing a previously unrecognised role in the decline of island birds.

1) Ph.D. Project 1: Does the composition of preen wax and the ontogeny of preen wax production vary with predation risk? Predation is the greatest source of nest failure for continental birds, and it is not unusual for 50-80% of nests to be lost to predators. Most predation is due to mammals which locate nests through the odours of eggs or nestlings. In contrast, birds on many oceanic islands, including New Zealand, evolved in the absence of predatory mammals. This difference in risk should

select for reduced odours in continental species, in order to camouflage nests from predators locating prey by olfaction. In this part of the project, the candidate will test this hypothesis by comparing the composition of preen waxes of a variety of island and continental birds. If predation has shaped the evolution of avian odours, then the preen waxes of island species should be relatively more volatile than those of their closest continental relatives. Differences in the ontogeny of preen wax, and the seasonal pattern of preen wax production are also expected to differ between island and continental species. This project will involve field work in New Zealand, Australia and several offshore islands.

2) Ph.D. Project 2: Do the odours of island birds increase their risk of predation from exotic mammalian predators? The vulnerability of island birds to exotic predators (e.g. rats, feral cats) is well known and has been attributed to their behavioural naivety towards novel predators and life histories that limit their ability to tolerate high predation rates. As island birds also appear to have more conspicuous odours than continental birds that co-evolved with mammals, the production of more volatile preen waxes may also increase the probability that island birds and their nests are detected by exotic mammalian predators. In this part of this study, the candidate will test if the odour of island birds and their nests increases the risk of predation by exotic mammalian predators using a variety of field and lab-based studies. Field work is required in New Zealand, Australia and offshore islands.

Applicants for either position require either a B.Sc. Honours or M.Sc. in Biology. Candidates must be prepared to work in remote field locations and travel for several months at a time. Scholarship includes stipend of \$NZ 25,000 per year and cost of tuition fees. Duration of scholarship is 3 years. Non-residents of New Zealand will be required to obtain a student visa for the period of study.

Application deadline: 1 March 2011 Start date: by negotiation but before 1 June 2011

To apply: Please send C.V. and cover letter to Dr. James Briskie (address above) or by email (Jim.Briskie@canterbury.ac.nz).

This email may be confidential and subject to legal privilege, it may not reflect the views of the University of Canterbury, and it is not guaranteed to be virus free. If you are not an intended recipient, please notify the sender immediately and erase all copies of the message and any attachments.

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UEdinburgh Plant Taxonomy

MSc Degree/Postgraduate Diploma in the Biodiversity and Taxonomy of Plants

Royal Botanic Gardens Edinburgh/ University of Edinburgh

Programme Philosophy The MSc in Biodiversity and Taxonomy of Plants was established by the University of Edinburgh and the Royal Botanic Garden Edinburgh (RBGE) to address the growing worldwide demand for trained plant taxonomists and whole-plant scientists. A detailed knowledge of plants and habitats is fundamental to their effective conservation. To communicate such knowledge accurately and effectively, training is required in plant taxonomy - "the discipline devoted to plant diversity and evolution, relationships, and nomenclature. The MSc is perfect for those wishing to develop a career in many areas of plant science:

Survey and conservation work in threatened ecosystems
Assessment of plant resources and genetic diversity
Taxonomic research
Management of institutes and curation of collections
A stepping stone to PhD research and academic careers

Edinburgh is a unique place to study plant taxonomy and diversity. The programme and students benefit widely from a close partnership between RBGE and the University of Edinburgh (UoE). RBGE has one of the worlds best living collections (15,000 species across our four specialist gardens - "5% of world species), an herbarium of three million specimens and one of the UKs most comprehensive botanical libraries. The School of Biological Sciences at UoE is a centre of excellence for research in Plant Sciences and Evolutionary Biology. Recognised experts from RBGE, UoE, and from different institutions in the UK deliver lectures across the whole spectrum of plant diversity. Most course work is based at RBGE, close to major collections of plants, but students have full access to the extensive learning facilities of the university.

Aims and Scope The MSc provides biologists, conservationists, horticulturists and ecologists with a wide knowledge of plant biodiversity, as well as a thorough understanding of traditional and modern approaches to

pure and applied taxonomy. Apart from learning about the latest research techniques for classification, students should acquire a broad knowledge of plant structure, ecology, and identification.

Programme Structure This is an intensive twelve-month programme and involves lectures, practicals, workshops and essay writing, with examinations at the end of the first and second semesters. The course starts in September of each year and the application deadline is normally 31 March.

Topics covered include: Functions and philosophy of taxonomy
Evolution and biodiversity of the major plant groups, fungi and lichens
Plant geography
Ecology of plants and ecosystems
Conservation and sustainability
Production and use of floras and monographs
Biodiversity databases
Phylogenetic analysis
Population and conservation genetics
Tropical field course, plant collecting and ecology
Curation of living collections, herbaria and libraries
Plant morphology, anatomy and development
Cytotaxonomy
Molecular systematics

Fieldwork and visits to other institutes are an integral part of the course. There is a two-week field course to a tropical country in which students are taught field collection and identification of tropical plants ecological survey techniques. The summer is devoted to four months of a major scientific research project of the students choice or a topic proposed by a supervisor. These research projects link in directly with active research programmes at RBGE.

Entry Requirements Applicants should ideally hold a university degree, or its equivalent, in a biological, horticultural, or environmental science, and above all have a genuine interest in plants. Relevant work experience is desirable but not required. Evidence of proficiency in English must be provided if this is not an applicants first language.

Funding The University of Edinburgh provides a limited number of studentships. Other international funding bodies have supported overseas students in the past. More information can be obtained in the course handbook.

Further Information For further details on the programme, including a course handbook please visit the RBGE website: <http://www.rbge.org.uk/-msctaxonomy> You can also contact the Course director or Education Department at RBGE, or the Postgraduate Secretary of the University of Edinburgh:

MSc course Director, Dr Louis Ronse De Craene
Royal Botanic Garden Edinburgh
Tel +44 (0)131 248 2804
Email: lronsedecraene@rbge.ac.uk
Postgraduate Secretary, The University of Edinburgh School of Biologi-

cal Sciences, Darwin Building The Kings Buildings, Edinburgh EH9 3JR, UK Tel +44 (0)131 650 7366 Email: icmbpg@ed.ac.uk

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UHalle BeeParasiteInteractions

Two PhD positions on honey bee-parasite interactions and host bee behaviour

Two PhD students are sought for a project on the ecology of honey bee V parasite interactions within the labs of Robin Moritz and Robert Paxton at the University of Halle, Germany. The goals of the research are to understand interactions among bee parasites and their impact on honey bee behaviour. The doctoral students will contribute to the recently funded BML (German Federal Ministry of Agriculture and Food) project FIT BEE (collaborating partners are spread across Germans many state bee institutes) that explores recent issues in honey bee health in relation to bee management. Research will involve lab and field-based experiments as well as molecular genetic analysis of honey bees and their pathogens. We seek highly motivated individuals with an interest in host-parasite interactions as well as molecular genetic skills.

The working language of the labs is English, though knowledge of German or willingness to learn German is of advantage. The two groups of Moritz and Paxton make for a strong profile in bee biology and genetics at the University of Halle (<http://www.mol-ecol.uni-halle.de/>). The positions are available for 3 years and we aim for a start date in spring 2011. Halle is a delightful, historical city approximately 1.5 hours SW of Berlin. The salary is on the standard German PhD scale E13 (half), which translates to approximately Euro 17,500 per annum dependent on experience.

Further details of the position can be obtained from Robert Paxton (robert.paxton@zoologie.uni-halle.de) or Robin Moritz (robin.moritz@zoologie.uni-halle.de).

Please send applications to posts D 33/2011 - D 34/2011 as a single pdf file to include a cv, a statement of research interests and goals (maximum 1 page), and contact details of two referees, to

petra.weber@zoologie.uni-halle.de by 24th February 2011.

Robert Paxton <robert.paxton@zoologie.uni-halle.de>

UHelsinki SocialEvolution

PhD position, 4 years: Genomic consequences of low relatedness in ant societies University of Helsinki, Department of Biosciences

The differentiation into queen and worker castes is the foundation of advanced insect sociality, and is based on differences in gene expression between the castes. Caste specific expression also affects how natural selection works on the genes. Because workers do not reproduce themselves, selection on genes expressed in workers depends on the relatedness between workers and the queens they help. In ants, relatedness between queens and workers varies widely, but little is known about how this affects selection on genes based on their expression pattern.

In order to study these questions, the project 'Genomic consequences of low relatedness in ant societies', funded by the Academy of Finland and carried out at the University of Helsinki, Finland, is looking for a highly motivated PhD student. The ideal candidate has an MSc in biological sciences, with experience of molecular genetics lab work and analyses of gene sequence data), ability and desire to acquire new skills, enthusiasm for research and applying genetical methods to evolutionary questions, and an ability to work independently as well as in a team.

The PhD student is expected to analyse sequence variation and signatures of selection on genes with caste specific expression patterns, and set the results in a comparative framework. The main focus will be on comparing selection in uniclonal ants (such as the Argentine ant and uniclonal *Formica* wood ants) that have extremely low relatedness societies with their non-uniclonal relatives. In addition to this main approach, the project can be expanded to include other directions, depending on the skills and interests of the student, the progress of the project and the increasing availability of genomic resources in ants.

The position is funded for four years, with a salary according to the University of Helsinki salary system (ca. 2000 €-permonth). The starting date is flexible, but June -

July2011ispreferred.

The PhD thesis will be supervised by Dr. Heikki Helanterä and Prof. Pekka Pamilo, and carried out in close collaboration with The Centre for Social Evolution at the University of Copenhagen (Prof. Jacobus J. (Koos) Boomsma, Dr. Jes S. Pedersen, Dr. Morten SchiÅtt). The research group of Dr. Heikki Helanterä is part of the group studying social evolution in ants at the Department of Biosciences at the University of Helsinki (Prof. Lotta Sundström, Prof. Pekka Pamilo, Dr. Perttu Seppä and others).

Send your application to heikki.helantera@helsinki.fi. Attach (as pdfäs) a CV, publication record, contact details of two references, and a two page (max) description of your research interests and why you would be a suitable candidate for the project. Screening of the applications will start on 1st of March 2011, and will continue until a suitable candidate is found.

More info: heikki.helantera@helsinki.fi <http://www.helsinki.fi/science/ants/Heikki.htm> <http://www.helsinki.fi/science/ants/>

heikki.helantera@helsinki.fi

ULausanne ModelingSpeciation

PhD position in mathematical modeling of speciation

A PhD position is open for a collaborative project between the labs of Prof. Marc Robinson-Rechavi (Evolutionary Bioinformatics) and Dr. Nicolas Salamin (Phyloinformatics). The project concerns the mathematical modeling of speciation and extinction rates of species. The model will be applied to phylogenetic and genomic data, and linked to fossil data, in collaboration with Prof. Phil Donoghue (University of Bristol). The student will participate to research projects on plant and vertebrate evolution.

The project is expected to shed light on the impact of genome evolution on the diversity of species, with implications for our understanding of the history of life, as well as for conservation biology. The student will receive training in bioinformatics / biomathematics and in evolutionary biology.

We are looking for an autonomous and ambitious student, with a strong mathematical background, and knowledge of biology. Previous experience with evolutionary biology is a plus but not a requirement. En-

thusiasm for inter- disciplinary work is necessary: the student will need to interact productively with evolutionary biologists, genome biologists, computer scientists, and paleontologists, and read the corresponding range of scientific literature.

Please send a CV and contact information of two references to: marc.robinson-rechavi@unil.ch; nicolas.salamin@unil.ch

Websites for additional information: <http://bioinfo.unil.ch/> <http://www.unil.ch/phylo> –

Nicolas Salamin Department of Ecology and Evolution University of Lausanne 1015 Lausanne Switzerland

tel: +41 21 692 4270 fax: +41 21 692 4165 <http://www.unil.ch/phylo> Swiss Institute of Bioinformatics http://www.isb-sib.ch/groups/Computational_Phylogenetics.htm nicolas.salamin@unil.ch

ULausanne PopulationGenomics

PhD position in population genomics of adaptation to nutritional stress in *Drosophila* University of Lausanne, Switzerland

We are looking for an autonomous and motivated PhD student for a project focusing on the genomic bases of tolerance to chronic larval malnutrition in *Drosophila*. The project will use Illumina cDNA sequencing (RNAseq) to study changes in gene expression profiles, coding polymorphisms, and splicing variants resulting from >100 generations of experimental evolution under nutritional stress, aiming to identify candidate molecular mechanisms of larval malnutrition tolerance. It has been increasingly recognized that responses to nutritional stress during development may have far-reaching consequences for adult life, including the rate of aging. At the same time, mechanisms of responses to nutritional environment seem highly conserved. Thus understanding how evolution shapes these responses is likely to throw light on early-life determinants of human aging and metabolic disease.

The PhD student will be co-supervised by Tad Kawecki (Department of Ecology and Evolution, http://www.unil.ch/dee/page47578_en.html) and Ioannis Xenarios (SIB Swiss Institute of Bioinformatics, Department of Integrative Genomics, <http://www.unil.ch/cig/page16826.html>) at the University of Lausanne, Switzerland. The candidates should have a background

in biology and strong computational skills (bioinformatics, statistics, and/or computer programming). The project will involve laboratory experiments (fly breeding, RNA extraction), but the main workload will be in data analysis and interpretation.

The position will be available from late spring 2010; a later starting date could be negotiated. It is offered in the framework of a ProDoc program in Population Genomics and the students will have an opportunity to profit from specialized courses in that area. The candidates are required to have completed a Masters degree before the beginning of the PhD. Funding is available for three years (an extension is possible but not guaranteed) with a salary of CHF 40800 per year plus a possible supplement for contribution to teaching. English is the language of the lab, and pre-existing knowledge of French is not required; however, learning some French would make life in Lausanne much easier.

Lausanne is a medium-sized city on the shores of Lake Geneva, surrounded by a wine growing region and within one hour of the Alps. It offers a great variety of cultural, recreational and outdoor opportunities.

To apply, send a single pdf or rtf file with a motivation letter, cv, description of your research experience and interest, and names of 2-3 referees to tadeusz.kawecki@unil.ch, putting "PhD position" in the subject line. The review of applications will start on March 15, 2011 and will continue until suitable candidates are found.

Tad Kawecki

– Tadeusz J. Kawecki Associate Professor Department of Ecology and Evolution University of Lausanne Biopôle CH 1015 Lausanne, Switzerland

tadeusz.kawecki@unil.ch

logical organization (physiology, behavior, population ecology). The types of questions that our lab is interested in are: (1) what are the effects of parasites on hosts? (2) Why don't hosts evolve resistance to parasites (trade-offs between anti-parasite defenses and other life history traits)? (3) What factors determine parasite virulence? The prospective PhD student is welcome to come up with his or her own thesis project. The University of Neuchâtel has a strong group of parasitologists that study host-vector-pathogen interactions across a wide range of biological organization (molecular biology, physiology, and evolution and ecology).

Job requirements: The position requires an independent, highly motivated, enthusiastic, and scientifically curious individual with a strong background in ecology, evolutionary biology, or related fields. Molecular techniques, field experience, and statistical data analysis skills are useful. The applicant must have a Master's degree. The position requires teaching of undergraduate biology labs in French so language skills are useful.

Start date: The position is available on June 1, 2011. Salary is determined by the Institute of Biology.

Application requirements: Formal applications should be in English and include: (1) a 1-2 page cover letter indicating research interests, (2) your CV (including a list of publications), and (3) two letters of reference. Informal enquiries and formal can be submitted by email to: maarten.voordouw@unine.ch

Maarten Voordouw Institute of Biology University of Neuchâtel Rue Emile-Argand 11 CH-2000, Neuchâtel Switzerland Tel. 0041 32 718 3114

The website is still a work in progress www2.unine.ch/Jahia/site/labpar/op/edit/pid/15585

Maarten Voordouw <mjvoordouw@gmail.com>

UNeuchatel LymeDiseaseEvolution

2

PhD position in Ecology & Evolution of Lyme disease Department of Biology, University of Neuchâtel

One PhD position is available for research on the ecology and evolution of Lyme disease, which is caused by the bacteria, *Borrelia burgdorferi*, and is transmitted among vertebrate hosts by *Ixodes* ticks. Our lab is interested in studying the interactions between the three players (pathogen, tick, host) at various levels of bio-

UNorthCarolina Wilmington PopulationGenetics

PhD assistantship - marine population genetics We seek a PhD student in marine population genetics. The goals of the project are to combine population genetic, life history, morphological, and demographic data to characterize stock structure of southern flounder in North Carolina and US South Atlantic waters. The project is management-oriented and is funded by the North Carolina Marine Resources Fund, yet the ideal candidate would have general interests in evolution and spatial

analysis of marine populations.

The student is expected to focus on molecular genetic aspects of the project, but also to integrate information coming from the life history, morphological, and demographic components of the study. We are particularly interested in exploring spatially explicit “seascape genetic” analyses. The strongest candidate would have a background in quantitative analysis in evolution and/or ecology. Specific experience in landscape genetic or population genetic analysis would be a plus, but is not mandatory. Also a plus is some background in technical aspects of the molecular biology, which in this case will include mitochondrial DNA sequencing and AFLP DNA fingerprinting. The ideal student will have completed an MS degree in evolutionary biology, marine ecology, fisheries, or a related field and should be able to demonstrate strong academic ability, but exceptional candidates possessing only a BS degree will also be considered.

The project represents a collaborative effort by UNCW researchers Fred Scharf (fisheries ecology) and Michael McCartney (molecular ecology), and NC Biologist Chris Batsavage. McCartney will serve as the major advisor for the student, but they will have the opportunity to collaborate and build relationships with multiple researchers from UNCW, NC Sea Grant, NCDMF, and NOAA.

Home department: Department of Biology and Marine Biology, University of North Carolina Wilmington, 601 South College Rd., Wilmington, NC 28403.

Start date: August 2011 Salary: Annual stipend of \$22,000 with full tuition support. Contact: Interested students should contact (via email) Michael McCartney (mccartneym@uncw.edu) or Fred Scharf (scharff@uncw.edu). Please include a recent CV and contact information for three references.

Michael A. McCartney Associate Professor Center for Marine Science UNC Wilmington 5600 Marvin Moss Lane Wilmington NC 28409 (910)962-2391 voice (910)962-2410 fax

“McCartney, Michael” <mccartneym@uncw.edu>

UOslo AvianEvolutionaryGenomics

Centre for Ecological and Evolutionary Synthesis (CEES) PhD Research Fellow in evolutionary biology, ref. no. 2011/2162

The CEES is a centre of excellence for integrative biological research and is well-funded. It provides a stimulating research environment, situated at the Department of Biology, with many young international and Norwegian scientists working on a variety of theoretical and empirical topics within ecology, evolution, population genetics, genomics, phylogenetics, molecular biology, and statistical methodology. The CEES is chaired by Nils Chr. Stenseth and currently employs 16 permanent employees, 43 postdocs/researchers, 32 PhD students and 30 MSc students. Information about the centre can be found at <http://www.cees.uio.no/> The PhD fellow will be part of a project funded by The Norwegian Research Council. The position as PhD is tentatively available from April 1st on the project “On the evolutionary genomics and behavioral ecology of homoploid hybrid speciation in Passer sparrows”.

The PhD position is for a period for 3 years.

Job Description We seek to employ a candidate on the project: “On the evolutionary genomics and behavioral ecology of homoploid hybrid speciation in Passer sparrows.” The successful candidate will work in a research team that works on evolutionary processes related to speciation. The project focuses on different species of sparrows and in particular the Italian sparrow (*Passer italiae*) that appears to be a stabilized hybrid form between the house sparrow (*P. domesticus*) and the Spanish sparrow (*P. hispaniolensis*). The project includes “comparative genomics using 454-technology” “analysis of genetic variation across transects through hybrid zones” “phylogeographic studies of the species complex” “association studies of traits affecting reproductive barriers using a candidate gene approach” “ecological and behavioural studies related to assortative mating in aviaries and in the field” “breeding experiments in aviaries to investigate the inheritance of mate preferences and potential genetic incompatibilities between the species.

The successful candidate will be involved in 3-4 of these subprojects pending on qualifications and interests. Requirements

We search for a candidate with a strong background in evolutionary biology. Experience with evolutionary genetic methods is required. Experience with evolutionary ecological or behavioural work on free-living or captive animals is a further asset. Applicants must hold a MSC-degree (or equivalent).

The purpose for the fellowship is research training leading to a successful completion of a PhD degree. The fellowship requires admission to the research training program at the Faculty of Mathematics and Natural Sciences. Appointment to a research fellowship is con-

ditional upon admission to the Faculty's research training program. An approved plan for the research training must be submitted no later than one month after taking up the position, and the admission approved within three months. C

A good command of English is required for all students attending the University of Oslo. International students who are not native speakers of English must document their proficiency in English.

Salary Pay Grade 48-56 (NOK 383 700 - 440 500 per year, depending on qualifications)

The application must include a cover letter including a statement of interest, summarizing the applicant's scientific work and interests and describing how she/he fits the requirements for the position, a CV including a list of published and unpublished works, transcripts of records, copies of certificates and grades from bachelor and master level, two letters from reference persons or names and addresses of two reference persons, and copies of relevant published papers. Applicants may be called in for an interview.

To apply for the position, please see <https://uio.easycruit.com/vacancy/application/-166821195605002bd72a9a6f572090fb/514022/-64421?iso=gb> Foreign applicants are advised to attach an explanation of their University's grading system. Please remember that all documents should be in English or a Scandinavian language.

In accordance with the University of Oslo's equal opportunities policy, we invite applications from all interested individuals regardless of gender or ethnicity.

UiO has an agreement for all employees aiming to secure rights to research results a.o.

Region: Oslo Job type: Contract Working hours: Full-time Working days: Day Application deadline: February 25th 2011 Location: Blindern, Oslo Reference number: 2011/2162 Home page: <http://www.matnat.uio.no>

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11 PhD AND POST-DOC POSITIONS IN EVOLUTIONARY BIOLOGY AND GENOMICS AT THE EVOLUTIONARY BIOLOGY CENTRE, UPPSALA UNIVERSITY

A Centre of Excellence in the interface of evolutionary biology and genomics has been established at the Dept of Evolutionary Biology of the Evolutionary Biology Centre (EBC) of Uppsala University. The environment consists of several relatively young research groups (Urban Friberg, Anders Gotherstrom, Simone Immler, Mattias Jakobsson Hanna Johannesson, Tanja Slotte and Jochen Wolf) with Hans Ellegren being Head of the unit. Currently, there are about 20 PhD students, 15 post-docs and some bioinformaticians working within these groups, with the great majority having a background from international universities. Thanks to a number of competitive grants recently obtained, the environment will now significantly expand by recruiting several new PhD students and post-docs.

An overview of the research activities in the environment can be found at our web pages (<http://www.ebc.uu.se/Research/IEG/evbiol/>). A common theme is that we address key questions in evolutionary biology, like speciation, local adaptation, life history evolution, and molecular evolution, using genomic approaches. Study organisms include natural bird and plant populations, Neurospora, Drosophila, zebra fish, domestic animals and humans. We have tight connections with several other research programs at the Evolutionary Biology Centre (see <http://www.ebc.uu.se/Research/IEG/> and a centre-wide graduate school "The genomics of phenotypic diversity in natural populations" (<http://www.ebc.uu.se/education/postgrad-gradschool/>) is organized from here.

Below are brief descriptions of the positions currently open. Further details about each of these, including necessary qualifications, are available at http://www.ebc.uu.se/Research/IEG/evbiol/-open_positions/ or can be obtained from the named group leader. Informal inquiries and applications should be sent to the respective supervisor. Common to all positions is that we ask applicants to provide a CV, a statement of research interests and the name and contact details of at least two references. The positions remain open until filled.

1. PhD position: Haploid selection in animals Sexual reproduction in eukaryotic organisms entails the existence of two sexes (males and females) and two life phases (haploid and diploid). Selection acting differently in the two sexes and the two phases causes conflicts, which affect evolutionary processes. This PhD project aims to address questions about the causes and

consequences of sexual selection across ploidy levels in animals. Experimental work using the zebrafish *Danio rerio* as a model system will bring answers to these questions. For more information please see our web pages or contact Simone Immler (Simone.Immler@ebc.uu.se).

2. PhD position: Natural selection on gene regulation
Changes in gene regulation have long been hypothesized to underlie adaptive phenotypic evolution. In this project, we aim to test this hypothesis and quantify the long-term impact of selection on regulatory sequences. The project will involve the use of genomic methods to study sequence and gene expression variation in the emerging plant model system *Capsella*. For more information please see our web pages or contact Tanja Slotte (Tanja.Slotte@ebc.uu.se).

3. PhD position: Whole-genome analysis of microsatellite evolution
Next-generation sequencing (NGS) allows gathering a wealth of information on microsatellite variability both within and between species. Using recently assembled whole-genome sequences from multiple avian and mammalian species, this project aims to increase our understanding of the evolution of microsatellites and polymorphism at these loci. Moreover, this project also aims at using NGS microsatellite data to identify genomic regions subject to strong selective sweeps in natural populations of ecological model organisms, using microsatellites. For more information please see our web pages or contact Hans Ellegren (Hans.Ellegren@ebc.uu.se).

4. PhD position: Speciation genomics in a famous avian hybrid zone
The hybrid zone between carrion and hooded crows (*Corvus [corone] corone / cornix*) is a text book example of incipient speciation that is well characterized from an ecological and behavioural perspective. We investigate its genetic architecture with a set of genomic tools currently including genome assembly, re-sequencing of several European populations and RNAseq-based transcriptome analyses. For more information please see our web pages or contact Jochen Wolf (Jochen.Wolf@ebc.uu.se).

5. PhD position: Sex differences in aging



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UPretoria Evolutionary Biol

Two positions available at the Forestry and Agricultural Biotechnology Institute (FABI), in association with the Department of Zoology and Entomology, at the University of Pretoria. FABI is a world-class, internationally recognized institute dedicated to understanding and promoting health in native and plantation forests, with a strong focus on insect and fungal ecology, genetics/genomics, systematics and biological control (<http://www.fabinet.up.ac.za/>). Specific projects can be tailored to student interests and background, but primary focal areas include: 1) understanding population feedbacks between the introduced pine woodwasp (*Sirex noctilio*) and various native and introduced organisms (including but not limited to: pine weevils, bark beetles, fungi, and baboons), and 2) assessing ecological and evolutionary processes driving insect community overlap between native and exotic trees (e.g. spillover of introduced insects from exotic hosts onto native trees, and host expansion/switching of native fauna onto exotic plantation species). More information is available upon request. Both projects are funded, and include a student bursary to cover University fees and living expenses.

Pretoria, the administrative capital of South Africa, is a modern city situated in the northern center of the country in the highveld (high elevation savanna). The area is has a moderate climate with wet summers and dry winters, is culturally diverse with 11 official languages (English is the language of choice at FABI, where students come from over 40 countries). The University is located within driving distance of many amazing locations including the Drakensburg Mountains and Kruger National Park, with hiking and biking (together with giraffe, wildebeest and all manner of fascinating biodiversity) within the city limits.

PhD students will typically have completed an MSc degree (except under special circumstances). An interest in insect, plant and/or fungal ecology and evolution is essential, as is a working facility with English. Students with a drivers license and field/lab experience preferred. Please send a CV, statement of interest and a short writing sample to Dr. Jeff Garnas (jeff.garnas@fabi.up.ac.za).

Jeff Garnas <jeff.garnas@fabi.up.ac.za>

USheffield Evolutionary Theory Disease

Dear colleagues, please consider disseminating details on this PhD position among your final-year undergraduates. Applications from UK home-students and EU citizens are welcome.

Best wishes, James Marshall

PhD in Evolutionary Theory and Disease

This PhD will investigate evolutionary aspects of disease. Many diseases have at their root a failure of one level of biological complexity to exert sufficient control over a lower level; examples include cancer (failure of the body to control replication of cell-lines) and certain genetics disorders such as Down's syndrome (failure to ensure fair chromosomal segregation during gamete formation). Still other diseases are caused by pathogens that must cooperate in order to achieve and sustain the infection of a host; one well-known example of this is acquired antibiotic resistance in some bacterial strains. Over the past 50 years theory to describe the evolution of social behaviour between genetic relatives, and across multiple levels, has been developed. The theory, however, is typically abstract, and aims to determine conditions under which altruism will or will not succeed due to natural selection. The challenge of this project will be to translate such theory and consider its potential application to understanding diseases. New theory on evolution in finite populations may also need to be applied or developed.

This project is deliberately underspecified, and the successful candidate will be an exceptional individual, who will have great freedom to pursue directions that interest them and seek out novel research collaborations. They will have a background in a numerate discipline such as mathematics, computer science, or physics, ideally with some knowledge of probability, statistics and stochastic modelling. A demonstrated interest in biology and medicine is a definite advantage. They will become part of the newly established Behavioural and Evolutionary Theory Lab at the University of Sheffield, Department of Computer Science, under the direction of Dr James Marshall.

About the Behavioural and Evolutionary Theory Lab

The Behavioural and Evolutionary Theory Lab is an interdisciplinary collection of individuals interested in

how and why behaviours evolve. We are interested in behaviours and behavioural mechanisms, and their evolutionary function. We apply a range of theoretical approaches, from mathematics and statistics, decision theory, computer science, and physics. Particular topics of interest are currently the evolution of social behaviour, such as altruism and cooperation, and optimal decision-making mechanisms in groups, such as social insects, and in individuals. The Lab is part of the Department of Computer Science, University of Sheffield, and is physically based in the interdisciplinary Kroto Research Institute.

Applications are invited from UK home students and EU citizens. Fees and a stipend will be paid for the duration of the studentship. Apply online or contact Dr Marshall if you require further information. Closing date: Feb 27th.

Bibliography

- [1] Burt, A. and Trivers, R. (2006) *Genes in Conflict: the Biology of Selfish Genetic Elements*. Harvard University Press. [2] Foster, K.R. (2005) Hamiltonian medicine: why the social lives of pathogens matter. 308, 1269-1270. [3] Merlo et al. (2006) Cancer as an evolutionary and ecological process. *Nature Reviews Cancer* 6, 924-935. [4] Okasha, S. (2006) *Evolution and the Levels of Selection*. Oxford University Press.

James A. R. Marshall Department of Computer Science University of Sheffield <http://staffwww.dcs.shef.ac.uk/people/J.Marshall/> James Marshall <James.Marshall@sheffield.ac.uk>

UTasmania Avian Conservation Genetics

Scholarship for MSc/PhD study at the School of Zoology, University of Tasmania, Hobart, Australia

Topic: Conservation genetics of the Providence Petrel

A fully funded research project with scholarship is available for immediate start.

Background to project: Petrels are often important seabird species with respect to nutrient inputs to oceanic islands, where they commonly nest. However, on Norfolk Island (southwest Pacific) a huge colony of Providence Petrels (>1 million breeding pairs) was hunted to extinction by humans during the early 1800's. In the following 200 years the vegetation of Norfolk Is-

land has declined, with ensuing problems of erosion, and degradation of habitat for other imperiled taxa such as the endemic Norfolk parakeet. For these reasons, managers seek to re-establish a population of Providence Petrel on Norfolk Island by releasing individuals sourced from Lord Howe Island (over 1000 km away). Similar colony re-establishments have already been performed successfully for petrel species on other islands. However, in this case an important conservation implication is the fate of a small Providence Petrel colony at Phillip Island (~30 individuals, only 4 km from Norfolk... not the "Phillip Island" near Melbourne). Individuals at Phillip Island exhibit different behaviour from those at Lord Howe (e.g. time of return to colony), and could represent the sole-perilously small- population of a distinct species.

The aim of this study is to assess the distinctiveness of Lord Howe and Phillip Island Providence Petrels. The project will use a variety of genetic techniques (nuclear introns, microsatellites, mitochondrial DNA) to determine whether the Phillip Island colony may require consideration before proceeding with re-establishing a Norfolk Island colony. Molecular analysis will also be performed on paleontological Norfolk Island material, to assess the genetic distinctiveness of this now extinct colony. Comparisons of morphology and call dialect will also be performed. The breeding season occurs in May, and a field trip to Phillip Island to collect blood samples in 2011 is a possibility if a student can enroll in time. The scope of the project can be varied to represent either an MSc or PhD study.

The project is based at the University of Tasmania (<http://www.utas.edu.au>), one of Australia's oldest universities, with great opportunities for intellectual development and also outdoor recreation. The Central Science Laboratory contains a large, well-equipped molecular genetics facility. Work on the paleontological material will be conducted with Dr. Trevor Worthy (University of New South Wales) and Dr Jeremy Austin at the Australian Centre for Ancient DNA (<http://www.adelaide.edu.au/acad/>). Dr David Priddel and Nicholas Carlile from the NSW Department of Environment and Climate Change will oversee fieldwork.

Applicants require a BSc with a substantial research component to part of their study (the latter may have been achieved by different means depending on the country of study; within Australia this typically represents a BSc Honours degree). Demonstrated expertise with molecular laboratory procedures is desirable (DNA extraction, PCR, DNA sequencing, microsatellite genotyping) but not essential, as are interests in conservation biology, molecular ecology, and species delineation.

The Scholarship comprises \$AUS 22,500 per year (2 years for MSc; 3 years for PhD with a possible 6 month extension). Student fees will be required if the you are not an Australian or New Zealand citizen, or an Australian permanent resident (\$AUS 18,400 per year for MSc; \$AUS 19,376 per year for PhD), unless you are able to attract your own scholarship, in which case the fees will be waived. Students from a non-English speaking background will require proof of English-language ability (e.g. an IELTS of 6.5).

To apply: Please send a cover letter expressing your interest (in the form of an e-mail), contact details of at least two referees, and an curriculum vitae to Dr. Chris Burridge (chris.burridge@utas.edu.au). Applications remain open until the position is filled.

Chris Burridge School of Zoology University of Tasmania Private Bag 5 Hobart, Tasmania 7001 Australia

e-mail: chris.burridge@utas.edu.au phone: +61 3 6226 7653 fax: +61 3 6226 2745 web: <http://fcms.its.utas.edu.au/-scieng/zoo/pagedetails.asp?lpersonId=5232>
Chris.Burridge@utas.edu.au

U**Vienna CompBiol ConserGenetics**

Graduate position: University of Vienna

Two PhD student positions (3-year contract with an annual salary of 25000 Euros) are available at the Center for Integrative Bioinformatics Vienna (CIBIV) headed by Prof. Arndt von Haeseler. The prospective PhD students will develop algorithmic approaches to tackle computational challenges arising in conservation genetics, e.g., integrating ecological/economical/geographical factors into conservation planning using genetic sequence data and phylogenetic methods. The project is also involved with real data analysis of, e.g., the Cape flora of South Africa or the European mammals.

The positions are funded through the Vienna graduate school in computational science, a newly founded graduate school of the University of Vienna. The three-year PhD program is run entirely in English and will start with an international group of students in summer 2011. The doctoral school covers a wide areas of fields from Physics (Prof. Dellago), Chemistry (Prof. Hofacker), Bioinformatics (Prof. von Haeseler) to Mathematics (Prof. Scherzer) and Computer Science (Prof. Hen-

zinger). Every student will have two advisors from two different fields.

The successful candidate should be self-motivated with a masters degree (or equivalent) in Bioinformatics or Computer Science. We require very good English skills. Applications should be sent to the office of the graduate school and, therefore, include: CV, motivation letter and preferred research areas, abstract of your master thesis (not obligatory), transcript of grades of your undergraduate and master studies, two letters of recommendation, proposed starting date.

Applications may be sent by February 15, 2011 by email in one printable pdf file with files included in the above order to Ms. Claudia Muellauer: [claudia.daniela.muellauer\(AT\)univie.ac.at](mailto:claudia.daniela.muellauer(AT)univie.ac.at). At the end of March or beginning of April the shortlisted candidates will be invited to an interview in person in Vienna.

For further questions please contact Ms. Claudia Muellauer.

BUI Quang Minh <minh.bui@univie.ac.at>

UWyoming PlantPopulationGenetics

Graduate Assistantship available in Restoration Ecology and Genetics at the University of Wyoming

A doctoral assistantship is available in the Dept of Renewable Resources at the University of Wyoming to study restoration ecology and genetics of native plant species beginning August 2011. A long-term goal of the lab is to characterize adaptive traits in native flora that are key for restoration success. The candidate who is awarded this graduate student assistantship may participate in current projects, or develop his/her own research direction. The available stipend will also include tuition and fees as well as health care. Prospective students with a background in ecology and evolution, population genetics, and/or natural resources are encouraged to apply.

Applicants should send a cover letter and copies of transcripts, GRE scores, resume and contact information for 3 references to: khufford@uwyo.edu Please submit applications by February 25, 2011.

Kristina Hufford, Assistant Professor

Dept. of Renewable Resources

University of Wyoming

1000 E. University Ave.

Dept. 3354

Laramie, WY 82071

Office:(307) 766-5587

Department info. <http://www.uwyo.edu/renewable/>-

Application info. <http://www.uwyo.edu/renewable/-info.asp?p=3D22152>

The University of Wyoming is located in Laramie, a town of 27,000 in the heart of the Rocky Mountain West. Wyoming is investing in its university, helping to make it a leader in academics, research and outreach. The university has state-of-the-art facilities in many areas and is a cultural center for the state. Located on a high plain between the Laramie and Snowy Range mountains, Laramie has more than 200 days of sunshine a year and near year-round outdoor activities that include skiing, hiking, camping, bicycling, fishing and climbing. The community provides the advantages of a major university and a distinctive identity as an important city in a frontier state. Laramie is near many of Colorado's major cities and university communities (Fort Collins: 1 hour; Boulder: 1.5 hours; Denver: 2 hours; Colorado Springs; 4 hours).

khufford@uwyo.edu

UZurich MonkeyBehaviour

PhD-position on the causes and consequences of between group conflicts in vervet monkeys

Hiring Organization: Anthropological Institute and Museum, University of Zurich Winterthurerstrasse 190 8057 Zurich, Switzerland

Position Description: Within the framework of a large collaborative project between the universities of Neuchatel (Prof. Dr. R. Bshary), St. Andrews (Prof. Dr. A. Whiten) and Zurich (Prof. Dr. C.P. van Schaik & Dr. M. Krützen) on the evolution of social behaviour in vervet monkeys (*Cercopithecus aethiops*), the Anthropological Institute and Museum (AIM) at the University of Zurich offers a three year, full-time PhD-position to investigate the causes and consequences of between-group conflicts in South African vervet monkeys. The successful candidate is expected to spend a considerable amount of time at our field-site in Kwazulu-Natal -up to a minimum of 10 months per year over the first two years- collecting and supervis-

ing the collection of: 1) behavioural (both observational and experimental) and ranging data (GPS- and VHF-telemetry) on ten habituated groups, and 2) detailed information on the local vegetation (structural and floristic make-up as well as phenology). In addition, genetic samples will be collected to allow detailed genetic analyses on, e.g. population structure, within- and between-group relatedness, and paternity. For the genetic part of this project, the PhD-student will receive all required training at the AIM.

Qualifications/Experience: We invite applications from students holding (or expecting to obtain prior to July 2011) an MSc.-degree in Biology/Anthropology or other relevant academic field. Previous experience collecting and analyzing behavioural and movement data, especially in a (sub-)tropical environment will be highly advantageous. Applicants should moreover be proficient in written and spoken English, have excellent social skills, and be able to work both independently and in a large, interdisciplinary team.

Salary/funding: The salary will be in accordance with Swiss national regulations for doctoral students and amounts to CHF 40,200.- over the first year, up to CHF 46,200.- over the third year. In addition, an annual contribution of up to CHF 2,000.- will be made to cover travel expenses between Zurich and the field site in South Africa.

Term of Appointment: Initial appointment will be for a 1 year period which, after satisfactory evaluation, will be extended to a total duration of 3 years. The successful candidate is expected to start by 01.07.2011.

Application Deadline: Applications will be accepted until the position is filled. Promising candidates will be invited for an interview and oral presentation of their MSc-thesis or other relevant work in the week of 11 -15 April.

Contact Information: Applications consisting of a cover letter stating research experience and interests, a detailed curriculum vitae (up to 2 pages), and the names and e-mail addresses of two referees can be sent electronically to Dr. Erik Willems, e.willems@aim.uzh.ch. A more detailed project description can be obtained upon request.

Dr. Erik P. Willems Postdoctoral Researcher Anthropological Institute and Museum University of Zurich Winterthurerstrasse 190 8057 Zurich Tel: +41-(0)4463 55435 Fax: +41-(0)4463 56804

e.willems@aim.uzh.ch

VrijeU Netherlands EvolutionOfLearning

PhD student in Evolutionary Ecology (f/m)

The department of Animal Ecology, Vrije Universiteit Amsterdam, The Netherlands has a PhD position available for the project:

“Evolution of learning rate in parasitoid insects”

Insects are excellent learners, but it is unclear if learning behaviour evolves independently for each different learning context. This project studies learning rate of parasitic wasps which use olfactory and visual cues to find hosts and food. The two most important questions are if the rate of learning is correlated between learning with different cues and rewards, and are there common genetic mechanisms underlying learning in different contexts. Experimental work will include sequence and expression analysis of candidate genes involved in learning processes, selection experiments and behavioural assays. The research will be carried out at the VU University in Amsterdam, in collaboration with the Netherlands Institute of Ecology (NIOO-KNAW) in Wageningen. This project is funded by the Netherlands Organization for Scientific Research (NWO-ALW) awarded to prof. dr. Jacintha Ellers.

Tasks - Executing scientific research as detailed in the project description. - Publication of results of the research in scientific journals as well as in a thesis. - Assisting in undergraduate courses given within the Institute of Ecological Science. - Following the PhD educational programme as prescribed by the institute.

Required skills and education - MSc degree in Biology, preferably with advanced courses in animal ecology, evolutionary biology, molecular biology, and animal behaviour, or equivalent. - Proficiency in both written and spoken English. - Excellent social skills, ability to work independently and high motivation will be assets.

Details The initial appointment will be for a period of 1 year. After satisfactory evaluation of the initial appointment, it can be extended for a total duration of 4 years. This period has to result in a written thesis. You can find information about our excellent fringe benefits of employment at www.workingatvu.nl Salary The salary will be in accordance with university regulations for academic personnel, and amounts 2.042,- gross per

month in the first year up to 2.612,- in the fourth year (salary scale 8.5) based on a full-time employment.

Information and applications Upon request, applicants can obtain the complete project description from DÃ©sirÃ©e Hoonhout (tel. +31 20 5987004; desiree.hoonhout@falw.vu.nl). Further information can be obtained from Prof. Dr. J. Ellers (tel. +31 20 5987076; jacintha.ellers@falw.vu.nl). Please, send your application, including your expression of interest (with a brief statement of your personal research aims and interests), a detailed resume, and two reference names before January 30th, 2011 addressed to Prof. Dr. B. Oudega, Dean Faculty of Earth & Life Sciences, Vrije Universiteit. You may also send your application by e-mail at: falw-vacatures@falw.vu.nl.

Please mention the vacancy number 1.2010.00338 in the e-mail header or at the top of your letter and on the envelope.

Jacintha Ellers <jacintha.ellers@falw.vu.nl> Jacintha Ellers <jacintha.ellers@falw.vu.nl>

Wageningen Genetic Variation

PhD Research position: Genetic variation in mechanisms underlying seasonal timing in the wild.

The vacancy is at the Netherlands Institute of Ecology (Wageningen) and the research group Chronobiology, Centre of Behaviour and Neurosciences, University of Groningen.

Seasonal timing of reproduction and growth has major fitness consequences. Due to climate change species are shifting their timing but not all at the same rate, leading to directional selection on timing. To predict the rate at which species may adapt to their warming world a better understanding of the genetic variation within the mechanisms underlying seasonal timing is essential. The research will be carried out on winter moths and great tits, part of the well studied food chain of oak, winter moth and great tit. While the research on great tits will be correlative and experimental field work studies the research on winter moths will be mainly laboratory based experimental work. The project is at the forefront of interdisciplinary research on evolutionary

ecology and physiological mechanisms, making an important contribution to our insights in the evolutionary and ecological impact of climate change.

The PhD student will be appointed at the University of Groningen but the research will be carried out at the Animal Ecology Department of the Netherlands Institute of Ecology (NIOO-KNAW) in Wageningen (see www.nioo.knaw.nl) in close collaboration with the research group Chronobiology at the University of Groningen.

For more information you can contact Prof. Marcel Visser, phone +31 317 473439, e-mail: m.visser@nioo.knaw.nl, Prof. Domien Beersma e-mail: d.g.m.beersma@rug.nl or Dr Roelof Hut, e-mail: r.a.hut@rug.nl

You should have an MSc or equivalent in Biology or a related discipline, preferably with a strong background in Behavioural Ecology, Evolutionary Ecology or Evolutionary Physiology. You are expected to have an excellent academic record (list of examination marks from your university study) and be curious, creative and ambitious. You should be able to write scientific articles and reports (to be proven by your graduation thesis or another comparable report) and be fluent in English both in writing and speech.

The University of Groningen offers a salary of minimal EUR 2,042 gross a month in the first year to maximal EUR 2,612 gross a month in the final year based on a full-time position. It is a temporary assignment for a period of 4 years. First you will get a temporary position of 1.5 years with the perspective of prolongation with another 2.5 years. After the first year, there will be an evaluation as to the feasibility of successful completion of the PhD thesis within the next three years.

Closing date 14 March 2011

Apply via a web form at:

<http://www.tangram-tis.nl/10378/Kandidaten/-Inschrijven/00347-0000004566> Prof. Dr Marcel E. Visser Head of Department Animal Ecology Netherlands Institute of Ecology (NIOO-KNAW)

New address: P.O. Box 50, 6700 AB Wageningen, The Netherlands Phone: +31-317-473439 E-mail: m.visser@nioo.knaw.nl Personal page: www.nioo.knaw.nl/users/mvisser

“Visser, Marcel” <M.Visser@nioo.knaw.nl>

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BardCollege NY Biostatistics

The Biology Program at Bard College is seeking applicants for a full-time, one-year visiting faculty position at the assistant professor level, beginning in the fall of 2011. The successful candidate will teach a biostatistics course, a 100-level course each semester, and an advanced seminar course one semester. The candidate's specific area of expertise is flexible but should complement the program's existing strengths in ecology, evolution, microbiology, molecular biology and biochemistry. The successful candidate will possess a Ph.D. and will be expected to involve undergraduates in their research. More information about the curriculum and current faculty research can be found at <http://biology.bard.edu>. Bard is a highly selective private liberal arts college with approximately 1,900 students, located 90 miles north of New York City on the Hudson River. Applicants should submit curriculum vitae, research and teaching statements, and the contact information for three references by email only to: Professor Philip Johns at hr11007@bard.edu. Review of applications will begin on March 21st and will continue until the position is filled. Bard College is an equal opportunity employer and we welcome applications from candidates who contribute to our diversity. AA/EOE.

philip johns

Assistant Professor Biology Program Bard College
Annandale-on-Hudson, NY 12504

johns@bard.edu bugs@bard.edu 845.752.2338

johns@bard.edu

Dexter NM LabManager PopulationGenetics

Dexter National Fish Hatchery & Technology Center in Dexter, NM is seeking applicants for the Molecular Ecology Program with experience in lab management and conservation, evolutionary and population genetics. The following position is now open through the USAJobs website, please click on the link below to view/print the full vacancy announcement. For questions concerning the vacancy please contact Izhar Kahn (Izhar_Khan@fws.gov) or Manuel Ulibarri (Manuel.Ulibarri@fws.gov) at 575-734-5910 ext 16 and 12.

R2-11-442217-MS-DEU Interdisciplinary (Genetics/Lab Manager) GS-0401/0482-9/11 Term Appointment NTE 13 Months, but may be extended up to 4 years at management's discretion Dexter NFHTC, Dexter, NM

Open: 02/23/11 Close: 03/08/11

Manuel.Ulibarri@fws.gov

FloridaStateU FruitFlyAllometry

Position open for a 15 month project investigating allometry in fruit fly wings in the laboratory of David Houle, Florida State University. This Laboratory Technician position will involve measurement of flies, qrt-PCR, data management, fly husbandry, and supervision of undergraduate assistants. Required qualifications are a Bachelor's degree in science or equivalent experience, and knowledge of computer software. Some programming experience is desirable. This project will provide excellent experience in research in evolutionary biology in a pleasant working environment, and is likely to result in authorship on publications for a capable, enthusiastic employee. Salary from \$28,000, depending on experience. Contact Rosa Moscarella rmoscarella@bio.fsu.edu for more information.

rmoscarella@bio.fsu.edu

Geneva MuseumDirector

Position announcement for Museum Director (Geneva, Switzerland)

The Museum director is responsible for ensuring the management of the Muséum d'histoire naturelle of the City of Geneva (Switzerland) and its subsidiary, the Musée d'histoire des sciences.

Candidates are expected to provide leadership for both the scientific missions and the management of these institutions and contribute to the cultural policy of the City of Geneva.

The assignment implies varied responsibilities. Candidates are expected to develop exhibition programs and multidisciplinary scientific projects ; to ensure the quality of the exhibitions and the good dissemination of knowledge ; to set objectives and find sponsors for the exhibitions, the management of collections and the scientific research ; to feed and develop collaboration with the scientific community, in Switzerland and abroad. The successful candidate will be assisted by the administrator for the financial and HR management.

Person specification : PhD (or equivalent) degree in Zoology or Geosciences ; a solid experience in project and HR management ; a good acquaintance with the museum fields, attested by a strong record of scientific and general-public publications. Excellent French language skills. English and German language skills required.

General conditions for formal application are available on www.ville-geneve.ch Closing date for application : April 1, 2011 Selection process : late Spring 2011 Starting date to be discussed

Contact : Danielle Decrouez, Director
danielle.decrouez@ville-ge.ch +41 22 / 418 63 21

Natalie Gressot Assistante de direction Direction du dÃ©partement T. +41(0)22 418 65 11
natalie.gressot@ville-ge.ch

DÃ©partement de la culture Route de Malagnou 19
Case postale 9 1211 GenÃ©ve 17 www.ville-ge.ch/culture

Natalie.Gressot@ville-ge.ch

GeorgeWashingtonU CommunityEvolution

Faculty Position in Community Evolution Department of Biological Sciences, The George Washington University

The Department of Biological Sciences of the George Washington University is accepting applications for a tenure-track faculty member at the rank Assistant Professor with expertise in the field of Community Ecology. We are searching broadly for candidates who study the ecological and evolutionary factors structuring communities, including anthropogenic factors such as invasive species, pollution, fragmentation, or climate change. Research interests could encompass terrestrial, freshwater, or marine communities or investigations of urban ecology using a community approach. Teaching responsibilities would include an undergraduate course in global ecology and a graduate course in his or her area of expertise. The successful candidate will carry out research capable of attracting external grants and help us build a program with a strong environmental biology or ecological research focus. Basic Qualifications: a Ph.D. in an appropriate discipline, postdoctoral experience, ability to teach global ecology, and accomplishments in biological research in community ecology demonstrated by publications in peer-reviewed journals.

Application Procedure: to be considered please send electronically a complete curriculum vitae, brief descriptions of teaching and research plans, three publications, and the names and contact information for three references to John Lill at GWecosearch@gmail.com

Only complete applications will be considered. Review of Applications will begin on March 13, 2011, and will continue until the position is filled.

The George Washington University is an Equal Opportunity/Affirmative Action Employer. The University Search Committee seeks to attract an active, culturally and academically diverse faculty of the highest caliber.

John T. Lill, Ph.D. Associate Professor George Washington University Department of Biological Sciences 2023 G Street, NW, Suite 340 Washington, DC 20052 (202) 994-6989 (202) 994-6100 [FAX] lillj@gwu.edu

John Lill <lillj@gwu.edu>

IndianaU EvolEcol SummerStudent

The Rieseberg lab at Indiana University is looking for a highly-motivated student to participate in an evolutionary genetics research project this summer. The project will examine the evolutionary and ecological basis for flowering time divergence in the silverleaf sunflower, *Helianthus argophyllus*, which is native to coastal south Texas.

The project participant will gain experience in fieldwork and data collection by independently managing one site of a large evolutionary genetics experiment, either at the Welder Wildlife Foundation Park near Sinton, TX or the Mission-Aransas National Estuarine Research Reserve headquarters in Port Aransas, TX. Participants will also have the opportunity to develop an independent project of their own design.

The successful applicant will be efficient, self-motivated, and pay careful attention to detail. Applicants must be able to tolerate (or enjoy) working outdoors in any type of weather, must have a valid driver's license, and must be current full-time students (undergraduate or graduate) at an accredited post-secondary institution. Unfortunately, students who are graduating Spring 2011 are not eligible for this position. Previous research experience and access to a vehicle are helpful, but are not required. The participant will receive a stipend of \$4,000 for the summer.

To apply, please send a cover letter and curriculum vitae along with two references (academic or work-related) to Brook Moyers (brook.moyers@gmail.com). Applications are due March 4, 2011. To apply, please send a cover letter and curriculum vitae along with two references (academic or work-related) to Brook Moyers (brook.moyers@gmail.com). Applications are due March 4, 2011.

For more information, contact Brook Moyers (brook.moyers@gmail.com) or check out the Rieseberg lab at <http://www3.botany.ubc.ca/rieseberglab/> brook.moyers@gmail.com

Kadoorei 3 Conservation Botany

Kadoorie Farm & Botanic Garden Corporation

Notice of Vacant Post: Senior Conservation Geneticist

JOB SUMMARY Applications are invited for a permanent Senior Conservation or Population Geneticist position at Kadoorie Farm and Botanic Garden (KFBG) in Hong Kong. The general remit of the post is to improve the integration of genetic information into conservation programmes and to manage a Genetic Laboratory. The successful candidate will study the effect of habitat fragmentation on the genetic diversity and the adaptability of populations of South Chinese and Indochinese plants at various geographical and temporal scales. The obtained results will be used to develop a decision-making framework for integrating genetic information into conservation programmes. Key conservation genetics concepts and research findings should be summarised and communicated in user-friendly handbooks, scientific publications and online resources for conservation practitioners and conservation management.

Applicants should have a PhD in the field of population or conservation genetics. Strong communication skills (written and oral), advanced knowledge of population and statistical genetics, and computational skills are required. Additional knowledge in genomics, analysis of high-throughput sequencing data and computer programming (Perl/Python/R/) are a plus.

Daily duties will include managing the genetic laboratory and projects, supervising junior laboratory staff as well as analysing genetic samples and interpreting the results.

Application Method Interested parties should send a detailed CV, expected salary, and a short essay (de-

scribing relevant work experience and reasons for interest in the post) to:

Dr. Gunter Fischer, Head of Flora Conservation Department, Kadoorie Farm & Botanic Garden Corporation Lam Kam Road, Tai Po, N.T., Hong Kong Email: gfisher@kfbg.org

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Kadoorie Farm & Botanic Garden Corporation

Notice of Vacant Post: Botanist (Plant Identification and Records Officer)

JOB SUMMARY Applications are invited for a permanent Botanist position at Kadoorie Farm and Botanic Garden (KFBG) in Hong Kong. The general remit of the post is to identify specimens collected at field surveys in South China and Indochina, assist in herbarium management and to manage the specimen database. The successful candidate will conduct field work and participate in survey projects in Hong Kong, South China and Indochina, work on taxonomy and conservation status assessment of plant genera, handling and processing botanical information, conducting plant conservation research and providing capacity building.

Applicants should have a PhD in plant taxonomy, plant biodiversity and/or plant conservation. Strong communication skills (written and oral) and knowledge of the local flora are required. Additional knowledge in herbarium management software, phylogenetics, GIS and computer programming are a plus.

Interested parties should send a detailed CV, expected salary, and a short essay (describing relevant work experience and reasons for interest in the post) to:

Dr. Gunter Fischer, Head of Flora Conservation Department, Kadoorie Farm & Botanic Garden Corporation Lam Kam Road, Tai Po, N.T., Hong Kong Email: gfisher@kfbg.org

—
Kadoorie Farm & Botanic Garden Corporation

Notice of Vacant Post: Botanist (Plant Ecology and Forest Restoration)

JOB SUMMARY Applications are invited for a permanent Botanist position at Kadoorie Farm and Botanic Garden (KFBG) in Hong Kong. The general remit of the post is to use the findings of research into the ecology of plants to conduct forest restoration projects. The successful candidate will conduct field work and participate in survey projects in Hong Kong, South China and Indochina, map forest ecosystems using fieldmap technology, develop an understanding of the life-cycle dynamics of plants to pinpoint which factors

are causing population declines, conduct projects to understand biotic and abiotic habitat requirements of plants and conduct forest enrichment and restoration projects.

Applicants should have a PhD in plant ecology or forest restoration. Strong communication skills (written and oral) and knowledge of the local flora are required. Additional knowledge in herbarium management software, soil science, GIS and computer programming are a plus.

Daily duties will include managing our native tree nursery and supervising work teams and junior staff.

Interested parties should send a detailed CV, expected salary, and a short essay (describing relevant work experience and reasons for interest in the post) to:

Dr. Gunter Fischer, Head of Flora Conservation Department, Kadoorie Farm & Botanic Garden Corporation Lam Kam Road, Tai Po, N.T., Hong Kong Email: gfisher@kfbg.org

gfisher@kfbg.org

Munich ChairPaleontology

Munich, Germany: Research Associate (“Wissenschaftlicher Assistent”) position at the Chair of Paleontology & Geobiology, Molecular Geo- & Paleobiology Lab.

We invite applications for a research associate (“Wissenschaftlicher Assistent”) at the Chair of Paleontology & Geobiology (Molecular Geo- & Palaeobiology Lab) of the Department of Earth- and Environmental Sciences and the GeoBio-CenterLMU of the Ludwig-Maximilians-Universitaet (LMU) München.

The successful candidate will join a young, international and dynamic lab that applies a molecular geo- and palaeobiological approach â including molecular biology, genomics, and molecular phylogenetic techniques in reconciliation with the fossil record â in a research programme that focusses on temporal and spatial aspects of the evolution, diversification and biomineralization of geobiologically important marine invertebrate taxa like sponges, corals, and echinoderms â lately also vertebrates. More information about the lab can be found at < www.mol-palaeo.de >.

You will have access to newly refurbished and fully equipped >200 sqm molecular labs including two

seawater aquaria systems, stereo- & compound (fluorescent) microscopes (< <http://www.palmuc.de/mol-labs-en.html> >), in-house stable isotope and geo-histology labs and a 64-core Linux cluster. Further equipment is available through the GeoBio-CenterLMU (< <http://www.geobio-center.uni-muenchen.de> >), through which you will also have access to the Bavarian Natural History Collections (< <http://www.snsb.de> >), with >30 Mio. items one of the largest biodiversity collections in Germany.

We are seeking a highly motivated applicant with an excellent track-record of international publications. The working language of the group is English, and applicants from abroad are encouraged to apply.

Requirements: PhD in Geosciences, Biology or related field less than four years ago; 1-2 years of Post-Doc experience preferred; excellent English language skills. German language skills (or willingness to acquire those quickly) is certainly an advantage for teaching undergraduate courses. SCUBA diving license, bioinformatics/computer programming or molecular skills are a bonus but not mandatory.

Duties: â Support the Chair of Paleontology & Geobiology in research and teaching â Develop own research projects that supplement the themes of the research group â Acquire third-party funding through national and/or international funding agencies â Teach courses in the Bachelor and Masters Programs in Geosciences (various geo- & paleobiology topics) for 5 hours per week â Participate in the academic self-administration

The position is intended for further qualification (German “Habilitation”) and is available for 2 times three years (starting from 01.07.2011). If the “Habilitation” is successfully completed after the first of six years, the position can be extended for another four years, depending on performance. The position will be paid according to the German public servant salary scheme A13 (“Beamtenbesoldung”, Akademischer Rat auf Zeit).

Application: Send application including CV, Publication list, PDFs of your three most significant publications, a maximum one-page research statement, and details of 2 referees in a single PDF document (only) by email to Mrs. Monika Brinkrolf (Secretary): m.brinkrolf@lrz.uni-muenchen.de. Application deadline is March 31, 2011. Informal enquiries about the position may be directed to Prof. Dr. Gert Wörheide (woerheide@lmu.de).

The Department of Earth- and Environmental Sciences (Section Palaeontology & Geobiology) of the Ludwig-Maximilians-Universität Munich offers an ex-

cellent multidisciplinary research environment, one of its particular strength being due to the close interaction between Geosciences and the Biological Faculty in the framework of the GeoBio-CenterLMU (< <http://www.geobio-center.uni-muenchen.de> >).

The LMU Munich is the leading research university in Germany, with a more than 500-year-long tradition, and builds upon its success in the Excellence Initiative, a Germany-wide competition promoting top-level university research. Munich has also been repeatedly voted Germany’s most livable city.

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

– Prof. Dr. Gert Wörheide Molecular Geo- & Palaeobiology Department of Earth and Environmental Sciences & GeoBio-CenterLMU Ludwig-Maximilians-Universität München Richard-Wagner-Straße 10 80333 München Germany

Phone: +49 (89) 2180-6718 Fax: +49 (89) 2180-6601 E-Mail: woerheide@lmu.de www.palmuc.de | www.mol-palaeo.de

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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>

NHM Paris BacterialGenomics

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

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

in theoretical and modern population genetics (bioinformatics, modelisation, ABC, demogenetics) as well as an interdisciplinary research environment based on national and international collaborations (Institut Pasteur, Max-Planck Institute).

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

Informal inquiries as well as applications (including a CV, copies of relevant publications and contact information for at least two references) should be emailed to both Thierry Wirth at wirth@mnhn.fr and veuille@mnhn.fr The starting date can be as early as October 2011.

Prof. Thierry Wirth

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

NorthernArizonaU Bioinformatics

Faculty Position in Bioinformatics, Northern Arizona University

The College of Engineering, Forestry and Natural Sciences invites applications for a tenure track position in the area of Bioinformatics at either the assistant or associate level, to begin August 2011. Although outstanding candidates from all areas of Bioinformatics will be considered, we are particularly interested in committed educators with strong practical experience in bioinformatics software development and application. The successful candidate will be expected to play a leadership role in the development of an undergraduate training program in bioinformatics, requiring a solid combination of technical, program development, communication, and leadership skills. Candidates must be particularly committed to undergraduate education, and must be able to teach core software development

courses in a Bioinformatics program, as well as upper-division and graduate courses in their specialty area. Candidates must also have a strong commitment to developing a scholarly record in either Bioinformatics or related pedagogy.

The position requires an earned doctorate in Computer Science or a Biological Science for either the assistant or associate level. Additionally, for the associate level candidates will be required to have teaching, research and service experience consistent with COFS guidelines for promotion to Associate Professor. Please see <http://home.nau.edu/provost/> for more information on COFS guidelines.

Preferred qualifications include: For appointment at rank of Assistant Professor: - Demonstrated skill in applied software development and application, particularly in the bioinformatics area. - Demonstrated skill in pedagogy and undergraduate education. - Demonstrated skill teaching core courses in Computer Science, Biology or Biochemistry. - Outstanding oral and written communication skills. - Demonstrated administrative and program management skills. - Candidates with a demonstrated commitment supportive of the multicultural needs of Northern Arizona University and the surrounding area are strongly desired.

For appointment at rank of Associate Professor: - The preferred qualifications for the Assistant rank, AND; - Strong scholarly or industry record in bioinformatics or related pedagogy. - Direct experience in design, deployment, and development of new academic programs, particular in the bioinformatics area.

Northern Arizona University has a student population of about 25,000 at its main campus in Flagstaff and at about 30 sites across the state. Committed to a diverse and civil working and learning environment, NAU has earned a solid reputation as a university with all the features of a large institution but with a personal touch, with a faculty and staff dedicated to each student's success.

While our emphasis is undergraduate education, we offer a wide range of graduate programs and research. Our institution has carefully integrated on-campus education with distance learning, forming seamless avenues for students to earn degrees.

Flagstaff has a population of about 62,000, rich in cultural diversity. Located at the base of the majestic San Francisco Peaks, Flagstaff is 140 miles north of Phoenix at intersection of Interstate 17 and Interstate 40.

The Bioinformatics position described here is inherently interdisciplinary in nature, spanning the departments of Electrical Engineering and Computer Science, Chem-

istry, and Biological Sciences, all of which are housed in the College of Engineering, Forestry, and Natural Sciences. NAU has a strong history of dedication to undergraduate education, with graduate degrees offered in selected fields, including a doctoral program in Biology, and Masters and Masters of Engineering programs in Chemistry and Computer Science, respectively.

To apply, send: (1) a cover letter highlighting your particular qualifications for this position; (2) a curriculum vitae; and (3) names and contact information for three references, to: Dr. Eck Doerry, BioInformatics Search Committee Chair, Box 4073 MGEN, Northern Arizona University, Flagstaff, AZ 86011-5600. Only complete application packets sent in hardcopy to this address will be reviewed.

The search will remain open until the position is filled or closed; however, the screening committee will begin reviewing applications on February 28, 2011.

NAU is an Equal Opportunity/Affirmative Action Employer and is responsive to the needs of dual-career couples. We are committed to a diverse faculty and specifically seek individuals supportive of the multicultural needs of Northern Arizona University and the surrounding area. Minorities, women, veterans and persons with disabilities are encouraged to apply. Please see <http://www.cefn.nau.edu/> for further information about the college, NAU or the Flagstaff area.

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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>

RhodesU SystematicEntomology

Senior Lecturer/Lecturer: Systematic or evolutionary entomology

Recognising that diversity is important in achieving excellence, Rhodes University especially encourages South African members of designated groups to apply. Responsibilities will include teaching at an Honours, and all undergraduate levels, with significant contributions to evolutionary biology (including some genetics) and entomology. The successful candidate is expected to carry out postgraduate supervision within the de-

partment, take on some departmental administration, and develop a strong research programme.

To apply, please email your completed application form, accompanied by a substantial letter of motivation, curriculum vitae, academic transcripts and copies of certificates to: jobs-yellow@ru.ac.za Or you can post your application to: Recruitment & Selection Section, Rhodes University, P O Box 94, Grahamstown, 6140. For more information please contact 046 603 7265.

It is essential that prospective candidates read the further particulars relating to this post and University and that all relevant documentation is submitted. Failure to submit such documentation will result in an application not being considered.

For more information about the Department of Zoology and Entomology, kindly visit their website on: <http://www.ru.ac.za/zoologyandentomology/> Closing Date: 12h00, 28 February 2011

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/~~~\ Martin H. Villet _ _ \ / Dept of Zoology & Entomology | / Rhodes University _*/ Grahamstown, South Africa 6140

Email: M.Villet@ru.ac.za Tel +27 [0]46 603 8527 FAX: +27 [0]46 622 4377 Editorial board, Psyche - <http://www.hindawi.com/journals/psyche/> Editorial board, Open Forensic Science Journal

Martin <M.Villet@ru.ac.za>

UAuckland ComputationalEvolution

The University of Auckland is looking for a top academic to join its diverse and internationally renowned Department of Computer Science. The successful appointee will have a PhD, demonstrated excellence in research, and a commitment to high quality research-informed teaching.

The Department is interested in candidates in the area of design and application of statistical models and computational methods to tackle problems in computational biology using genomic data. The successful candidate is expected to develop her/his own independent research program, but would also be expected to work with existing faculty members including Associate Professor Alexei Drummond and Dr Stephane Guindon, who are both lead authors of popular software packages in the field of computational evolution, BEAST

and PhyML, which are being developed at the University of Auckland.

The appointee will also be expected to teach at undergraduate and postgraduate levels in their specialist area, at introductory levels more widely, and to engage in research and publication both personally and by the supervision of research students.

The appointment will be made at Lecturer level. This is a 5-year fixed term, full time position based on the University of Auckland's city campus

For further information please contact Professor Gill Dobbie, Head of Department of Computer Science on +64-9-3737 599 ext 83949 or email g.dobbie@auckland.ac.nz For further information about the Department please visit <http://www.cs.auckland.ac.nz/>. For the official job advertisement, please visit <http://www.auckland.ac.nz/uoa/-/home/about/opportunities/> (Job ID: 12789)

– Stephane Guindon Department of Statistics University of Auckland <http://www.stat.auckland.ac.nz>
s.guindon@auckland.ac.nz

UBern FieldAssist BirdEvolution 4

Field assistants in evolutionary ecology of Great tits (*Parus major*)

We are seeking highly motivated field assistants interested in taking part in field studies in Bern, Switzerland. Applicants will be part of the evolutionary ecology team (Institute of Ecology and Evolution, University of Bern).

Our projects aim to investigate: - Interactions of parasite and predator-induced maternal effects; - The expression of carotenoids and sexual signals. and are all based in Bern (Switzerland)

We will require field assistants that will help with all the aspects of the work, including checking nests, ringing the birds, catching adults, performing treatments, and more. Applicants with a Msc in Biology/Ecology and/or with bird handling or field experience would have an advantage. Motivation will play a key role; the work is hard and demanding, takes place in changing weather and requires long hours at times. One of the studies will start around the 15 of March 2011 until the end of June 2011 and the other ones in the end of March/beginning of April until the end of June. Fluent

English, French or Italian speaking and a valid European driving license are required.

Travel expenses will be paid and accomodation will be covered; additionally, the field assistants will receive another salary per month to cover the expenses.

Applicants can send us a letter + CV as soon as possible and ask for further details or questions on the following email addresses:

Alessandra Basso Institute of Ecology and Evolution University of Bern Baltzerstr. 6 3012 Bern E mail: ale84.basso@tiscali.it Phone: +41 31 631 30 18 Mobile: +41 78 696 11 19

Viviana Marri E mail: viviana.marri@iee.unibe.ch Phone: +41 31 631 30 18 Mobile: +41 76 798 33 81

Lea Maronde E mail: leamaronde@gmx.de

Phone: +41 31 631 30 20 Mobile: +41 78 798 20 06

"ale84.basso@tiscali.it" <ale84.basso@tiscali.it>

UCincinnati CavefishEvolution

Jr. Research Associate (210UC2195) Cavefish Evolutionary Genetics/Genomics.

A full-time technician is available starting this Winter Quarter, 2011, in the laboratory of Dr. Josh Gross, in the Department of Biological Sciences, at the University of Cincinnati. Dr. Gross's lab studies the evolution of regressive and constructive changes in blind Mexican cavefish. Duties will include working at UC's Uptown Campus in Cincinnati, OH. For benefits eligibility, a one-year commitment is required. Preference will be given to a candidate who can commit to a second year. The technician will be responsible for basic lab maintenance, monitoring and maintenance of a fish husbandry room, and performing molecular genetic, phenotypic, and statistical analyses. While experience with quantitative trait locus (QTL) analysis and linkage mapping is not required, a willingness to learn such techniques and train others is necessary. Experience with basic molecular techniques, such as DNA/RNA isolation, PCR, cloning, as well as basic microscopy, are required.

The candidate should have a BA or BS in biology, genetics, molecular biology, or a related degree, have previous experience performing independent research, the ability to work well in a group environment, and a willingness to supervise undergradu-

ates. The position is ideal for a highly motivated person interested in gaining field and laboratory skills prior to starting graduate school or other work in the life sciences. Salary is commensurate with experience. If you should have any questions about this position, please feel free to email Dr. Josh Gross at joshua.gross@uc.edu. In order to apply, go to: < <https://www.jobsatuc.com/applicants/jsp/shared/-frameset/Frameset.jsp?time=1297278562351> > . The position number is 210UC2195.

grossja@ucmail.uc.edu

rhizal techniques, or next-generation sequencing (esp. 454 pyrosequencing). Salary range: \$30-35,000/year for up to 3 years. To apply, please submit a cover letter and CV/resume to: http://www.hr.uga.edu/-recruitment/employment/hire_app.html Please email me at ralankau@uga.edu with any questions. Sincerely, Richard Lankau

Assistant Professor Department of Plant Biology University of Georgia

ralankau@gmail.com

UGeorgia ResTech InvasivePlants

A research professional with previous experience in molecular biology techniques is needed to help perform research on the impacts of an invasive plant on native plants and soil microbial communities at the University of Georgia, in Athens, GA. This NSF funded project seeks to understand how native plants and garlic mustard have evolved in response to one another over the course of this 150 year old invasion, and the role that soil microbes (especially mycorrhizal fungi) have played in this interaction. This technician will be responsible for performing and overseeing laboratory and greenhouse research on plant-soil microbe interactions. In the laboratory, this will entail extracting and purifying DNA from soil and root samples, amplifying specific gene regions with PCR, and preparing products for analysis by core facilities. Laboratory work may also require clearing and staining root samples and quantifying fungal infection under microscopes. In the greenhouse, the technician will help with propagating native and invasive plants from seeds, and in establishing and maintaining greenhouse experiments. Some field work in nearby locations may be required, but will not be the primary focus of this position. Finally, the technician will be responsible for maintaining a functional lab by keeping stock of supplies and ordering when necessary, will ensure that data are properly recorded and backed-up, and will help supervise undergraduate assistants. Education and experience required: Master's degree or equivalent experience, including experience with DNA extraction, PCR amplification, gel electrophoresis, sequence analysis, plant propagation. Preference will be given to applicants with experience in ecological, evolutionary, or agricultural research with plant systems, and/or those with experience in microbiology, fungal culture, mycor-

UHull EvolutionaryBiol

We would welcome applications from all types of evolutionary biologist, to join Hull's strong, diverse and international Evolutionary Biology Group. You do not have to be primarily a 'zoologist', just to be prepared to contribute to the teaching of the zoology degree programme. The official advert is below. Closing Date: 17 February 2011 Dave

Lecturer in Biological Sciences University of Hull - Department of Biological Sciences

We seek to appoint a Functional Ecologist/Evolutionary Biologist (with expertise in Zoology) ready to make a contribution to the high quality research and research led teaching which characterizes our department.

The Department of Biological Sciences has an international reputation for research in areas of Functional Ecology, Evolutionary Biology, Environmental Management and Biomedical Science. It has an excellent reputation for research led teaching and learning.

Currently the department has strengths in a number of interrelated areas of organismal, evolutionary and molecular biology and in experimental ecology in both terrestrial and aquatic environments. Current research includes microbial functional ecology, eco-toxicology, chemical ecology, ecosystem services, and physiological, behavioural and evolutionary studies.

The successful applicant will be an experienced researcher with a strong publication record in an area which will strengthen the Department's submission to the UK Research Excellence Framework (REF) specifically in the areas of evolutionary biology and/or functional ecology. They will have a proven ability of publishing international quality research and attracting in-

dependent research funding as well as a strong desire to contribute to the teaching of zoology in the department.

To discuss this role informally, please contact Dr Graham Scott on 01482 466424 or email: g.scott@hull.ac.uk

For information about the Department of Biological Sciences visit www.hull.ac.uk/biological_sciences For the application procedure: <http://www.jobs.ac.uk/-job/ACD571/lecturer-in-biological-sciences> Closing Date: 17 February 2011

Dr Dave Lunt Evolutionary Biology Group Department of Biological Sciences University of Hull Hull HU6 7RX UK

d.h.lunt@hull.ac.uk +44 (0)1482 465514 <http://www.hull.ac.uk/biosci> <http://davelunt.net>
D.H.Lunt@hull.ac.uk

UKansas ResTech PhenotypicVariation

An NIH-funded Research Technician position is available in Stuart Macdonald's lab in the Department of Molecular Biosciences at the University of Kansas. The Macdonald lab explores the genetic basis of complex phenotypic variation within and between species using *Drosophila* as a model system. We seek an enthusiastic individual to supervise and carry out large-scale genetics/genomics projects, and to oversee various lab activities. The responsibilities of the technician will include maintaining and using a large panel of *Drosophila* strains, and helping with quantitative genetic experiments. The successful candidate should be motivated, organized, and careful, and should have excellent oral and written communication skills. Salary will be commensurate with experience and will include benefits.

Required qualifications are a Bachelors degree in biology or a related field, and demonstrable experience conducting research in a (broadly-defined) genetics or molecular biology laboratory. Preference will be given to candidates with significant experience in the laboratory (including troubleshooting and optimizing protocols). Prior experience with *Drosophila* is not essential, but would be an asset.

The position is open and review of applications will begin on Feb 15 and continue until the position is filled. Informal inquires are welcome and can be directed to Stuart Macdonald (sjmac@ku.edu). To apply, complete an online application at <https://jobs.ku.edu> (position

number 00207629). Attach a cover letter (describing your interest in the position and any relevant expertise), a full CV, and complete contact information for 3 referees. EO/AA Employer.

Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321 email: sjmac@ku.edu web: <http://web.ku.edu/~sjmac/> sjmac@ku.edu

ULondon MolecularEvolution

Senior Lecturer / Reader in Molecular Ecology and Evolution School of Biological Sciences Royal Holloway, University of London, UK

Applications are invited for the above post, to commence by 1 September 2011. The position is for a Senior Lecturer or Reader (roughly equivalent to an American Associate Professor), and we are therefore seeking an individual with an excellent research record. Royal Holloway has established a reputation for innovative research in ecology and evolutionary biology, and the successful candidate will complement existing activities, especially in the areas of evolutionary ecology, ecological genetics, macroecology, systems biology and molecular phylogenetics.

Informal enquiries are welcome to the Head of School, Professor Peter Bramley (+44 1784 443555; p.bramley@rhul.ac.uk), the Director of Research, Professor Vincent Jansen (+44 1784 443179; vincent.jansen@rhul.ac.uk) or the Head of Ecology, Evolution and Behaviour, Dr Ian Barnes (+44 1784 443652; ian.barnes@rhul.ac.uk).

Further details about the position and the department, and an application form, are available to download at <http://www.rhul.ac.uk/jobs/home.aspx>. The closing date for applications is 12 noon, 14th March and we will be holding interviews on the 29th March.

Ian.Barnes@rhul.ac.uk

UMarseille EvolutionaryBiol

A Professor position is open in 2011 for the EBM lab

Research profile:

The candidate will be a theoretical biologist, with research experience in one or more of the following areas:

Population genetics, Evolutionary Biology, Phylogeny, Comparative genomics and Post genomics.

The successful candidate will be encouraged to develop its own research project and to interact with biologists, mathematicians, and informaticians, of the EBM team.

Education Profile:

The candidate will teach :

Population Genetics, Comparative genomics and post genomic at master and bachelor level.

the CV and other files should be load at

A Professor position is open in 2011 for the EBM lab

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the necessary files can be loaded between the 02/24 to the 03/24 at the following adress

<https://www.galaxie.enseignementsup-recherche.gouv.fr/ensup/candidats.html>
Pierre
Antoine Pontarotti

UMR 6632 Université de Aix Marseille/CNRS . <http://sites.univ-provence.fr/evol/>

USDA WashingtonDC ParasiteEvolution

The Animal and Natural Resources Institute, Agricultural Research Service, USDA is looking for a Research Leader for the Animal Parasitic Diseases Laboratory.

The incumbent serves as a member of the management team, providing research coordination and administrative leadership to a scientifically diverse staff.

The incumbent serves as the Research Leader in the Animal Parasitic Diseases Laboratory (APDL), Animal and Natural Resources Institute, Beltsville, MD. As the Research Leader in APDL, the incumbent is responsible for directing multidisciplinary and multi-faceted research programs that address animal and zoonotic parasitic diseases problems. The research program encompasses eight research projects with total funding of \$6.9 million per year and nearly \$1 million of additional funds through grants and CRADAs. The incumbent provides scientific leadership as well as coordinates interactions between ARS scientists and federal and state agencies, universities, and foreign institutions. The incumbent's personal research is directed at population genetics, phylogeography and molecular systematics related to exploring the development and dissemination of drug resistance by nematode parasites in ungulates while contributing to a broader understanding of population structure and diversity among animal and zoonotic parasites.

Major research objectives related to ruminants and helminths are to: (1) explore fine scale population structure based on appropriate mitochondrial and nuclear markers for economically important gastrointestinal and other nematodes in ruminants; (2) explore the distribution and dissemination of the genes that define multi-spectrum drug resistance in nematode populations; (3) contribute to defining diversity (genetic and genealogical) for nematode faunas in domestic and wild ungulates. Classic methods related to animal sampling and epidemiology will be used to obtain sufficient sample numbers and with ample geographical distribution for proper analysis. It is expected that molecular techniques such as PCR and DNA sequencing will be used to process and genetically define the samples. These and other molecular techniques will be applied to existing as well as user developed protocols which may utilize pre-defined genetic markers or require developing new genetic markers for genus, species and/or isolate identification. Demonstrated expertise working with currently available as well as user modified computer programs which compile and statistically evaluate the data will be required to achieve research goals.

The position is located in the vicinity of Washington, D.C. (in nearby Beltsville, Maryland)

The full announcement may be found here:

<http://snipurl.com/1ykuhw> Applications accepted through March 4, 2011

“Rosenthal,
<Benjamin.Rosenthal@ARS.USDA.GOV>

Benjamin”

USheffield ResAssoc BehaviouralEvolution

Research Associate in Computational Complexity and Behavioural Evolution University of Sheffield, UK Duration: 18-months with potential for extension Deadline: 25th March 2011

This post will develop novel approaches to understanding the evolution of animal behaviour, by applying computational complexity and information theoretic approaches to the analysis of mechanisms for implementing animal behaviour. The classic approach to understanding behavioural evolution is in terms of models of optimal behaviour. Optimality theory is invaluable as a benchmark to assess a given behaviour or behavioural model against, but typically requires unrealistic limitations on the behaviour under consideration, and hence results in 'complex models for simple environments' [2]. However, real animals inhabit complex environments, and use simple rules of thumb to deal with them [1]. There is clearly a trade-off between the marginal fitness gain from having a more and more complex behavioural model for an environment, and the fitness costs of the additional resources required for implementing that model. To date, the approach to understanding this trade-off has been somewhat heuristic. This project will seek to apply computational complexity theory and information theory in an attempt to gain a more quantitative understanding of the trade-off between behavioural complexity and behavioural optimality. It is expected that the successful candidate will quickly take a lead in developing a research programme and securing funding to continue it. Researchers who have demonstrated an ability to direct their own research programme, whether during doctoral studies or subsequently, are therefore particularly encouraged to apply. We particularly welcome applications from theoretical computer scientists, theoretical physicists, and mathematicians. A demonstrated interest in biology would be an advantage. The successful candidate will become part of the newly established Behavioural and Evolutionary Theory Lab at the University of Sheffield, Department of Computer Science, under the direction of Dr James Marshall (<http://staffwww.dcs.shef.ac.uk/people/J.Marshall/>). It is anticipated that there will be opportunities for interaction with the Modelling An-

imal Decisions research group directed by Professors Alasdair Houston and John McNamara (Mathematics) at the University of Bristol (<http://www.bristol.ac.uk/biology/research/behaviour/mad/>).

References — [1] Gigerenzer, G., Todd, P.M. et al. (1999) Simple Heuristics that Make Us Smart. Oxford University Press. [2] McNamara, J.M and Houston, A.I. (2009) Integrating function and mechanism. Trends in Ecology and Evolution 24, 670-675.

For access to the full job advert, visit http://staffwww.dcs.shef.ac.uk/people/J.Marshall/lab/Join_Us.html — James A. R. Marshall Department of Computer Science University of Sheffield <http://staffwww.dcs.shef.ac.uk/people/J.Marshall/> James Marshall <James.Marshall@sheffield.ac.uk>

UWisconsin ClimateAdaptation

ASSISTANT PROFESSOR—CLIMATE CHANGE & NATURAL RESOURCES

The Department of Forest and Wildlife Ecology, University of Wisconsin-Madison announces an Assistant Professor position in the area in climate change research (including evolutionary responses). Focus is on impacts of climate change on wild birds and/or mammals and their habitats and the adaptive management of natural resource systems emphasizing climate change impacts.

9 month tenure-track academic position—75% Research/25% Teaching

This position will emphasize climate change mitigation and adaptation in the adaptive management of complex ecological systems. Focus on natural resource systems in the region and their resident mammals and birds. The successful candidate will be expected to work closely with natural resource agencies and other groups involved in climate change research and response.

In addition to developing an externally-funded research program, the successful candidate will be expected to teach 1 new undergraduate course on climate change impacts and response. Additional responsibilities include participation in faculty-led graduate seminars including those related to her/his area of expertise, mentoring graduate students (masters and doctoral level) and post- doctoral researchers.

Degree and area of specialization:

Earned Ph.D. prior to appointment in a topic consistent with impacts of climate change on wildlife and forests and the adaptive management of climate change impacts on natural resource systems. Relevant disciplines could include (but are not limited to) wildlife ecology, forestry, natural resources, climate science, decision sciences/ decision analysis and/or applied decision methods, etc. We will consider candidates from the social and biological sciences, and those who bridge the two. Applicants must be eligible to work in the USA and possess excellent English-language communication skills.

Minimum number of years and type of relevant work experience:

Post-Ph.D. research and teaching experience is desirable but not essential. Preference will be given to candidates that present evidence of excellent teaching skills, a record of publishing in peer-reviewed journals, success attracting extramural funding.

To apply: to ensure full consideration, please apply by March 7, 2011. Submit in a single PDF file a cover letter, CV, statements of research and teaching (not to exceed two pages each) and the names of your three references. Please have the 3 letters of recommendation sent directly to Laurie Ballentine via email lsballen@wisc.edu or FAX (608-262-9922)

Please name your application file `Climate-Change.YourLastName.pdf` and Email it to Laurie Ballentine, lsballen@wisc.edu with a subject line: Climate Change Position.

Queries should be directed to Professor Scott Craven, Chair, Search Committee srcraven@wisc.edu (608 263-6325)

carollee@wisc.edu

UWisconsin Madison
PopGenQuantGenEvolGen

Tenure tracks FACULTY POSITIONS in Population, Quantitative, Computational, and/or Evolutionary Genetics, College of Agricultural and Life Sciences, UNIVERSITY OF WISCONSIN-MADISON

The College of Agricultural and Life Sciences at the University of Wisconsin (UW) Madison has long been a world leader in experimental and theoretical population and quantitative genetics. To continue to build strength in these areas, we seek to hire two tenure-track

assistant professors in the areas of population, quantitative, computational, and/or evolutionary genetics. Candidates for these positions will be considered in three broad research areas:

Integration of population genetics and genomescale approaches to elucidate evolutionary mechanisms within and between populations

Quantitative genetics of economically important animals or crops

Integration of experimental, computational, and/or theoretical approaches to population and quantitative genetics

In addition, the successful candidates will help to promote a deeper and more profound understanding of population, quantitative and evolutionary genetics in UW undergraduate and graduate students. Faculty members hired through the initiative will be expected to spend part of their teaching efforts in courses that serve departmental needs and part of their efforts in courses that serve a broader collegewide and campuswide community.

Areas of interest include experimental and theoretical research that draw fundamental insights into the connections between molecular function and genetic variation, experimental evolution, ecological genetics, and research that addresses emerging issues in human health, ecology, natural resources or food security; and quantitative and computational approaches that foster genetic improvement of agriculturally important animals or crops. Four departments have worked collaboratively to outline the vision and needs for the initiative: Agronomy, Animal Sciences, Entomology, and Genetics. Each faculty position will be located in one of these four departments.

The successful candidates will be capable of developing a strong, independent, extramurallyfunded research program; developing an innovative undergraduate and graduate teaching program; building collaborative relationships in research and instructional programs; and contributing to service and outreach functions of the Department, College, University and professional societies. Earned doctorate with expertise in population, quantitative, computational, and/or evolutionary genetics is required. Postdoctoral experience is highly desirable. Interested individuals are welcome and encouraged to contact Professor Irwin Goldman directly by phone at (608) 2627781 or by email at ilgoldma@wisc.edu to discuss this position opportunity.

HOW TO APPLY: Send CV, a 12 page statement of research interests and plans, a statement of teaching philosophy, and arrange to have three letters of refer-

ence sent to Dr. Irwin Goldman, pvl66521, by mail to CALS/UWMadison, 240 Agricultural Hall, 1450 Linden Drive, Madison, WI 53706 OR electronically to pvl66521@cals.wisc.edu.

Applicants can find further information on the Evolution Institute web site at www.evolution.wisc.edu or each of the four departmental websites: Agronomy: <http://agronomy.wisc.edu/> Animal Sciences: <http://www.ansci.wisc.edu/> Entomology: <http://www.entomology.wisc.edu/> Genetics: <http://www.genetics.wisc.edu/> Applicants furnishing all materials by March 31, 2011 will receive priority in consideration.

NOTE: Unless confidentiality is requested in writing, information regarding the names of applicants must be released upon request. Finalists cannot be guaranteed confidentiality. The College of Agricultural and Life Sciences views recruiting women and minority faculty members as central to its strategic goals. The University of Wisconsin is an Equal Opportunity and Affirmative Action Employer.

jbrunet@wisc.edu

UWisconsin Madison Population Genetics

TENURE-TRACK Faculty Positions in POPULATION, QUANTITATIVE, COMPUTATIONAL, and/or EVOLUTIONARY GENETICS, College of Agricultural and Life Sciences, UNIVERSITY of WISCONSIN-MADISON

The College of Agricultural and Life Sciences at the University of Wisconsin (UW) -Madison has long been a world leader in experimental and theoretical population and quantitative genetics. To continue to build strength in these areas, we seek to hire two tenure-track assistant professors in the areas of population, quantitative, computational, and/or evolutionary genetics.

Candidates for these positions will be considered in three broad research areas:

Integration of population genetics and genome-scale approaches to elucidate evolutionary mechanisms within and between populations

Quantitative genetics of economically important animals or crops

Integration of experimental, computational, and/or

theoretical approaches to population and quantitative genetics

In addition, the successful candidates will help to promote a deeper and more profound understanding of population, quantitative and evolutionary genetics in UW undergraduate and graduate students. Faculty members hired through the initiative will be expected to spend part of their teaching efforts in courses that serve departmental needs and part of their efforts in courses that serve a broader college-wide and campus-wide community.

Areas of interest include experimental and theoretical research that draw fundamental insights into the connections between molecular function and genetic variation, experimental evolution, ecological genetics, and research that addresses emerging issues in human health, ecology, natural resources or food security; and quantitative and computational approaches that foster genetic improvement of agriculturally important animals or crops. Four departments have worked collaboratively to outline the vision and needs for the initiative: Agronomy, Animal Sciences, Entomology, and Genetics. Each faculty position will be located in one of these four departments.

The successful candidates will be capable of developing a strong, independent, extramurally-funded research program; developing an innovative undergraduate and graduate teaching program; building collaborative relationships in research and instructional programs; and contributing to service and outreach functions of the Department, College, University and professional societies. Earned doctorate with expertise in population, quantitative, computational, and/or evolutionary genetics is required. Postdoctoral experience is highly desirable. Interested individuals are welcome and encouraged to contact Professor Irwin Goldman directly by phone at (608) 262-7781 or by email at ilgoldma@wisc.edu to discuss this position opportunity. HOW TO APPLY: Send CV, a 1-2 page statement of research interests and plans, a statement of teaching philosophy, and arrange to have three letters of reference sent to Dr. Irwin Goldman, pvl66521, by mail to CALS/UW-Madison, 240 Agricultural Hall, 1450 Linden Drive, Madison, WI 53706 OR electronically to pvl66521@cals.wisc.edu.

Applicants can find further information on the Evolution Institute web site at www.evolution.wisc.edu or each of the four departmental websites:

Agronomy: <http://agronomy.wisc.edu/> Animal Sciences: <http://www.ansci.wisc.edu/> Entomology: <http://www.entomology.wisc.edu/> Genetics: <http://www.genetics.wisc.edu/> Applicants furnishing all

materials by March 31, 2011 will receive priority in consideration.

NOTE: Unless confidentiality is requested in writing, information regarding the names of applicants must be released upon request. Finalists cannot be guaranteed confidentiality.

The College of Agricultural and Life Sciences views recruiting women and minority faculty members as central to its strategic goals. The University of Wisconsin is an Equal Opportunity and Affirmative Action Employer.

jbrunet@wisc.edu

UWyoming WildlifeConservation

Assistant Unit Leader-Wildlife | U.S. Geological Survey | Wyoming Cooperative Fish and Wildlife Research Unit | Department of Zoology and Physiology | University of Wyoming

Salary: \$71,901 - \$93,470

Closing: 02 March, 2011

Responsibilities: Conduct innovative research on the ecology, conservation and management of terrestrial non-game wildlife species in the Great Plains and Rocky Mountain region; address research needs of state and federal resource management agencies, especially the Wyoming Game and Fish Department; participate as faculty in the Department of Zoology and Physiology.

Qualifications: Education: PhD in wildlife science, ecology, zoology, conservation biology, or related field. Experience: Postdoctoral, agency, or faculty research

experience in wildlife management, animal ecology, or conservation biology. Other: Record of publishing in the peer-reviewed literature; interest in building a research program that integrates basic and applied aspects of non-game wildlife species; record of obtaining research funding; ability to develop research program involving academic and agency collaborators.

The University and Laramie: The Zoology and Physiology Department has a vibrant group of researchers focused on fish, wildlife, and ecology. The department has 65 graduate students, making it one of the largest and most productive departments at the University (total enrollment is a 11,000). Several outstanding outdoor laboratories are available in Wyoming, including the Greater Yellowstone Ecosystem and numerous mountain and plains systems. Field and laboratory facilities off campus include the Red Buttes Environmental Labs (captive animal facilities) and the UW-NPS AMK Field Station located at the base of the Tetons on the shore of Jackson Lake. Laramie, Wyoming is a small university town of approximately 27,000, nestled between the Laramie Range to the east and the Snowy Range to the west. On the high plains at 7,200 ft elevation within the Rocky Mountain region, Laramie's neighboring mountains and plains provide numerous opportunities for hiking, skiing, biking, hunting and fishing and a high quality of life.

Apply: <http://www.usajobs.gov> Announcement: ATL-2011-0321

Contact: Dr. Matthew Kauffman mkauffm1@uwyo.edu

Matt Carling Asst. Professor Department of Zoology & Physiology Berry Biodiversity Conservation Center University of Wyoming

www.uwyo.edu/carlinglab (p) 307.766.6169

mcarling@uwyo.edu

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AlgonquinPark VolFieldAssist PlantEvol

We are seeking a volunteer field assistant for work being conducted in Algonquin Park (Ontario, Canada) this summer. We are looking for an individual who can commit to a minimum of two weeks in the field anytime between mid-July and the end of August.

The conditions are quite rugged. We camp in the interior of the park. This is not a campground. There are no facilities, meaning there is: 1.no running water, other than the river, 2. no indoor plumbing, 3. no electricity, 4.no cell phone reception. All necessary camping gear and food will be provided.

The study is of a population of flowering plants that grows along the shores of the Petawawa river. Generally, we are interested in the reproductive biology, and evolution of mating systems in flowering plants. Individuals with an interest in evolutionary biology, and specifically plant mating system evolution will be preferred.

Interested applicants should contact Maggie at mbartkow@dal.ca

– Magdalena Bartkowska, M.Sc. Biology Department
Dalhousie University phone:494-8005

Magdalena Bartkowska <MBARTKOW@dal.ca>

AncientDNA from MuseumBirds

Dear EvoLDir Members:

I am going to start with ancient DNA analysis of galliforms resident in museums and aged between 50 and 150 years. We are going to loan classic toe pads from mounted birds or skins. As beginner in the field (I had just past experience in collaboration with Spanish and US colleagues that have done this work in their labs), I would like to receive some feedback about the use of commercial DNA extraction kits. Especially given my samples are from not so ancient specimens, after having read many literature records, I feel that commercial kit such as Promega DNA IQ (or others similar to) could work well.

Is there anyone who has successfully employed DNA IQ kit on toe pads from stuffed birds ?

All suggestions are really welcomed

Thanks

Filippo Barbanera Department of Biology Via A. Volta,
6 I - 56126 Pisa (PI) Italy

Filippo Barbanera <fbarbanera@biologia.unipi.it>

AncientDNA from MuseumBirds answers

ANSWERS

USEFUL PAPERS LISTED AT THE END

(1) Here is a paper about turkey DNA, some of the samples used were toe clippings. you should email Dr. Camilla Speller for more questions, she did the research. I am sure she can help you with this. her email is:

(2) We extracted DNA from foot pad tissue by using a traditional Proteinase K digest, followed by a PureGene protocol, but any other protocol for ProtK and tissue sampels should work well. Before the procedure starts

you should let the tissue soak for 1-2 days in the ProtK buffer (ProtK added). Then do a few cycles of freezing +thawing the tissue with the buffer in liquid nitrogen to break cell walls (say, 10 times or so). Then probably a few more days with ProtK and the tissues will dissolve (add ProtK newly after every night or so.). We will soon submit a manuscript in which that method is used, please let us know if you want to try it out.

Robert H. S. KRAUS PhD student Resource Ecology Group Wageningen University, The Netherlands Email robert.kraus@wur.nl

(3) Have a look at the papers by Giri Athrey; he did the same kind of work very recently. His email: giri.athrey@tamu.edu

Eric Pante Department of Biology University of Louisiana at Lafayette P.O. Box 42451, Lafayette, LA 70504 Lab: (337) 482-6494 Web: www.uill.edu/~egp0628 (4) I haven't worked on birds, but I have extracted DNA from equivalent age mouse specimens, using the Qiagen Blood and Tissue DNA kits. I used pretty much the standard protocol, leaving the tissue to lyse overnight in the proteinase K (rather than the minimum 3 hrs) and, to get more concentrated DNA at the end, eluted the sample with half the amount of elution buffer. Obviously, contamination is potentially a huge problem to be aware of.

Good luck,

Eleanor eleanor.jones@ebc.uu.se

(5) I haven't used the kit you are asking about, but I have had success with the Chargeswitch Forensic DNA Purification Kit from Invitrogen and with the DNeasy Tissue kit from Qiagen (see attached paper). Incubations with prot K were overnight. Note that I rehydrated the samples first, this makes it a lot easier to cut them up into very small pieces.

Sanne Boessenkool Postdoctoral Researcher NCB - National Centre for Biosystematics Natural History Museum University of Oslo P.O. Box 1172 Blindern NO-0318 Oslo, Norway Visiting address: Sars' gate 1, TÅyeyen Phone: +47 22851777 www.nhm.uio.no/forskning-samlinger/forskning/forskningsgrupper/-ncb/ (6) What kind of markers do you intend to use? We have used similar samples for SNPs and the Puregene DNA isolation kit worked fine, although I advise you to test on the fragment length and amount of DNA always and assume that half of your samples may have been degraded too much.

Rudy Jonker M.Sc. Ph.D. Candidate Resource Ecology Group Wageningen University e: rudy.jonker@wur.nl i: www.reg.wur.nl/UK/Staff/Jonker t: +31(0)317-

485304 Skype: rudyjonker

(7) I have ventured on a similar thing a couple years ago (see attached paper). We used the Quiagen Kit (I think you should be able to find my query in the archives of evolDir, from somewhere between summer 2007 and summer 2008). DNA extraction was no problem, contamination was one. Archive DNA usually comes in small quantities, and is easily contaminated. To ensure that your results are really from your samples, you might want to make use of a lab that is specialised on ancient and archive DNA processing. We ended up having the samples run in Allan Bakers Lab (Toronto), but the facility here in Sheffield can also do such things.

Julia Schroeder Research Associate Dept of Animal and Plant Sciences University of Sheffield Sheffield, S10 2TN Tel: +44 (0)114 222 0112 http://julia-schroeder.staff.shef.ac.uk/JSchroederSite/Research_interests.html julia.schroeder@gmail.com

(8) I used the Qiagen DNeasy spin columns purification kit for extracting DNA from bird foot pads 40 - 120 years of age. Sometimes it worked quite well, sometimes worse, depending on the museum where I got the samples from. The amount of DNA was always low, the concentration was adjustable by using less of elution buffer down to a given minimal amount. We used very small amplicons for sequencing (150 - 300 bp). This worked quite well in most of the samples given that they came from a museum collection where it worked well at all. The reason for why my professor wanted me to use a kit instead of a manual maxiprep was that he wanted to have very standardised and well comparable results.

Severin Uebbing Dept. Evolutionary Biology Evolutionary Biology Centre (EBC) Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

(9)

— / —

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>

Expected Heterozygosity

Hi,

I am doing a project on population genetics using ISSR-

PCR. I have calculated expected heterozygosity but was wondering if it is safe to directly compare with the expected heterozygosity calculated from other studies that use different molecular markers? Also would anyone know if using ISSR-PCR to calculate expected heterozygosity is safe, bearing in mind that it is dominant data?

Thankyou, Adam

adam radage <adam_radage@msn.com>

FIS calculation

I have three populations of 45 individuals each. They were genotyped for microsatellites in order to get FIS and FST. I would like to have a FIS value for each population, considering all loci together and after that, I would like to know if each FIS is statistically different from zero. I have tried Genepop and Arlequin with no success.

– Hozana Dantas Laboratório de Genética Aplicada
Universidade Federal Rural de Pernambuco

hozanadantas@gmail.com

Himalayan ClimateAdaptation

Dear all, I am finishing a PhD on the evolutionary and physiological ecology of predator population responses to climate change along the Western Antarctic Peninsula. I am interested in connecting with researchers working on climate change issues in the Himalaya Mountains. I would greatly appreciate any information you can offer. Please email me at: kgorman@sfu.ca

Kind regards,

Kristen

kgorman <kgorman@sfu.ca>

Honduran FrogPopulationGenetics

Hi,

I am doing my dissertation on population and landscape genetics of two frog species using ISSR-PCR. I have collected 20 specimens of each species from 3 different locations (60 in total) and I am looking at whether elevation is having a differential effect on the gene flow of the two species. I am having trouble with the Mantel test, which I am obtaining from GenAlEx. At the moment I have been using euclidean distance which has given a higher correlation for one species ($r=0.418$) than the other ($r=0.356$). The species with the higher correlation has also given larger unbiased Nei's genetic distances and a larger amount of genetic variation has been partitioned among groups in AMOVA, leading me to conclude that elevation is causing this. This has also fitted well, because this species has lower elevational tolerances than the other. Is this what the mantel test also suggests from the r values I have given, that is, does a larger r suggest elevation is effecting gene flow of this species? I have also seen in papers that a Partial Mantel test is used, which from what I understand looks at other possible routes the species could be taking and incorporates this into the analysis to see if the correlation is better, would anyone know if my understanding is correct? Also would anyone know how to perform a partial Mantel test? On GenAlEx? At the moment for the Mantel test using euclidean distance, I have been using global positions of each individual, I cannot see how other distances would be incorporated and this is my main problem. Also if someone could explain the use of looking at euclidean distance in a Mantel when three sites are involved, especially in relation to possible barriers that would be very helpful.

I hope someone can help me out, Adam.

adam radage <adam_radage@msn.com>

Hudson paper request

Hi all,

Does anyone have a pdf version of the following article?

Bruce Hudson, David A. Clayton, and Jerome Vinograd, 1968. Complex Mitochondrial DNA. Cold Spring Harb Symp Quant Biol 33: 435-442. doi:10.1101/SQB.1968.033.01.050

Thanks a lot in advance.

E

Ehsan Kayal PhD Candidate Department of Ecology, Evolution, and Organismal Biology Iowa State University 253 Bessey Hall Ames, IA 50011 ekayal@iastate.edu ehsan.kayal@gmail.com

Hello all,

I'm hoping to find a program that will simultaneously display two competing topologies in a mirrored image (which illustrates topological discordance). I have two large trees with equivalent taxon samples (n9), but it will be a pain to illustrate topological discordance by hand in Adobe.

Any help or info is appreciated!

Mike Sandel - University of Alabama

Michael Sandel <kwksand@yahoo.com>

IJEB issue

Kyoichi Sawamura, Chau-Ti Ting, Leonie Moyle, and I are putting together a special thematic issue on speciation for the International Journal of Evolutionary Biology. We hope to organize a collection of papers that will address speciation from as many different perspectives as possible: molecular mechanisms, phylogenetic patterns, quantitative genetics, relationship between intra- and interspecific variation, evolutionary and ecological forces, etc. We think that putting together a multifaceted and well-rounded portfolio of work will raise the prominence of each paper and showcase every contribution in the best possible light.

The link to the official call for papers is included below. Interested authors can get in touch with any of the editors (about the science), or with Yasmine Moussa, Editorial Staff member at Hindawi Publishing, regarding any logistical and administrative issues.

Best wishes,

Artyom

<http://www.sage-hindawi.com/journals/ijeb/sipen.html> – Artyom Kopp Department of Ecology and Evolution University of California - Davis One Shields Ave Davis CA 95616 office (530) 752-8657 lab (530) 752-8328 fax (530) 752-9014 <http://www.eve.ucdavis.edu/kopplab/> akopp@ucdavis.edu

Large mirrored trees

Malaysia VolFieldAssist WaspBehaviourEvolution

VOLUNTEER FIELD ASSISTANT needed for 3 months starting early May 2011, for study of hover wasp behavioural ecology in peninsular Malaysia (note: these are small wasps that do not sting, with average colony sizes <5 individuals!). The work will involve helping a PhD student to census and observe colonies as part of experiments to elucidate the basis of helping behaviour in these wasps. The successful applicant must be prepared to work hard and have an interest in behavioural/evolutionary biology and enthusiasm for fieldwork. A driving licence is essential and, because the work involves recording colour marks on individual animals, the job would not be suitable for someone who is colour-blind! For further details of how to apply and the research that we do, see: <http://www.sussex.ac.uk/lifesci/fieldlab/>. Accommodation will be provided, and air fare (from the UK) will be reimbursed on successful completion of the field trip, with the applicant needing to pay for only their own food/personal expenses, which are relatively cheap in Malaysia. Accommodation will be a room in a small flat shared with the PhD student and (for the first 2-3 weeks) supervisor - relatively good for tropical research (shower, cooking facilities, TV etc.), and is in a small village which is a centre for bird-watchers.

APPLICATION PROCEDURE

Applicants should send a covering letter and a CV, including contact details (including e-mail addresses/telephone nos.) for the applicant and 2-3 referees who would be available to provide references during February and March 2011. Applicants must be available for interview in the UK during that time, and review of applications will begin 18 March and continue

until the position is filled.

Applications should be sent to:

Professor Jeremy Field, School of Life Sciences, John Maynard Smith Building University of Sussex Brighton BN1 9QG, UK.

Or e-mail your application as a single Word document to: j.field@sussex.ac.uk.

Jeremy Field <j.field@sussex.ac.uk>

Migrate 3 0 query

Recently I have run multiple DNA sequence data sets with the program Migrate 3.0 and run into a similar problem with each one. Often, about midway through sampling, one of my values for theta will jump wildly from, say, ($\theta = 0.8$) to ($\theta > 1 \times 10^{12}$). In some cases, multiple theta values will do this, sometimes it is only one theta. I can run the same data set twice and different thetas will do this in different runs. Has anyone else run into this problem, and can it be fixed?

Joel Anderson <Joel.Anderson@tpwd.state.tx.us>

MillionTaxa DistanceTree

if someone has an enormous table with pairwise distances between 1 million protein sequences, and he wants to build a tree out of that (say, using neighbor joining), is there a way to do that?

Thanks,

Rutger

Dr. Rutger A. Vos School of Biological Sciences Philip Lyle Building, Level 4 University of Reading Reading RG6 6BX United Kingdom Tel: +44 (0) 118 378 7535 <http://www.nexml.org> <http://rutgervos.blogspot.com> rutgeraldo@gmail.com

MillionTaxa DistanceTree answers

Dear EvolDir,

a few days ago I posted a query about how to construct a distance tree for 1 million taxa. I posted this query on behalf of someone else (the "OP", if you like), who has assembled a very large dataset of pairwise Smith-Waterman distances between various proteins. The OP's plan was to use these distances to give some structure to a landscape of proteins (orthologs and paralogs from a variety of taxa) by clustering them by distance. Various responders assumed/hoped that the OP also has a sequence alignment, but that's actually not the case.

Here's a summary of the responses received:

Several responders suggested tools that operate directly on distances. Sergios-Orestis Kolokotronis suggested that QuickTree/QuickJoin (<http://www.daimi.au.dk/~mailund/quick-join.html>) might be of use. Jeff Boore suggested a pipeline called PHRINGE (<http://oomycetes.genomeprojectsolutions-databases.com/>) that is quite close, in spirit, to what the OP is trying to achieve.

A number of responders (Jason Stajich, Paramvir Dehal, Mark Holder) suggested FastTree (<http://www.microbesonline.org/fasttree/>). However, this requires a protein alignment, which the OP doesn't have.

Brian Foley discussed the problem of aligning this many sequences, with some special case suggestions for doing this using an HMMer model. Not really the situation that the OP is dealing with, but an interesting problem nonetheless.

Others (Xuhua Xia, Jason Caravas) discussed the issue of allocating memory for this many pairwise distances - the implication being that, if that's taken care of, number-crunching thru all these pairs using neighbor-joining (however implemented) is something that is done in linear time and therefore manageable.

For example, Xuhua Xia suggested that this could be done using DAMBE, memory requirements permitting. Jason Caravas suggested that one could also re-implement the neighbor-joining algorithm, which isn't that complex (and usefully described in Joe Felsenstein's book "Inferring Phylogenies").

Ruchira S. Datta recommended a paper (<http://bioinformatics.oxfordjournals.org/content/24/13/i41.abstract?keytype=ref&ijkey=tHbUa129vtj6z>) that discusses algorithms that don't require the entire distance matrix in memory at once.

Thank you all for your responses!

Rutger

– Dr. Rutger A. Vos School of Biological Sciences Philip Lyle Building, Level 4 University of Reading Reading RG6 6BX United Kingdom Tel: +44 (0) 118 378 7535 <http://www.nexml.org> <http://rutgervos.blogspot.com> rutgeraldo@gmail.com

NESCent seeks Hackathon Whitepapers

The National Evolutionary Synthesis Center (NESCent), in keeping with its objective to promote collaborative development of open-source, reusable, and standards-supporting informatics resources, sponsors highly collaborative, face-to-face software development events, called “hackathons” (see [1]). To ensure that this program continues to be responsive to user needs and to tap into the expertise and creativity of the evolutionary biology community, NESCent is soliciting short whitepapers (2-6 pages) [2] on potential target areas for future hackathons.

To further encourage submissions, we have now distilled specific guidelines for proposing hackathon events, based on the experiences gained from events we have sponsored in the past: <http://informatics.nescent.org/wiki/Hackathon.Whitepaper.Guidelines> The Center’s Call for Informatics Whitepapers [3] includes not only hackathons, but also a large spectrum of other initiatives to be undertaken by the Center, including training, software development, collaborative ontology development, and coordination of data standards. Whitepapers are accepted at any time and reviewed on an on- going basis.

URLs: [1] Collaborative cyberinfrastructure events and programs organized by NESCent: http://informatics.nescent.org/wiki/Main_Page

[2] NESCent Call for Informatics Whitepapers <http://www.nescent.org/informatics/whitepapers.php>

[3] Hackathon Whitepaper Guidelines: <http://informatics.nescent.org/wiki/Hackathon.Whitepaper.Guidelines> [4]

Past NESCent-sponsored hackathons: http://informatics.nescent.org/wiki/Main_Page#Hackathons hlapp@nescent.org

NSF EvoDevoNetwork

We would like to announce a new funding and networking opportunity for researchers in evolutionary and ecological developmental biology: a National Science Foundation Research Coordination Evo-Devo-Eco Network called EDEN (<http://edenrcn.com/>).

The major aims of EDEN are the following: To fund research exchange grants allowing active interchange of tools and techniques among labs working on emerging model systems. To fund undergraduate internships in the field of Evo-Devo-Eco with an emphasis on emerging model systems. To document the tools and techniques being used and developed in these organisms and make them publicly available for future users. To promote interactions across the Evo-Devo-Eco community through conference funding and the sponsorship of workshops. EDEN’s first deadline for funding applications is October 31, 2010. You can read about the funding available at <http://edenrcn.com/funding/>. If you are working at the interface of the fields of development, evolution, and ecology, and/or with non-traditional model organisms, you have probably found yourself developing new techniques and tools. Perhaps you have used well-established protocols from traditional model organisms as a starting point, but have had to modify these protocols by painstaking trial and error, without the benefit of a large research community to support work on your organism.

If you are working with well-established model organisms, perhaps you would like to add an evolutionary or comparative dimension to your work, but have not worked with other organisms before.

With the support of the National Science Foundation, we have developed a new research coordination network called EDEN (Evo-Devo-Eco Network) to help address these challenges. You can read about EDEN’s activities and opportunities at <http://edenrcn.com/>. Please consider “joining” EDEN by filling out a brief survey about your lab’s areas of expertise. You can complete the survey on our website at

<http://edenrcn.com/join/> or by clicking here

<http://www.surveymonkey.com/s/JoinEDEN> This survey will allow your lab to be added to a searchable database of scientists, organisms and techniques that will soon be available on the EDEN website. With this

database, other researchers in development, evolution and ecology will be able to learn about your work, hopefully facilitating new and useful networks and collaborations.

We encourage you to go to EDEN's website to read more about it, and to check back frequently for future calls for applications, protocols, and workshop and symposia announcements.

Please feel free to email us at edenrcn@fas.harvard.edu with questions about the program, and forward this email to colleagues who you think would be interested in EDEN.

Barbara Perlo <perlo@fas.harvard.edu>

Problematic Barcode datasets

Dear colleagues,

I am working on a manuscript comparing different methods for analyzing DNA barcodes and am looking for 'problematic' barcode datasets (i.e. species are not reciprocally monophyletic in a NJ tree).

Preferably, these datasets are published and contain at least 4 non-monophyletic species (and >10 sequences per species). Also, they should be reasonably clean of identification errors.

If anyone has a dataset matching most of these criteria (or knows where to find one), please let me know.

Obviously, authors of the datasets used will be cited.

Thanks!

Robin

robin.vanvelzen@wur.nl

Robin van Velzen PhD student Biosystematics Group Wageningen University

Wageningen Campus, Radix building 107, Room W4.Aa.095 Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands PO Box 647, 6700 AP Wageningen, The Netherlands Tel. +31 (0)317 483425 <http://www.bis.wur.nl> Robin.vanVelzen@wur.nl

Queensland VolFieldAssist

Field assistant position available to study limits to adaptation in Australian rainforest *Drosophila*

The deadline for applications for this position has been extended to 7th February 2011

We are looking for a motivated, hardworking volunteer to help conduct fieldwork in northern Queensland as part of a project examining limits to adaptation in rainforest *Drosophila*. This project is based at the University of Bristol, UK (PI Dr Jon Bridle, postdoc Dr Eleanor O'Brien), and involves collaboration with researchers at the University of Queensland (Professor Mark Blows) and the University of Melbourne (Professor Ary Hoffmann). This position represents an excellent opportunity to be involved in exciting research in evolutionary biology, and would suit someone seeking direct experience of a field-based project in this area.

The role of the volunteer will be to assist with collection of *Drosophila* at several locations in the rainforest in northern Queensland, sort field-collected specimens, maintain live stocks and perform other duties as required. Training will be provided in *Drosophila* identification and maintenance, although previous experience would definitely be helpful.

Essential requirements: (1) BSc in evolutionary biology, genetics, ecology or a related discipline. (2) Willingness to spend long days working in rainforest in hot, humid conditions. (3) Ability to work carefully and meticulously, with close attention to detail. (4) Enthusiasm and the ability to work closely as part of a team. (5) A full driving licence.

Previous fieldwork experience and 4 wheel-driving experience would also be an advantage.

The volunteer must be able to spend up to 8 weeks in the field from mid-March - May 2011. Full living expenses (meals and accommodation) will be paid during this period. We are also able to make a contribution of up to 400 GBP (approx. \$AU630) towards the costs of travel to the field site.

Applications should be received by the 7th February 2011, and must include a cover letter and CV, including the names of two referees.

To request further information about this position, or to apply, please contact Dr Eleanor O'Brien (eleanor.obrien@bristol.ac.uk).

– Dr. Eleanor O'Brien Postdoctoral Researcher School of Biological Sciences University of Bristol

Ph: +44 (0)117 928 7470

Eleanor.OBrien@bristol.ac.uk

RockyMountains VolFieldAssist SquirrelEvolution

Field Assistants Required-Columbian ground squirrels
Sheep River Provincial Park, Alberta, Canada

We are looking for 3 volunteers to assist with fieldwork for the period of April 07 to Aug 30, 2011. The project investigates the evolutionary ecology of Columbian ground squirrels. As a member of the study, assistants will be involved with monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals. Fieldwork will involve live-trapping and handling of animals, behavioural observation and assistance with the measurement of physiological (metabolism) traits on free-ranging animals. This is an excellent opportunity to gain experience working with a collaborative research team on a long-term study of a wild mammal. Opportunities exist for side-projects for interested and motivated applicants. All fieldwork is carried out in the spectacular Rocky Mountains of western Alberta, Canada, home to some of the most majestic wildlife in North America. We will be staying at the University of Calgary's R.B. Miller research station in Sheep River Provincial Park, Alberta (<http://bgs.ucalgary.ca/facilities/facilities>). You will interact with other researchers working with ground squirrels on a diversity of projects in behavioural and population ecology. Additionally, the field station is home to a number of other researchers working on a variety of projects, ranging from insects to large mammals.

Food, accommodation and travel to and from Calgary or Edmonton, Alberta are provided. Training will be provided and no experience is necessary, but candidates should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal behaviour. Periods of time will be spent camping and, as such, successful applicants need to enjoy the outdoors, be up-beat, positive, responsible and work well as a member of a team.

If you wish to apply for one of these posts then please send a CV with a cover letter and contact details of three references (with e-mail addresses), by email to Jeff Lane (contact info below), by March 01, 2011.

Contact:

Dr. Jeff Lane
Centre d'Ecologie Fonctionnelle et Evolutive
Centre National de la Recherche Scientifique
34293 Montpellier Cedex 5
France
u.columbianus@hotmail.com
Jeff Lane <u.columbianus@hotmail.com>

Software MetaPIGA2

Dear all,

Thanks to the feed back of users, we have fixed bugs and added several functionalities to *MetaPIGA2* (a robust implementation of the Metapopulation Genetic Algorithm (metaGA) for large phylogeny inference under Maximum Likelihood).

Most importantly, a bug WAS CAUSING OUT-OF-MEMORY PROBLEMS WITH LARGE DATASETS when using the Likelihood Ratio Test (LRT), the Akaike Information Criterion (AIC), or the Bayesian Information Criterion (BIC) for automated selection of substitution models that best fit the data. This has now been solved. By the way, general memory requirements have also been reduced by half and the likelihood computation is approximately 20% faster.

Multi-core processing has been extended to model testing as well. Multiple minor bugs have been fixed (all described in the "change log").

For updating MetaPIGA2, either download the new version from <http://www.metapiga.org> or launch your previous version of MetaPIGA2 while connected on the internet (and the auto-update system will propose you to update).

MetaPIGA2 is described in: Helaers & Milinkovitch BMC Bioinformatics 2010, 11: 379 <http://www.biomedcentral.com/content/pdf/1471-2105-11-379.pdf> The metaGA algorithm is described in: Lemon & Milinkovitch; PNAS, 99: 10516-10521 (2002) <http://www.pnas.org/content/99/16/10516.full.pdf> Stay tuned for protein models, soon to be implemented in MetaPIGA.

Best wishes, Michel and Raphaël.

Prof. Michel C. Milinkovitch Laboratory of Artificial & Natural Evolution Dept of Genetics & Evolution

University of Geneva Sciences III, 30, Quai Ernest-Ansermet 1211 Genève 4, Switzerland

Michel.Milinkovitch@unige.ch

Tel +41(0)22 379 67 85 Fax +41(0)22 379 67 95

www.lanevol.org Michel.Milinkovitch@unige.ch

Software RAxML-Lightv1 0 0

Dear Community,

RAxML-Light v 1.0.0 is now available for download under GNU GPL at: <http://www.kramer.in.tum.de/-exelixis/software.html> RAxML-Light is a strapped-down RAxML version for conducting tree searches on very large trees under the CAT approximation of rate heterogeneity.

It's key features are:

1. A light-weight efficient checkpointing and restart capability
2. A highly optimized fine-grain MPI parallelization that allows you to concurrently compute the likelihood of a single tree on hundreds or thousands of processors, provided that you have a low latency interconnect.

A usage manual is included in the source code archive.

This is the first release of this code, so please send me an email in case of problems, bugs, incomplete documentation etc.

Cheers,

Alexis

Dr. Alexandros Stamatakis

Group Leader: Scientific Computing Group (Exelixis Lab & HPC Infrastructure) Heidelberg Institute for Theoretical Studies (HITS gGmbH)

Schloss-Wolfsbrunnenweg 35 D-69118 Heidelberg Germany

Tel: +49 162 8541515 (Mobile) +49 6221 533240 (Office) Fax: +49 6221 533298 Skype: stamatak Email: Alexandros.Stamatakis@h-its.org WWW: <http://www.kramer.in.tum.de/exelixis/> <http://www.hits.org/english/research/sco/index.php> Amtsgericht Mannheim/HRB 337446 Managing Directors: Dr. h.c. Klaus Tschira/Prof. Dr.-Ing. Andreas Reuter

alexandros.stamatakis@gmail.com

Spittlebug samples

Dear all,

I am a PhD student from the Faculty of Sciences of Lisbon University, Portugal, and I am currently interested in the study of the genetic structure and the genetic basis of the dorsal colour polymorphism of the spittlebug *Philaenus spumarius* (Insecta, Hemiptera, Aphrophoridae) and related species of the same genus. I am having some difficulties getting samples from some geographic regions. I would greatly appreciate the contacts of some people who would be able to help me to get samples from *P. spumarius* from Balkans and east of Europe, *P. loukasi* and *P. signatus* from Greece, *P. arslani* from Liban and *P. italosignus* from Italy.

Thank you,

Ana Rodrigues

Computational Biology and Population Genomics research group (CoBig2, * <http://cobig2.fc.ul.pt>).

Centro de Biologia Ambiental

Departamento de Biologia Animal

Faculdade de Ciências da Universidade de Lisboa

Edifício C2, sala 2.3.22

1749-016 Lisboa

Portugal

Ana Sofia Rodrigues <ana87bartolomeu@gmail.com>

SSB ErnstMayrAward

Society of Systematic Biologists Ernst Mayr Award (Graduate Student Award)

The Ernst Mayr Award is given to the presenter of the outstanding student talk in the field of systematics at the annual meetings of the Society of Systematic Biologists. The award consists of \$1000, a special certificate, and a two-year subscription to the journal Systematic Biology.

Who is Eligible. Members of the Society who are stu-

dents or have completed their Ph.D. within the last 15 months are eligible. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to be considered (to join go to: <http://systbio.org/?q=node/6>). Previous Mayr award winners are not eligible.

Application Procedure. Applications should be sent to the current SSB Awards Committee Chair (Sydney Cameron), at ssb-apps@life.illinois.edu. E-mail submissions are required. IN THE SUBJECT LINE OF THE E-MAIL, please indicate the SSB award category as "Mayr Award" followed by first name initial and last name.

Applicant Procedure:

1. To be eligible for this award, you will need to email a 400-word abstract of your talk to the SSB Mayr Awards Committee (ssb-apps@life.illinois.edu) by April 1, 2011. All candidates will be notified of their status no later than April 10, 2011. Please note that the cut-off date for talk submission is April 17, 2011, which coincides with the final day for "early bird" registration of the annual Evolution meeting, this year "Evolution 2011", hosted by the University of Oklahoma in Norman, OK. This gives you at least a week between notification of acceptance by the committee and talk submission deadline date.
2. If selected as a Mayr Award candidate, create a login on the Evolution 2011 registration site and register for the meeting.
3. After receiving verification of registration payment, you will receive a special code via email that will allow you to login to the Evolution 2011 Presentation Submission site. When you submit your title and keywords you will be given an option to declare your candidacy for the SSB Ernst Mayr Award.
4. Your presentation will be placed in the Ernst Mayr Student Presentation Award session for Evolution 2011. Again, you must first register and pay for the meeting before we can place your talk into the session.

Judging. Based on the submitted abstracts, the Mayr Awards Committee (appointed by the Awards Chair) will select a maximum of 16 applicants for inclusion in the Ernst Mayr Award session, which will be held at a single venue as a continuous session.

Talks will be judged on creativity, quality, excellence of research, and quality of presentation. Abstracts should clearly indicate methods used, conclusions, and the relevance to systematics. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible.

Co-Authors. The paper may be co-authored. It is understood that the ideas, data and conclusions presented

are primarily and substantially the work of the student presenter, and the intention is that the student presenter will be senior author on the published version of the paper.

Notification of Winner. The winner of the award will be announced at the SSB business meeting in Normal and again during the banquet awards ceremony (complimentary ticket provided) at the conclusion of the Evolution Meetings, whereupon the winner will be given an award certificate. An announcement of the winner will also be published in *Systematic Biology*.

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

ofc ph. 217-333-2340 lab ph 217-333-2170 cell ph 217-766-5631 scameron@life.illinois.edu

www.life.illinois.edu/scameron Sydney Cameron
<scameron@life.illinois.edu>

SSB GradStudResearchAward

Society of Systematic Biologists Graduate Student Research Award

The Society of Systematic Biologists (SSB) announces the 2011 annual Graduate Student Research Award competition. The purpose of these awards is to assist students in the initiation (first two years) of their systematics projects and in the collection of preliminary data to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: <http://systbio.org/?q=node/6>). Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply. Awards will range between \$1,200 - \$2000 and approximately seven to ten awards will be made. The list of awardees below includes examples of successful proposals for you to download.

How to apply All application materials must be in electronic format. Applicants and those writing letters of recommendation are required to use pdf format, rather than Word or some other application, to minimize diffi-

culties in file transfer. Applicants should send all materials (except letters of recommendation) in a SINGLE pdf file. Letters of recommendation should be sent separately by the referees in pdf format or in the text of an e-mail; please include the FULL NAME OF APPLICANT in recommendation letters.

Applicants must submit

1. a curriculum vitae (one page)
2. brief research proposal including objectives, methods, significance, and schedule (max. three single-spaced pages including literature cited and any figures and tables)
3. budget and budget justification (1 page)
4. and arrange for two letters of recommendation; one letter must be from the student's current graduate advisor.

The research proposal must clearly state the current stage of the proposed research and the current year and status of the student. PLEASE INCLUDE APPLICANT'S CONTACT E-MAIL ADDRESS AT THE TOP OF THE APPLICATION ITSELF. Both Masters and Ph.D. students in their FIRST TWO YEARS are eligible. Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work.

Please email all application materials and queries to SSB Awards Committee ssb-apps@life.uiuc.edu. IN THE SUBJECT LINE OF THE E-MAIL, PLEASE INDICATE "Student Research" FOLLOWED BY FIRST INITIAL AND LAST NAME.

To be considered for this year's award, application materials, including letters of recommendation, must be received electronically no later than March 31, 2011.

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

ofc ph. 217-333-2340 lab ph 217-333-2170 cell ph 217 766-5631 scameron@life.illinois.edu

www.life.illinois.edu/scameron Sydney Cameron
<scameron@life.illinois.edu>

StKilda Volunteer MousePopulations

Volunteer wanted for 5 weeks from 8th March 2011 (plus 2 days travel either side), to help with live trapping of field mice on St Kilda, a small archipelago 180km off the west coast of Scotland.

Responsibilities consist of helping to set up trapping grids on remote parts of the island, prepping and cleaning traps, handling mice and recording data. You will be living as part of a small group of researchers in restored cottages on the remotest field site in the British Isles; the accommodation is fairly basic but the scenery is spectacular! A great opportunity to acquire small mammal field experience.

A brief news report and footage of the project can be found on the BBC news website - <http://www.bbc.co.uk/news/uk-scotland-highlands-islands-11168757>

You must be available for the full duration of the field work, and preference will be given to people with a background in biological sciences. Volunteers must be fit and confident enough to carry 18kg backpacks over steep and rocky terrain, and happy to work in all weathers.

Helicopter flights between St Kilda and Benbecula (Outer Hebrides) will be provided, as will food and board whilst on St Kilda. Reasonable travel expenses within Scotland will also be reimbursed.

To apply for this volunteer position, please send a CV and brief covering letter, plus details of one or two referees who can be contacted at short notice by email to: Tom Black (t.w.black@sms.ed.ac.uk).

T.W.Black@sms.ed.ac.uk

Sweden FieldAssist BirdEvolution

Field assistants in evolutionary ecology of two sympatric flycatcher species (*Ficedula hypoleuca* and *F. albicollis*).

Pied and collared flycatchers are closely related migratory passerines that breed in Europe and co-occur on Baltic Islands of Öland and Gotland. In the contact zone they tend to compete over nesting sites and food resources; they also hybridize occasionally. A field work on flycatchers gives an excellent and rewarding opportunity to be involved in exciting research in evolutionary biology. It will give you an insight into interspecific interactions between competing species, impact of blood parasites on their hosts as well as into hands-on

research on long-studied wild bird populations. This position is perfect for someone who seeks direct experience of a field-based project.

The field stations are situated on Swedish island Öland. The field work will involve measuring and sampling flycatcher chicks, nest-box checking, song recording, collecting and managing breeding data. We won't cover travel or food expenses, but we offer a salary, free accommodation and a transport once on-site.

Training will be provided in species recognition and data collection, although previous fieldwork experience would definitely be an advantage. Essential requirements:

(1) Fluency in English (2) Willingness to spend long days working in the forest, sometimes in harsh weather

conditions (3) Ability to work efficiently but carefully at the same time (4) Enthusiasm and the ability to work closely as part of a team (5) A driving license.

Field assistants should be able to spend in the field 6-8 weeks between early May and late June 2011.

Applications should be received by the 6th March 2011, and must include a cover letter and CV.

To request further information about this position, or to apply, please contact Katarzyna Kulma (katarzyna.kulma@ebc.uu.se), Department of Animal Ecology; Evolutionary Biology Centre (EBC), Uppsala University

email: katarzyna.kulma@ebc.uu.se email: katarzyna.kulma@ebc.uu.se

PostDocs

Australian InstMarineSci CoralEvolution	74	UCambridge SequencingStatistics	88
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Australian InstMarineSci CoralEvolution

Super Science Fellowships

The Australian Institute of Marine Science is the leading national organisation researching tropical marine ecosystems. The Institute has world-class laboratory facilities, two modern research vessels and extensive technical support. Facilities are being enhanced with \$55M of capital funds from the Australian Government. This will include a state-of-the-art experimental ocean simulator in an extensive seawater precinct to support innovative research into coral spawning, water quality and climate change.

As part of the Australian Government's Super Science Initiative (Marine and Climate), AIMS has received competitive funding from the Australian Research Council to support three exceptional early-career researchers. Successful applicants will conduct original research within a Project entitled "A Changing Climate on the Great Barrier Reef: Present and Future Implications", with a focus on the following topics:

1. Interactive effects of changing climate and water quality on corals and coral reefs (Position No. 468)
2. Coral cellular microbes: community transitions and roles in a changing climate (Position No. 469)
3. Coral associated viruses: pathogens, mutualists or agents of evolution in a changing climate (Position No. 470)

These fellowships are available from 1 July 2011. Fellowship numbers 469 and 470 will address the roles of bacteria and viruses on the ecology and evolution of corals, e.g. the evolution of new traits through lateral gene transfer. Further, the bacterial and viral communities associated with corals will be identified using next generation sequence analysis, i.e., there is also relevance to the field of systematics. More information about these jobs and detailed application kits can be found at www.aims.gov.au/employment. Successful candidates will join a collaborative, multidisciplinary team addressing important questions about the future of coral reefs. Ideal candidates will be high achievers with up to 3 years of postdoctoral experience in directly relevant research. Positions are available for 3 years fixed term and will be based in Townsville, Queensland. Generous working conditions apply including a commencing salary of AU\$73,714 - AU\$81,091 plus superannuation and other benefits.

Project specific inquiries may be made to:

* Position No. 468 - Dr Katharina Fabricius (k.fabricius@aims.gov.au)

* Position No. 469 - Dr David Bourne (d.bourne@aims.gov.au)

* Position No. 470 - Dr Madeleine van Oppen (m.vanoppen@aims.gov.au)

General enquiries may be directed to AIMS Research Manager, Dr Lyndon Llewellyn (L.Llewellyn@aims.gov.au).

Closing date for all positions is 4 March 2011.

AIMS is an EEO Employer and promotes a smoke free work environment

Kylie Tomarchio <K.Tomarchio@aims.gov.au>

BangorU CichlidEvolution

A three-year postdoctoral position is available in the School of Biological Sciences to work with Professor G.F. Turner (george.turner@bangor.ac.uk) applying high-throughput sequencing and bioinformatic methods to the study of evolution and speciation. The focus of the research group is on speciation of African cichlid fishes, for which an increasing amount of molecular information is becoming available, including full genome sequences. The appointee will join the large, thriving team in the Molecular Ecology and Fisheries Genetics Group (<http://mefgl.bangor.ac.uk/>), in new purpose-built molecular laboratories in the Environment Centre, Wales, investigating the origins and significance of population and species biodiversity in animals.

Applicants should have a broad interest in evolution, genetics and ecology, excellent writing and interpersonal skills, with a strong willingness to work as part of a team, and to work to deadlines on research publications and grant applications. A background in molecular genetics or bioinformatics and an interest in using high-throughput sequencing methods is essential. The successful candidate will be expected to start as soon as possible.

Further details and application forms can be found at <http://www.bangor.ac.uk/corporate/-vacancies/home.php?jobdetails=1&reference=11-10/-10&category2=Academic> Closing date for applications: 1.00 p.m. Monday 7th March, 2011.

Interviews will be held on 28th March, 2011.

nitram8@hotmail.com

BiKf Germany PlantMolecularClocks

The Biodiversity and Climate Research Centre (BiK-F) is a new interdisciplinary institute with the mission to carry out internationally outstanding research on the interactions of biodiversity and climate change on the organism level. It has been founded by the Senckenberg Gesellschaft fuer Naturforschung, the Goethe-University Frankfurt am Main, and other partners. The Centre is funded by the Federal State of Hesse through its Initiative for the Development of Scientific and Economic Excellence (LOEWE). It provides a new, dynamic research environment that integrates a variety of disciplines from both natural and social sciences. The Project Area A "Evolution and Climate" invites applications for the position of a

Postdoctoral Researcher Plant Biogeography/Molecular Clocks Ref. A29b

The Department of Systematics, Evolution and Climate Change, lead by Prof. Alexandra N. Muellner (http://www.bik-f.de/root/index.php?page_id=262), is seeking a botanist with a research focus on plant evolution and historical biogeography. The successful applicant is expected to develop an extramurally funded research program, as well as collaborating with other staff members. The position entails basic teaching obligations.

Applicants should hold a Ph.D. in Botany or in another relevant subject and have a solid publication record. Preference will be given to applicants with skills in at least one of the following areas: historical biogeography, molecular clocks, ecological phylogenetics, evolutionary ecology. Competence in general biostatistical methods and knowledge of the Central European flora are an advantage. Excellent written and oral communication skills in English and the interest in joining a multidisciplinary team are required.

Salary and benefits are according to a public service position in Germany (TV-H E 13). The Research Centre BiK-F advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference. The contract shall start as soon as possible and will initially be restricted to three years. The duty station will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft fuer Natur-

forschung. Please send your application by e-mail attachment (pdf), mentioning the reference of this position (#A29b) and including a letter outlining your suitability for the position, a detailed CV, contact details of 2 referees and a copy of your PhD certificate before 2 March 2011 to: Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. E-mail to Service and Finances: recruiting@senckenberg.de, and cc to alexandra.muellner@senckenberg.de.

For scientific enquiries please write to Prof. Dr. Alexandra N. Muellner (e-mail: alexandra.muellner@senckenberg.de).

Many thanks and Kind regards

[recruiting <recruiting@senckenberg.de>](mailto:recruiting@senckenberg.de)

CNRS GifsurYvette EvolutionSexualReproduction

Post-doctoral Research Associate (22 months) in proteomic analysis at the CNRS (Gif-sur-Yvette France)

The "Centre National de la Recherche Scientifique" (CNRS) is starting a new program funded by the French National Research Agency "ANR", called Sex-Dro. The aim of the program is to study chemical signals (pheromones and seminal peptides) involved in sexual reproduction and their evolution. The project is coordinated by Dominique Joly (<http://www.legs.cnrs-gif.fr>).

The postdoc will perform comparative proteomic analyses on the seminal fluid of the species of the melanogaster subgroup. Work will be carried out at the mass spectrometry lab of the « Institut de Chimie des Substances Naturelles » of the « Centre de Recherches » at Gif-sur-Yvette (<http://www.icsn.cnrs-gif.fr>) located at 30 km south from Paris, 45 mn by suburban train.

The candidate will be in charge of the MS method development and validation and of computational analysis of the data. He (she) will use the data obtained by mass spectrometry using nano LC/MS/MS orbitrap after the digestion of proteins separated by SDS-PAGE. Skills in protein sequencing by tandem mass spectrometry will be a plus. The candidate will use the protein or genomic sequence databases to identify proteins of

interest. In this context a good knowledge of genomic and proteomic databases and their maintenance is required. Experience with label free quantification techniques would be also appreciated.

The successful candidate will work in collaboration with both evolutionary biologists and biochemists. Starting date will be flexible but preferentially not after September 31st.

The net salary will be around 1900 euros per month, including social security, depending on the applicant's experience.

Candidates should send the following information before March 31th 2011 : - a detailed CV; - a cover letter stating the research interests and experience describing the qualifications for this position; - two letters of recommendation; - a list of publications with the pdfs of the most appropriate papers regarding the position.

Please send these documents to both : Dominique Joly Laboratoire Evolution, Génomes et Spéciation Dominique.Joly@legs.cnrs-gif.fr and Jean Pierre LE CAER Institut de Chimie des Substances Naturelles lecaer@icsn.cnrs-gif.fr

With my very best regards, Dominique

Dominique JOLY Directrice-adjointe Laboratoire Evolution, Genomes et Speciation Equipe Génétique Évolutive, Reproduction et Adaptation des Drosophiles (GÉRAD) CNRS - UPR 9034 - bat 13 Avenue de la Terrasse F-91198 Gif sur Yvette Cedex France Tel: (33) 1 69 82 37 34 Fax: (33) 1 69 82 37 36 E-mail:joly@legs.cnrs-gif.fr Web:<http://www.legs.cnrs-gif.fr/> Dominique Joly <Dominique.Joly@legs.cnrs-gif.fr>

DukeU PopulationGenomics

Applications are welcomed from individuals interested in working with Marcy Uyenoyama and David L. Swofford on the development of sampling-based statistical methods for inference of rates of introgression between populations and the existence and location of incompatibility loci. Here, incompatibility loci are sites at which variants are neutral in their home context and deleterious in other contexts. Incompatibility loci may include factors contributing to reproductive isolation between different species or to local adaptation in subpopulations of a single species.

Applicants should have a background in statistics, computation, bioinformatics, population genetics, or a related field. The postdoctoral scholar may participate in research in one or more of the following key areas:

(1) Population genetics

First-principle analysis of the evolutionary dynamics of incompatibility loci and neutral sites elsewhere in the genome

(2) Genome-scale sequence analysis

Bioinformatic analysis of population samples of genomes

(3) Sampling-based inference

Construction and implementation of likelihood-based or likelihood-free methods for inferring the existence and location of incompatibility loci

Funding is presently available and the appointment may continue for up to three years. Please send a CV, a brief statement of research interests, and contact information for two or three references to marcy@duke.edu.

M. K. Uyenoyama Department of Biology 130 Science Drive Box 90338 Duke University Durham, NC 27708-0338 USA

Tel: 1-919-660-7350 Fax: 1-919-660-7293 email: marcy@duke.edu

marcy@duke.edu

ETH Zurich EvolutionFungicideResist

POSTDOC POSITION IN POPULATION BIOLOGY OF FUNGICIDE RESISTANCE AT THE ETH ZURICH

A postdoc position is available in the Theoretical Biology Group of Sebastian Bonhoeffer at the Institute of Integrative Biology, ETH Zurich. The main research area of the group is the population biology and genetics of infectious diseases. With the advertised position we are planning to expand our research to mathematical models of the evolution of fungicide resistance in plant pathogens. The ideal candidate has both strong quantitative skills (mathematics, programming, statistics) as well as background in the relevant areas of biology (population biology, infectious diseases, resistance, epidemiology).

In the Theoretical Biology Group postdocs can develop their research with a high degree of independence. The group provides a stimulating environment with a broad range of expertises and ample opportunities for collaboration. For more information on research and current members of the Theoretical Biology Group see www.tb.ethz.ch. The group has strong links with several experimental groups (Experimental Ecology: Paul Schmid-Hempel; Molecular microbial ecology: Martin Ackermann). Moreover a close collaboration with the Bruce McDonald's plant pathology group is foreseen.

The ideal starting date is May/June 2011. Salary is approximately 80,000 Swiss Franks per year. Zurich is a great place to live and to do research. It is the home of two big universities (the University of Zurich and the ETH), and is an attractive city in beautiful surroundings with a multinational population and many educational and recreational opportunities.

To apply send a letter describing your interest in this position, a CV and the names and contact addresses of two referees by email to sebastian.bonhoeffer@env.ethz.ch. To enable automatic e-mail filtering please mention "PPP-Application" as the subject of the mail. Review of applications will begin on March 1, 2011.

Sebastian Bonhoeffer Theoretical Biology, Institute of Integrative Biology, ETH Zurich www.tb.ethz.ch sebastian.bonhoeffer@env.ethz.ch

ETH Zurich Insect Differentiation

Postdoctoral Research Assistant in Molecular Entomology ETH Zurich, Applied Entomology

The project deals with worldwide patterns of genetic differentiation in an invasive moth pest that has followed its fruit tree hosts around the globe. To understand the processes by which this invasive species colonizes new regions, the postdoctoral research assistant will analyze samples (representing the global distribution of this insect species) at available polymorphic microsatellite loci, and evaluate structuring and differentiation of populations using state-of-the art techniques. Interpretation of data will link to historical records of infestation and routes of trade.

ETH Applied Entomology investigates insect-plant interactions, particularly as a basis for more sustainable pest and crop management, and projects range from

the molecular to the ecosystem level. Main languages spoken in the group are English and German.

Candidates with a PhD in a relevant discipline and strong experience with molecular methods are invited to apply. Expertise in entomology and in state-of-the-art population genetic analysis techniques is advantageous.

The position can be filled immediately, or upon agreement. The duration of the appointment is one year, with option for extension contingent on performance and opportunity.

Review of applications will start immediately and continue until a suitable candidate is found. Send Curriculum Vitae, a list of methods you are familiar with, indication of the earliest possible starting date, as well as addresses with phone numbers of three references to Prof. Dr. Silvia Dorn.

Prof. Dr. Silvia Dorn ETH Zurich / Applied Entomology (Subject: Postdoc Molecular Entomology) Schmelzbergstrasse 9 / LFO, 8092 Zurich, Switzerland or e-mail: silvia.dorn@ipw.agrl.ethz.ch; (Subject: Postdoc Molecular Entomology).

For informal inquiries, contact Dr. Dominique Mazzi e-mail: dominique.mazzi@ipw.agrl.ethz.ch

dominique.mazzi@ipw.agrl.ethz.ch

Frankfurt Conservation Genomics

Job Advertisement Ref 04-11002

Senckenberg Gesellschaft für Naturforschung has an international reputation in all fields of Natural History research. It runs six research institutes and two museums in Germany and is also custodian of the UNESCO World Heritage Site at Messel.

The Senckenberg Research Institute, department Limnology and Nature Protection Research, Gelnhausen is looking for a researcher for the following project:

PostDoc/PhD Positions available in Wildlife/Conservation Genomics

In the frame of a joint research project, the National Reference Center for Genetic Analyses of Large Carnivores at Senckenberg Research Institute in Frankfurt/Main and the Leibniz institute for Zoo and Wildlife Research in Berlin (IZW) invite applications for one postdoctoral, Frankfurt and one post-

doctoral (or two PhD) positions, Berlin in the field of Wildlife/Conservation Genomics: We are looking for candidates with a strong background in molecular biology, population genetics, and/or bioinformatics. Preferably, one candidate with experience in the development of SNP based marker panels and one person with experience in handling of large amounts of genotypic data will be chosen. Organizational skills and the willingness for frequent travels between the research partners in Frankfurt, Berlin, Munich, and further institutions among Europe are required. A proficiency of English is essential. The candidates develop and apply genome-wide, SNP based marker panels for endangered European carnivores. Markers will be used for genotyping large amounts of samples from Central Europe and adjacent regions. The ultimate goal of the project is to identify source regions, migration routes, and gene flow patterns in order to understand recent recolonization and spread of Central and Western Europe by elusive carnivores, such as wolf, lynx, otter, and further species. The implementation of a comprehensive genotype database will serve as the basis for understanding large scale dispersal patterns of European carnivores. The successful candidate will have a PhD in biology or a related discipline. This is a temporary position at the E13 level (fulltime) for Postdocs (or E13 half-time for PhD candidates), limited to 3 years and will be available from May, 1st, 2011. The position of IZW, Berlin may be split in two PhD positions, if suitable candidates apply. The Senckenberg Gesellschaft für Naturforschung and the Leibniz institute for Zoo and Wildlife Research (IZW) are equal opportunity employers and encourage women to apply for these positions. Equally qualified severely handicapped applicants will be given preference. The places of work will be Frankfurt am Main (Senckenberg station Gelnhausen) and Berlin. Please submit your application electronically with the usual documents until March 11th, 2010 to:

Administrative Director Dr. Johannes Heilmann c/o Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 D-60325 Frankfurt/Main E-mail: recruiting@senckenberg.de

For further information please contact by E-mail: cnowak@senckenberg.de

Many thanks and kind regards

recruiting <recruiting@senckenberg.de>

Institut Pasteur Microbial Population Genomics

2 years post-doctoral position in microbial population genomics, Institut Pasteur, Paris, FRANCE.

We seek a motivated and productive postdoctoral researcher to work on the population-level genomic diversity of pathogenic bacteria. The project is funded by the French Region Ile-de-France (DIM Malinf programme) and will focus on the evolutionary processes (gene flux, natural selection) that shape the diversity of *Klebsiella* and *Salmonella* genomes. The objectives also include the identification of novel pathogenicity and antibiotic-resistance determinants.

Institut Pasteur is one among leading institutes in the study of infectious diseases and in microbial genomics. The project is a collaboration among population and statistical geneticists (D. Falush, Germany; M. Achtman, Ireland), medical microbiologists, genomics platforms and microbiologists interested in functional aspects of host-pathogen interactions (P. Sansonetti's lab).

The successful candidate is expected to: - Analyze raw data from high-throughput sequencers - Contribute to annotation and perform comparative genomics of assembled genomes - Quantify gene flux within and among species - Detect selection footprints in genomes - Develop innovative bioinformatics tools to improve microbial comparative genomics.

The candidate should have a strong background in evolutionary biology or genomic data analysis, including some programming capabilities.

Duration: 2 years, available immediately; to be filled before June 1st, 2011.

Salary: 2,100 euro netto per month, plus social (medical insurance,...) advantages.

Application (detailed CV, cover letter, references): Dr. Sylvain Brisse - sylvain.brisse@pasteur.fr Genotyping of Pathogens and Public Health (PF8) Institut Pasteur, Paris, FRANCE

Sylvain Brisse <sbrisse@pasteur.fr>

InstZoology London BeeEvolution

Institute of Zoology Zoological Society of London

Postdoctoral Research Assistant in Molecular Ecology Two year fixed term contract Starting Salary GBP25,958 plus GBP3,554 London weighting

Applications are invited for a postdoctoral research assistant with experience in molecular ecology to work on a project investigating the biology of a range of bumblebee species, both estimating the dispersal distance of emerging queens to establish new colonies and the foraging range of worker bees. Candidates would ideally have an interest in social insect biology and experience in microsatellite loci genotyping and mitochondrial DNA sequencing.

The post is funded for 24 months under the Insect Pollinator Initiative and is available from 14th March 2011. Informal enquires and requests for further details can be directed to Bill Jordan (bill.jordan@ioz.ac.uk, 0207 449 6631).

Applications, with a covering letter, a current CV and names and full contact details of three academic referees, should be sent to Human Resources, Zoological Society of London, Regent's Park, London NW1 4RUK (email HR@zsl.org) by 28th February 2011.

Dr W C Jordan Institute of Zoology Zoological Society of London Regent's Park London NW1 4RY Tel: 0207 449 6631 Fax: 0207 586 2870 www.zsl.org/billjordan

bill.jordan@ioz.ac.uk

IPasteur PopStatGenetics

POSTDOC IN POPULATION AND STATISTICAL GENETICS, Pasteur Institute, Paris A postdoctoral position in population and statistical genetics is available in the Human Evolutionary Genetics Unit (Quintana-Murci's Lab), in the Department of Genomes and Genetics at Institut Pasteur in Paris. The lab combines large empirical datasets and computation approaches to study human population genetics, for more information see <http://www.pasteur.fr/>

research/heg. Current work in the lab focuses on a wide range of topics, including (i) the study of the relative effects of demography and natural selection in the shaping of human genome variability using next-generation sequencing data, (ii) the genomic control of gene expression related to both mRNA and microRNA and immunity-related processes, (iii) the influence of lifestyle (nomadic hunter-gathering to sedentary farming) on human adaptation to environmental pressures, but project details for the successful candidate are flexible. Our lab benefits from the large and outstanding community of researchers in population genetics, microbiology, immunology and computational biology at the Pasteur Institute, providing a working interdisciplinary research environment.

Applicants must have a strong background in statistics and computer science and a desire to do research in genetics and evolutionary biology, or a strong background in theoretical population genetics with experience analyzing genomewide datasets (expression and/or genetics data). Programming skills and proficiency in unix-based computational environments are essential.

Informal inquiries as well as applications (including a CV, copies of relevant publications and contact information for at least two references) should be emailed to Lluís Quintana-Murci at [<quintana@pasteur.fr>](mailto:quintana@pasteur.fr). The starting date is negotiable, and could be as early as June 2011.

Lluís QUINTANA-MURCI UP Human Evolutionary Genetics, CNRS URA3012 Institut Pasteur 25, rue du Dr. Roux 75724 Paris Cedex 15 France

Tel: +33 1 40 61 34 43 Fax: +33 1 45 68 86 39 e-mail: quintana@pasteur.fr

LundU ImmunityAdaptations

Post doc: Immunity adaptations & migration (ref number: PA 2011/113)

Centre for Animal Movement Research (CAnMove), Department of Biology, Lund University, Sweden.

A 2-year post doc stipend is available from 1 August 2011 in the project: 'Immunological and physiological adaptations to migration: comparing migrating V sedentary bird populations and species'.

Research on adaptations for migration in birds has traditionally focussed on traits affecting flight efficiency,

such as wing loading and body mass. However, different physiological and genetic adaptations (e.g., in basal metabolic rate (BMR) and immune function) in relation to variation in migration distance of populations/species can also be expected.

We offer a post-doc position on a project that focus on comparing immunological and physiological adaptations in long-distance versus short-distance/sedentary bird species. Initially, we have two projects in mind. (1) BMR and immunity in migratory and sedentary populations of robins (*Erithacus rubecula*). In this project, we will compare BMR, innate and acquired immunity between dark-legged medium- distance migrating robins (winter in S Europe) and light-legged sedentary robins (winter in S Sweden). Birds will be measured soon after capture when in migration mode as well as in mid-winter under indoor conditions. (2) Immune gene diversity in long- and short-distance migrating vs. sedentary songbirds. In the second project, we want to investigate if the broader range of parasites to which long-distance migrant birds are exposed in their tropical winter quarters as compared with e.g. sedentary temperate species, is reflected in the diversity of their immune genes (e.g., Major Histocompatibility Complex, MHC, genes). MHC diversity will be analysed using amplicon 454 sequencing on a set of individuals from sedentary, temperate and tropical migrant passerines taking phylogeny into account.

The successful candidate will be responsible for capturing and sampling of the robins in the indoor study, for conducting basic immunological and molecular lab work, and for analysing the data.

We are looking for a highly motivated and experienced postdoctoral co-worker with a background in e.g., molecular ecology, immunological ecology, animal behaviour, functional or evolutionary ecology. Applicants should have considerable experience of laboratory work using molecular and/or immunological (ELISA) methods (preferably both types of methods). Experience of analysing DNA sequence data and (simple) bioinformatics analyses will be seen as additional advantages. Moreover, the postdoc will work a lot with handling birds (when catching birds in the wild and when sampling captive birds), and we therefore also rate experience in handling birds as a further advantage,

Research environment:

CAnMove (www.canmove.ekol.lu.se) is a centre of excellence for trans-disciplinary research on the causes and consequences of animal movements, funded by a Linnaeus grant from the Swedish Research Council and Lund University. CAnMove research aims to resolve some of the most challenging questions in biology, such

as the genetic control programs of migration, the fluid dynamics of animal flight, and adaptations for and evolution of migration. In CAnMove we also study dispersal and speciation, spread of diseases, costs of migration and how climate change affect migrating animals.

Lund University (www.lu.se) is one of Europe's foremost universities and Sweden's strongest for research. Here, tradition combines with dynamic development and cutting edge qualifications. 46 000 students study at the university, which has 6 000 employees. The Ecology Building at Lund University is one of Europe's largest centres for Ecology with over 200 senior scientists, postdocs and PhD students.

Applications: Applications, marked with reference number (see below), and the documents the applicant wishes to cite (CV, publication list, reference letter, etc) shall be sent to Registrar, Lund University, Biologiska institutionen, Solvegatan 37, SE-223 62 Lund. All documents shall be attested.

Reference number: PA 2011/113 Last date of application: 7 March 2011 Start date: 1 August 2011 (or after agreement) Position: 2 years stipend 100%

For further information, please contact Dennis Hasselquist (dennis.hasselquist@zoekol.lu.se), Jan-Ake Nilsson (jan-ake.nilsson@zoekol.lu.se) or Helena Wester Dahl (helena.westerdahl@zoekol.lu.se).

Dennis Hasselquist / Professor Department of Biology Molecular Ecology & Evolution Group Lund University Ecology Building SE-223 62 Lund, Sweden Email: dennis.hasselquist@zoekol.lu.se

Dennis Hasselquist <Dennis.Hasselquist@zoekol.lu.se>

LundU ProtistMetagenomics

Lund University hereby announces the following vacant Stipend At the Department of biology within CAnMove and the project "Community metagenomics of Antarctic Protists - the importance of history versus environment".

Project description

This postdoc project concerns the recent scientific discoveries that eukaryotic microorganisms (protists) have cosmopolitan species as well as species with restricted biogeographies. In order to study microbial communities it is imperative to know their taxonomic diversity. Through the use of molecular techniques, the diversity

of protists has been shown to be much higher than what older methods indicated. Dispersal and subsequent colonization of new habitats have important consequences for community composition. An important question is thus whether community composition of aquatic protists is a consequence of environmental filtering, mass effects, historical processes or a mix of the previous processes.

In this project, marine and freshwater protist composition will be investigated in a lake metacommunity that includes marine-derived and glacial melt-water lakes. Lakes operate very much as islands, imposing certain geographic limitations to populations, as well as dispersal among populations. In a system of remotely located (Antarctica) recently formed lakes, the community composition of protists will be analyzed using 454-technology. Community similarity will be tested for both historical (biogeographical) and environmental effects (salinity). Samples collected from 20 Antarctic lakes on a gradient of salinity (0-300), distance from the sea, and lake age, are available for analyses. No travels to Antarctica will be conducted.

The postdoctoral project will include sample preparation for 454 sequencing as well as bioinformatic analyses of the sequence data using publicly available or custom made pipelines. Moreover, clonal cultures of dinoflagellates from a subset of the lakes are available for laboratory experiments related to the research topic.

CAnMove

CAnMove is a centre of excellence for trans-disciplinary research on the causes and consequences of animal movements, funded by a Linnaeus grant from the Swedish Research Council and Lund University. Our vision is to become a world-leading centre for research on animal movement. CAnMove research aims to resolve some of the most challenging questions in biology, such as the genetic control programs of migration, the mechanisms for animal navigation, the fluid dynamics of animal flight, and the evolution of migration. In CAnMove we also study dispersal and speciation, effects of movements on populations, spread of diseases and how climate change affect migrating animals. CAnMove aim to develop and use new tracking technology to track movements of organisms across scales, from small daphnia and insects to large albatrosses and sea turtles moving across wide areas of the globe.

Qualifications

The successful applicant is a highly motivated postdoctoral stipend with a strong interest in protist ecology and evolution. A PhD in limnology, marine biology, biological oceanography, microbial ecology, or equivalent,

is required. Specifically, the applicant should have substantial and documented experience with molecular techniques (PCR, sequencing) and previous experience of phylogenetic analyses, population genetic analyses and/or genomic analyses. He/she preferably has experience of culturing and/or microscopy of protists. Very good spoken and written English is required. As the postdoctoral stipend will be part of CAnMove - Centre for Animal Movement Research, a general interest in ecology as well as the ability to interact and collaborate with other members is considered an important quality.

To be eligible for a stipend a person must have successfully completed a PhD degree or have corresponding scientific competence in a relevant subject area. The applicant needs to have a PhD not older than 5 years from a non-Swedish university and can not have been employed at Lund University. Priority should be given to candidates who have completed their degree no more than three years before the last date for applications. Candidates who have completed their degree earlier than this should receive equal priority if special grounds exist, for example documented leave of absence because of illness or parental leave.

For information on stipend:

Karin Rengefors, Karin.Rengefors@limnol.lu.se
 , Phone: +46 46 2228427 Web: http://www.limnol.lu.se/limnologen/person_detalj.asp?id=3D28 For information on CAnMove postdoc program:

Lars-Anders Hansson, Lars-Anders.Hansson@limnol.lu.se , Phone: +46 46 2224169,

For information on CAnMove activities:

Susanne Åkesson, Susanne.akesson@zoekol.lu.se ,
 Phone: +46 46 2223705

Web page: www.canmove.ekol.lu.se/ Application

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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>

MichiganStateU EvolutionEducation

Post-Doctoral Research/Teaching Associate Evolution
 Education Michigan State University

Applications are now being accepted for a Post-doctoral Associate in Evolution Education at Michigan State University (MSU). This NSF-funded position involves the development, implementation and assessment of the effectiveness of a set of online integrative case studies to help undergraduate students learn evolutionary principles and concepts. Case study development and testing will occur as a member of an interdisciplinary team of educators and researchers in the Lyman Briggs College (LBC) and the College of Natural Science at MSU, led by Dr. Merle Heidemann and Dr. Jim Smith. The position also involves a mentored teaching experience in LBC. The post-doc will work as a teaching team member in the LBC Biology Program and will co-lead an Introductory Biology course in the 3rd semester of this 2- year position.

Candidates should have an earned doctorate in a biological discipline or in biology education. Experience assessing student learning is desirable, but not required.

This position is for 2 years and will begin on July 1, 2011. Applications review will begin Mar. 1, 2011 and will continue until the position is filled. Starting salary will be in the range of \$40 - \$42 K, depending on experience.

Applicants should send a statement of interest, curriculum vitae, and arrange to have three letters of reference sent to Dr. Jim Smith, either by email (jim-smith@msu.edu), or by US Mail (Lyman Briggs College, East Holmes Hall, East Lansing, MI 48825-1107).

MSU is an affirmative-action, equal-opportunity employer. Applicants who are not U.S. citizens or permanent residents must provide a document of employment authorization for the U.S. Persons with disabilities have the right to request and receive reasonable accommodation. MSU is committed to achieving excellence through cultural diversity. The university actively encourages applications and/or nominations of women, persons of color, veterans, and persons with disabilities.

Dr. James J. Smith Michigan State University Lyman Briggs College East Holmes Hall E. Lansing, MI 48825-1107 tel: (517) 353-3939 fax: (517) 432-2758

and:

Department of Entomology 201 CIPS E. Lansing, MI 48824 tel: (517) 432-2029 fax: (517) 353-4354

email: jimsmith@msu.edu web: www.msu.edu/user/-jimsmith Jim Smith <jimsmith@msu.edu>

Montpellier FishGenomics

18-month post-doctoral position in fish genomics, Université Montpellier 2, UMR CNRS 5554 Institut des Sciences de l'Evolution de Montpellier, Montpellier, FRANCE.

We seek a motivated and productive postdoctoral researcher to work on genomic aspects of fasting in sea bass (*Dicentrarchus labrax*), a major finfish aquaculture species in Europe. The project is funded by the French National Research Agency (ANR; RegulBASS programme) and aims to better figure out the determinism of starvation tolerance in this species. A draft of the genome is already available in this species, together with other genomic resources (e.g. RNA-seq runs were carried out during the project). The project encompasses acquisition and analysis of data from high-throughput sequencers, study of differential gene expression as well as identification of polymorphisms. Main objectives include (i) the delineation and identification of differentially expressed genes among selected individuals/families and (ii), among those genes, the search of relevant polymorphisms involved in the genotype/phenotype relationship and physiological performance of fish.

Located close to the Mediterranean Sea, the Université Montpellier 2 is a leading French university ranking eight among French universities, and third outside the Paris area. The UMR CNRS 5554 ISE-M (Institut des Sciences de l'Evolution Montpellier) is a leading European institute in evolutionary biology and is now dedicating a large portion of its activities to evolutionary genomics. The RegulBASS project gathers fish biologists, fish physiologists and quantitative geneticists, and benefits from the genomics and bioinformatics platforms located in the university or in the institute itself.

The position will involve both experimental and analysis work. The candidate should have a strong background in transcriptomics and in bioinformatics for the analysis of large sequence datasets (sequence trimming, assembly and annotation). The candidate should also be able to design and carry out experiments for analyzing gene expression. Knowledge of fish population genetics would be appreciated.

Basic skills in French would also be a plus.

Duration: 18 months, available immediately; to be

filled before June 1st, 2011. Salary: 1,800 euro per month, netto.

Application (detailed CV, cover letter, the names and contact information for 3 references): Dr. Bruno Guinand guinand@univ-montp2.fr Conservation & Domestication des Poissons Université Montpellier 2 UMR CNRS 5554 Montpellier, FRANCE

bruno.guinand@univ-montp2.fr

Montpellier Modelling Biodiversity

Postdoctoral position: **

Comprehensive modelling of agro-biodiversity in relation to seed exchange networks.

*Contacts: francois.massol@cemagref.fr; pierre.martin@cirad.fr; sophie.caillon@cefe.cnrs.fr

Host Institute: Center of Evolutionary and Functional Ecology (UMR 5175-CEFE), CNRS, Montpellier, France.

*Closing date for application: *April, 1 2011

*Starting date: *May 2011 (negotiable)

*Duration: *24 months

The postdoctoral project

The postdoctoral project is part of a global project (3 years) funded by the French Foundation for Research on Biodiversity (FRB) through its CESAB program (centre national de synthèse et d'analyse sur la biodiversité). This project deals with strengthening management of agro-biodiversity through social networks using an interdisciplinary method for analyzing how local seed systems impact the diversity of domesticated plants.

The goal of the project is to study the structure of seed exchange networks (SEENs) among farmers, i.e. the fluxes of 'seeds' (generic term for all plant propagation vectors, including true seeds and vegetative propagules) and provide comprehensive models relating plant biodiversity to socio-cultural and geographic factors. The general question is to assess how SEEN structure – the significations, directions and intensities of seed fluxes among individuals or groups exchanging seeds, and the distribution of genealogical, socio-cultural or geographical distance among these individuals or social entities – impacts agro-biodiversity.

The post-doctoral fellow will be the project's keystone person. He/She will lead the analysis of 12 datasets from 10 societies/countries and answer questions from distinct disciplines by interacting with the different specialists involved – anthropologists, ecologists, ethnobiologists, geographers and modelers. This multidisciplinary group will provide a large number of opportunities for the post-doctoral fellow to increase his/her connections to empirical disciplines, as well as assisting him/her with meta-analysis and network modeling.

Candidate requirements

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We seek a candidate with skills in network modelling and meta-analysis. The successful candidate will need to synthesize and compile data from various sources into a cohesive database and will personally conduct the network modelling and meta-analysis. He/She will need to show an interest in sharing knowledge with social scientists, and will need to coordinate the different tasks. We expected a candidate with strong skills in writing scientific articles.

/1. Publications/

Two types of articles are expected: (i) method paper(s), to publish the methodology and results on the main mechanisms of seed networks in international peer-reviewed journals (articles will be signed by all members of the team and the post-doctoral fellow will be first author), and (ii) other articles presenting the results of each study case (led by the principal investigator in charge of each dataset and signed by the post-doctoral fellow).

/2. Software and training/

A software will be developed for specialists in network analysis and researchers in social and natural sciences from Northern and Southern countries, resource managers, NGO stakeholders and farmers. The post-doctoral fellow will contribute to the development of this software through the implementation of network modeling algorithms, and participate in the training workshops dedicated to the use of this software.

Practical information

The post-doctoral fellow will be employed for 2 years starting in May 2011 (negotiable). He/she will be based at the Center for Functional and Evolutionary Ecology (UMR5175) in Montpellier, France (<http://www.cefe.cnrs.fr>). The gross salary will be 45,000 euros per year (35,000 euros net pay).

Please send a letter and a CV outlining research experience and interests, publications, a list of skills and other relevant professional information.

– Adeline Barnaud UMR DiA-PC, équipe DYNADIV IRD Montpellier 911, avenue Agropolis BP 64501 34394 Montpellier cedex 5 France

Tel : +33 (0)4 67 41 64 39 Fax : +33 (0)4 67 41 62 22 Website : <https://sites.google.com/site/plantbiodiversityadaptation/home> “adeline.barnaud@ird.fr” <adeline.barnaud@ird.fr>

Professor (concurrent), Department of Biological Sciences, Graduate School of Science, University of Tokyo Council Member (concurrent), Japan Science Council

Home Page: sayer.lab.nig.ac.jp/~saitou/ Postal address: Mishima, 411-8540, Japan TEL/FAX +81-55-981-6790/6789 Email: saitounr@lab.nig.ac.jp
nsaitou@genes.nig.ac.jp

NatInstGenetics MishimaJapan GenomeEvolution

Invitation to apply for NIG Postdoctoral Fellow Saitou Laboratory, National Institute of Genetics (NIG), Mishima, Japan Lab Home Page: <http://sayer.lab.nig.ac.jp/> We are studying various aspects of genome evolution in wide spectrum of organisms, from human to bacteria in our laboratory at NIG.

Kenta Sumiyama (<http://sayer.lab.nig.ac.jp/~sumiyama/index-e.html>), assistant professor in Saitou laboratory, is studying evolutionary mechanisms at genomic level regarding innovation in the body plan evolution of vertebrates. He aims to identify genomic regions that enabled phenotypic evolution, through bioinformatics and genetically engineered animal systems. His current theme is analyzing cis-regulatory elements of the mammalian homeobox genes that confer the body plan innovations. We are seeking for a motivated postdoc candidate for this project. Experiences in molecular biology and/or genetic engineering in developmental biology are desirable. Having skills in bioinformatics is preferable, but not prerequisite for application. One can learn computer analysis techniques after joining our lab. Please ask Kenta Sumiyama (ksumiyam@lab.nig.ac.jp) for project details.

Please download pdf file at “NIG Postdoctoral Fellows 2011” at NIG Home Page (<http://www.nig.ac.jp/index-e.html>) to obtain detailed information on this fellowship.

Expected date of job starting: April 1, 2011 Deadline of application: February 14, 2011 We will ask candidate person to give presentation via internet if one is currently out of Japan.

Saitou Naruya Professor, Division of Population Genetics, National Institute of Genetics Professor (concurrent), Department of Genetics, School of Life Science, Graduate University for Advanced Studies Pro-

NorthCarolinaStateU BiologicalComplexity

NC State University Distinguished Postdoctoral Fellows in Biological Complexity

* *

North Carolina State University is embarking on a new university-wide interdisciplinary initiative in biological complexity encompassing systems genetics, behavioral neurogenetics and neurogenomics, genome-environment interactions, ecological genetics, systems ecology, climate change, computational biology and bioinformatics.

Associated with the new initiative in biological complexity is a distinguished postdoctoral fellowship program. Applicants are expected to be near completion of a terminal doctorate degree, have a strong research record with evidence of exceptional scholarship, and embrace interdisciplinary research. Fellows will receive competitive stipends and independent research funds to initiate an innovative research program with guidance from a multidisciplinary mentoring committee in areas covered by the initiative in biological complexity.

To apply for faculty or fellowship positions, go to jobs.ncsu.edu/applicants/Central?quickFind=258 (position number 100552), and provide a cover letter, curriculum vitae, a three-sentence statement of the most significant scientific problem(s) to be addressed in the near future, and statements of research interests. Three letters of recommendation should be sent to Trudy Mackay (trudy_mackay@ncsu.edu). Review of applications will begin immediately, and continue until the positions are filled.

NCSU is an AA/EO employer. All qualified applicants will receive consideration for employment without regard to race, color, national origin, religion, sex, age, veteran status or disability. In its commitment to diversity and equity, NC State University seeks applications

from women, minorities, and persons with disabilities. NC State welcomes all persons without regard to sexual orientation. ADA Accommodations: please call 919-515-5727.

– Trudy F. C. Mackay, PhD, FRS William Neal Reynolds and Distinguished University Professor of Genetics Department of Genetics North Carolina State University Campus Box 7614 Raleigh, NC 27695-7614 Tel: 919-515-5810 Fax: 919-515-3355 Email: trudy_mackay@ncsu.edu

Trudy Mackay <trudy_mackay@ncsu.edu>

OhioStateU USDA InsectVectorEvolution

USDA-ARS: POSTDOCTORAL RESEARCH ASSOCIATE

We have a great opportunity for a recent Ph.D. to join the USDA, ARS, Corn and Soybean Research Unit at The Ohio State University, OARDC in Wooster, OH as a POSTDOCTORAL RESEARCH ASSOCIATE. This is a two year appointment to conduct team research with ARS scientists and OSU faculty and students to investigate evolutionary, comparative and population genomics of insect vectors of corn and soybean virus diseases.

Please refer to the announcement #RA-11-048-H at <http://www.afm.ars.usda.gov/divisions/hrd/hrdhomepage/vacancy/pstdclst.htm> . Thank you,

Andy

Andrew Michel Assistant Professor Dept. of Entomology 210 Thorne Hall Ohio Agricultural Research and Development Center The Ohio State University 1680 Madison Ave Wooster, OH 44691 Ph: 330-263-3730 Cell: 330-347-8652 Fx: 330-263-3686

michel.70@osu.edu

Oregon USForestService GrassPopulationVariation

Postdoctoral Research Associate, USDA Forest Service Pacific Northwest Research Station, Corvallis, Oregon

A postdoctoral research position is available at the USDA Forest Service Pacific Northwest Research Station in the Plant Genetics, Ecology and Management Team based in Corvallis, Oregon. The candidate will participate in genetics research to explore population variation in adaptive traits of native grasses and forbs of the interior western United States. Adaptive variation is studied using a genecological approach in which variation as expressed in common garden trials is related to the environments of seed sources. The employee will use the knowledge gained from genecology studies to evaluate alternatives for delineating seed zones and guiding population movement for reestablishing productive, healthy and diverse native plant communities, both in the short-term and in the long-term given different climate change scenarios. Qualifications include: US citizen; completed PhD in ecology, botany, forestry, biology, genetics or related field prior to beginning of employment; demonstrated knowledge of statistical analysis including general linear models and multivariate analysis; demonstrated skills in communicating science through publications and public speaking. The position is full-time for a minimum of 13 months and a maximum of 48 months and will be filled at the U.S. Government GS-11 or 12 level, dependent upon qualifications. Starting date is flexible, but the deadline for application is March 25, 2007. To apply, send curriculum vitae and cover letter indicating interests and qualifications, along with you publication list, college transcripts (unofficial okay), and contact information for at least three professional references to: Brad St.Clair, USDA Forest Service, Forestry Sciences Laboratory, 3200 SW Jefferson Way, Corvallis, OR, 97331; email: bstclair@fs.fed.us.

bstclair@fs.fed.us

Rockefeller InsectEvolution

Postdoctoral position in genomics and behavioral genetics

A two year postdoctoral position is available in the Laboratory of Insect Social Evolution (PI Daniel Kronauer) at Rockefeller University. The project will involve genomic analyses and large scale RNA-Seq experiments to understand the molecular underpinnings of social behavior, social regulation, and caste differentiation in an ant model system. Genome sequencing will be conducted in collaboration with a commercial facility, which will also provide bioinformatics analyses

and advanced training for the postdoc. The position starts in summer 2011 and an extension beyond two years is possible.

The Laboratory of Insect Social Evolution will be a newly established lab at the Rockefeller University campus on Manhattan's Upper East Side. More information can be found at: <http://newswire.rockefeller.edu/?page=engine&id=1091> Rockefeller University supports a vibrant research community in behavioral genetics and the successful candidate will have the opportunity to interact with leading researchers in the field.

The ideal candidate for the position will have a strong background in bioinformatics as well as an interest in behavioral genetics and large-scale gene expression analyses. Applications will be accepted until the position is filled.

To apply, please submit the following items to Daniel Kronauer at dkron@fas.harvard.edu - your CV - contact information for three references - a short cover letter describing your background and research interests (not more than one page)

I'm looking forward to hearing from you!

Best regards,

Daniel Kronauer

Present address: Museum of Comparative Zoology Labs / Harvard University / 26 Oxford St / Cambridge, MA 02138

Daniel Kronauer <dkron@fas.harvard.edu> Daniel Kronauer <dkron@fas.harvard.edu>

UAlgarve PlastidOrigins

POSTDOCTORAL POSITION

Applications are invited for a postdoctoral researcher position at the Centro de Ciencias do Mar (CCMAR), University of the Algarve (CCMAR - <http://www.ccmар.ualg.pt/>) in the research group of Cymon J. Cox (Plant systematics and bioinformatics). The successful applicant will participate in the project titled "The origin and early diversification of plants: a phylogenomic approach employing novel composition-heterogeneous methods" funded by the Portuguese Foundation for Science and Technology (FCT). The project will be conducted in collaboration with T.M. Embley (Newcastle University, UK) and P.G. Foster

(Natural History Museum, London, UK).

Background Plant chloroplasts are derived from an ancient endosymbiotic capture of a cyanobacterium by a heterotrophic eukaryotic ancestor, an event which led to the diversification of three primary plant lineages, namely, the glaucocystophytes, red algae, and green plants, and the eventual emergence of terrestrial ecosystems. The endosymbiosis marked a crucial episode in cell and Earth history, yet our understanding of the phylogenetic context surrounding this momentous event remains obscure in part due to the technical limitations of current phylogenetic methodology in relation to the reconstruction of deep evolutionary divergences.

The project will be conducted entirely in silico and implement novel non-stationary composition models in a phylogenomic context. Ideally, the successful candidate will have a strong background in phylogenetic analyses, Unix/Linux computing, and bioinformatics (biopython/bioperl, cluster management, relational databasing, etc). An extensive publication record will also be advantageous. The position is available immediately until the end of December 2012 and is open to all nationalities. The researcher will receive a salary of 1495 euros/month.

Applications should be submitted before 28th of February of 2011 to Cymon J. Cox (cymon@ualg.pt). Applicants should send a covering letter detailing their research interests, a current C.V., and the email addresses for 3 professional referees. Informal enquires are welcome to the same address.

CCMAR is located on the Gambelas campus, 4km from Faro, the capital city of the Algarve and close to Faro International Airport (FAO). http://www.ualg.pt/index.php?option=com_google_maps&Itemid=2311&lang=en FCT announcement (in Portuguese): <http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId=21992&lang=pt>

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Cymon J. Cox

Auxiliary Investigator Plant Systematics and Bioinformatics Research Group (PSB) Centro de Ciencias do Mar (CCMAR) - CIMAR-Lab. Assoc.

cymon.cox@googlemail.com

UArizona OriginMulticellularity

POSTDOCTORAL POSITION

Genomics and bioinformatics of the origin of multicellularity

A post-doctoral position in genomics / bioinformatics / computational biology is available immediately in the laboratory of Dr. Richard E. Michod (<http://www.eebweb.arizona.edu/Michod/>) in the Department of Ecology and Evolutionary Biology at the University of Arizona, Tucson (<http://www.eebweb.arizona.edu>). A major focus for this research group is the origin and evolution of multicellularity using the volvocine algal lineage as a model system. To better understand this transition, we have recently completed the genome sequencing of *Pleodorina starrii*, one of the key organisms in this group. We are currently sequencing the nuclear genomes of three other members (*G. pectorale*, *A. gubernaculifera* and *T. socialis*) in the lineage.

The project aims to understand the genetic and genomic underpinnings for the evolutionary transition to multicellularity in the volvocines, which involves investigating key steps (for example the emergence of specialized cell types) during this transition. We wish to understand the molecular basis for these processes using the sequence data we are generating and seek a postdoctoral fellow to help in performing these analyses. Interested parties would have a background in genomics, bioinformatics or computational biology. The requirements include an understanding of comparative and evolutionary genomics, phylogenetics, data mining as well as other skills for the analyses of large amounts of sequence data. The individual should be motivated, able to work independently and collaboratively with others in the lab.

To apply, please e-mail (michod@u.arizona.edu) with the following information: a statement detailing your research interests and qualifications, a CV, and the names and contact information of three references. Please describe what interests you about this post-doctoral position and whether you have any particular ideas that you wish to pursue. Please direct any inquiries about the position to Rick Michod (michod@u.arizona.edu) or Pierre Durand (pierre.durand@wits.ac.za).

The initial appointment is for one year, with an additional two years' funding possible conditional on satisfactory performance. The position is funded by an NSF grant, at 36K per year (plus benefits).

The University of Arizona is an EO/AA Employer.

Rick Michod <michod@u.arizona.edu>

UCalifornia SanFrancisco EvolutionaryGenomics

Postdoctoral Positions in Evolutionary and Computational Genomics

Postdoctoral positions are available in the laboratory of Dr. Ryan Hernandez at the University of California San Francisco (Mission Bay campus). The research focus will be in the general area of evolutionary and/or computational genomics, and is geared toward understanding the evolutionary forces that contribute to health disparities across human populations. In our computational lab, we use detailed simulations, modeling, and analysis of high throughput genome sequencing data in humans and other mammals. Research projects will focus on developing novel techniques for applying principals of population and evolutionary genomics to medical resequencing studies. Ongoing collaborations involve comprehensive studies of patterns of global genetic diversity as part of the 1000 Genomes Project, the genetic basis of asthma in admixed populations, and the genomics of host-pathogen interactions. Successful candidates will be expected to develop novel computational/statistical methods for addressing specific biological hypotheses, and to perform analyses of large-scale genomics data. Ideal candidates will have a background in a quantitative field (such as computer science, statistics, or applied mathematics), experience in performing genetics/genomics research, and a strong track-record of accomplishment in research.

Qualifications:

- Ph.D. in bioinformatics, computer science, statistics, genetics, molecular biology, applied mathematics, or a related field.
- Research experience (with first-author publications) in population genetics or a related field.
- Proficiency in programming, ideally in C or C++, scripting languages such as perl, and familiarity with R.
- Comfortable with large data sets, computer clusters, and databases.

Applicants should send a CV and the names and email addresses of at least two references to Ryan Hernandez <ryan.hernandez@ucsf.edu>. Informal inquiries are also welcome.

Ryan D. Hernandez, Ph.D. Assistant Professor Department of Bioengineering and Therapeutic Sciences, Institute for Human Genetics, and California Institute

for Quantitative Biosciences (QB3) University of California San Francisco UCSF MC 2552 Byers Hall Room 503C 1700 4th Street San Francisco, CA 94158-2330

Phone: (415) 514-9813

Email: ryan.hernandez@ucsf.edu Email: ryan.hernandez@ucsf.edu

UCambridge BehaviouralEvolution

Post-doctoral Research Associate - Behavioural Ecology Group

Reference: PF07806

Salary range: £27,319 - £35,646 per annum Limit of tenure applies

This position, based at the Department of Zoology, University of Cambridge, is available for up to 3 years from 1 June 2011 to work with Dr Rebecca Kilner and her team in the Behavioural Ecology group. For background information and examples of our recent work, please see <http://www.zoo.cam.ac.uk/zoostaff/-bbe/Kilner/Rebecca1.htm> The project 'Cooperation, conflict and mutualism in burying beetle family life' involves running laboratory experiments on a pedigreed population of burying beetles (*Nicrophorus vespilloides*) to identify sources of individual variation in cooperative behaviour.

To apply, and for Further Information, please see: <http://www.zoo.cam.ac.uk/zooone/-administration/vacancy.html> Anastasia Nezhentseva <an286@hermes.cam.ac.uk>

UCambridge EvolutionaryCancerGenomics

We are seeking a post-doctoral research associate to join a very active computational biology and statistics research group (see <http://www.compbio.group.cam.ac.uk/>) to work in the area of evolutionary cancer genomics. The position will be based in the Cancer Research UK Cambridge Research Institute (<http://www.cambridgecancer.org.uk/>).

A background in the application of probabilistic and

statistical methods in the biological or medical sciences is advantageous. Experience in stochastic computation is preferred. Applicants with experience in the analysis of high-throughput genomic data are encouraged to apply. Experience with R, Bioconductor and parallel/distributed computing is advantageous.

Further details may be found at: <http://www.admin.cam.ac.uk/offices/hr/jobs/-vacancies.cgi?job=7838> Simon Tavaré <st321@cam.ac.uk>

UCambridge SequencingStatistics

We are seeking a post-doctoral research associate to join a very active computational biology and statistics research group (see <http://www.compbio.group.cam.ac.uk/>) to work on the development of statistical methodology for sequencing technologies.

A background in the application of statistical methods in the biological and medical sciences is advantageous. Statistical bioinformatics experience, including familiarity with R and Bioconductor, is preferred. Applicants with experience in the analysis of high-throughput genomic data are encouraged to apply. Experience with parallel/distributed computing is advantageous.

The position will be based in the Cancer Research UK Cambridge Research Institute (<http://www.cambridgecancer.org.uk/>). Further details may be found at: <http://www.admin.cam.ac.uk/offices/hr/jobs/vacancies.cgi?job=7789> Simon Tavaré <st321@cam.ac.uk>

UGeorgia PlantEvolutionaryGenetics

A postdoctoral position in plant evolutionary genetics is available in the new lab of Andrea Sweigart in the Department of Genetics at the University of Georgia.

Research in the lab will focus on the genetics of speciation in the model flowering plant *Mimulus* (see www.mimulusevolution.org) using molecular and func-

tional approaches, field experiments, and population genomics. Projects in the lab will include mapping and characterizing hybrid incompatibility genes; characterizing the genetics of flowering time and habitat divergence; investigating the mechanisms and consequences of polyploid speciation; and studying the population genomics of divergence with gene flow. The postdoc will also be encouraged to develop his/her own independent research projects. The ideal candidate will have a background in evolutionary genetics, as well as strong skills in bioinformatics and/or molecular biology.

For more information about Univ. of Georgia's Department of Genetics, please visit:

<http://www.genetics.uga.edu/>

Additional information about my research can be found at:

<http://www.genetics.uga.edu/sweigartlab/> The start date may be as early as August 15, 2011. To apply, please email a CV, a brief statement of research interests, and contact information for 2-3 academic references to: andrea.sweigart@mso.umt.edu.

andrea.sweigart@gmail.com

UKansas BeetleSystematics

A POSTDOCTORAL RESEARCHER POSITION is available in the laboratory of Dr. Caroline Chaboo whose research area is chrysomelid beetle systematics. The selected candidate will help initiate a long-term survey and inventory of the arthropod faunas at multiple sites along an elevational transect in Peru and explore questions involving arthropod diversity in relation to elevation, climate change, and human impacts. The postdoctoral fellow will work within a highly active team comprising the PI, foreign collaborators, graduate students, and undergraduate students. Field teams will collaborate closely with investigators from the Entomology Department, Museo de Historia Natural, Universidad Nacional Mayor de San Marcos (MUSM) Lima, Peru. The postdoctoral work will focus on field collection, sorting and curation, identification, imaging, data-basing, and dissemination of entomological specimens. The candidate will assist in the oversight and training of undergraduate student employees. Additional training will be provided in molecular systematics, collection management software (Specify 6), grantsmanship, and statistical analyses. The successful

candidate will be expected to develop a research program within their taxon of specialization and communicate results in publications and at society meetings. The candidates will be required to have completed a Ph.D. in Ecology and Evolutionary Biology or Entomology earned within the past four years from an accredited university. The ideal candidate will have experience with arthropod sampling methods, curation, and making identifications. Funding is available for one year with possibility of extension. Apply to: <https://jobs.ku.edu> and search for Position 00208948. Application review date 02/26/2011. For more information see Chaboo website: <http://www2.ku.edu/~eeb/faculty/-chaboo.shtml> EO/AA employer.

Dorothy Johanning Program Assistant Ecology and Evolutionary Biology University of Kansas Lawrence, KS 66045 785/864-5889

"Johanning, Dorothy" <jdorothy@ku.edu>

ULeicester SticklebackEvolution

Post Doctoral Research Associate in Evolutionary Ecology

University of Leicester, UK

We seek an enthusiastic and highly motivated biologist to join a NERC- funded collaborative project, working with Dr. Iain Barber (PI: Biology, <http://tinyurl.com/barberlab>) and Dr. Ezio Rosato (Co-I: Genetics, <http://www2.le.ac.uk/departments/genetics/people/rosato/research>). The aim of the project is to investigate the impact of environmental change on the nest building behaviour and synthesis of Spiggin - a protein glue used in nest construction - by male three-spined stickleback fish, and to study the fitness consequences of these effects. The PDRA will design, run and analyze lab-based experimental behavioural studies investigating the effects of flow regime on stickleback nest construction and undertake molecular studies examining the expression of Spiggin genes in response to changing environments. The successful applicant will ideally be an evolutionary or behavioural ecologist with experience in the design, implementation and analysis of behavioural studies, and possess good molecular biology skills. Direct experience of qPCR would be an advantage, but is not essential. The position is full time and is available immediately to run to May 31st 2012. Informal enquiries are encouraged and should be addressed to Iain Barber (email: ib50@le.ac.uk,

tel: +44(0)116 252 3462). Salary: Grade 7 (pt 31) £30,747p.a.

Full details of application procedure and further particulars at:

<http://www.jobs.ac.uk/job/ACH393/post-doctoral-research-associate-in-behavioural-molecular-ecology/>

Dr Iain Barber Senior Lecturer in Animal Biology

Room 228b (through Lab 226) Adrian Building Department of Biology College of Medicine, Biological Sciences and Psychology University of Leicester Leicester LE1 7RH UK

Tel: +44(0)116 252 3462 Fax: +44(0)116 252 3330 email: ib50@le.ac.uk

Barber lab website: <http://tinyurl.com/barberlab>
ib50@leicester.ac.uk

UMelbourne AvianSocialEvolution

Research fellowship: Investigating the evolutionary ecology of personalities in social birds

Project outline:

In many animals, individuals differ consistently in suites of correlated and heritable behaviours, comparable to human personalities. Recent research suggests that personalities should influence key socio-ecological processes, but they have rarely been studied in this context. We will use an experimental approach to determine how a) personality affects critical social and life-history decisions in a cooperatively breeding bird and b) early social environment contributes to the development of personality.

The study will involve assaying the personalities of birds in a wild population of individually marked superb fairy wrens and conducting intensive field observations and manipulations to reveal associations between personality and dispersal, mate choice, cooperation and parental care. Moreover, we aim to disentangle the genetic and environmental factors that shape personality development, using cross-fostering experiments and molecular approaches to link polymorphism in candidate genes to personality variation. This research should have both fundamental and applied significance.

Investigators and funding:

The study is funded by the Australian Research Coun-

cil and is a collaborative project between A/Prof Raoul Mulder and Dr Michael Magrath (University of Melbourne, Australia) and Dr Niels Dingemanse and Prof Bart Kempenaers (Max Planck Institute for Ornithology, Germany).

The research fellowship:

The Research Fellow will be based at the Department of Zoology, University of Melbourne, Australia. They will be responsible for designing, executing, and analysing field experiments at a field site near Melbourne (Serendip Sanctuary), implementing field techniques ranging from mist-netting to captive behavioural assays, and focal observations. The fellow will coordinate field schedules and help direct a small team of research students and assistants. The fellow will also contribute to the preparation of manuscripts for publication and may contribute to molecular genotyping.

The fellow will receive an annual salary of between A\$65,852 - A\$76,299, depending on experience. The position is full-time (but part-time may be considered) and is available from 01/04/2011 (later start negotiable) until 31/12/2013.

Applications:

Application details, including specific selection criteria, can be found at www.jobs.unimelb.edu.au, Position number 00257256.

Online applications are preferred.

Applications will close Feb 28th 2011.

For further information please contact:

A/Prof Raoul Mulder

Tel +61 3 83446245

r.mulder@unimelb.edu.au

magrath@unimelb.edu.au

UMontana InsectSymbiontGenomics

A postdoctoral position in insect symbiont genomics is available in the laboratory of John McCutcheon, in the Division of Biological Sciences at the University of Montana in Missoula.

The McCutcheon lab is part of a team of USDA-funded researchers studying the spread of an invasive insect throughout the southeastern United States. The post-doc involved with this work will be responsible for se-

quencing the complete genome of a bacterial insect symbiont, and for performing population structure experiments using multi-locus genotype data. These projects will involve the generation and analysis of large next-generation sequencing datasets, and so candidates with bioinformatic experience are strongly preferred. However, interested applicants with molecular biology, microbiology, or entomology backgrounds are encouraged to apply.

The appointment is expected to be for 1.5 years, and could start as early as April 2011. Applications will be reviewed immediately and will continue until the position is filled. To apply, please email a cover letter, CV, and the names of three references to John McCutcheon (john.mccutcheon@umontana.edu). Further information about the lab and the university are available at the McCutcheon lab website (<http://mccutcheonlab.dbs.umt.edu/>).

john.mccutcheon@mso.umt.edu

UNewSouthWales ModellingViralEvolution

We are still accepting applications for a postdoc position in Sydney (see below). The salary package is \$71,000–\$76,000 plus superannuation and leave loading. The closing date for applications is 1 March 2011.

Post-doctoral position in mathematical modelling of viral evolution, Sydney, Australia

A post-doctoral position funded by the Australian Research Council is available at the University of New South Wales (UNSW), Sydney, Australia. The successful applicant will be part of a collaborative team involved in modelling the evolution and epidemiology of viruses. The investigators of the team are Mark Tanaka and Peter White (UNSW), Katia Koelle (Duke University) and Roland Regoes (ETH Zurich). The post-doctoral researcher will develop mathematical models, implement computer simulations, and design statistical methods to analyse genomic data. The successful applicant will have the opportunity to contribute to a range of projects.

The selection criteria are: a PhD in a quantitative discipline such as theoretical biology, bioinformatics, mathematics, statistics, physics or computer science; a strong research track record in mathematical modelling or biostatistics; an interest in viral evolution; proficiency with

Linux or Unix and computer programming languages, preferably C and R; excellent oral and written communication skills; the ability to work effectively as part of a team as well as independently; knowledge of OHS responsibilities and a commitment to attending relevant OHS training; knowledge of equal opportunity principles.

For the full information package see <http://www.hr.unsw.edu.au/services/recruitment/jobs/-26111020.html> Informal enquiries to Mark Tanaka, email: m.tanaka@unsw.edu.au

m.tanaka@unsw.edu.au

UNorthCarolinaChapelHill MaleMateChoice 2

Second posting: review of applications starts Feb 15.

Postdoctoral Position at the University of North Carolina, Chapel Hill

A position is available for a Postdoctoral Research Associate in the lab of Maria Servedio at the University of North Carolina, Chapel Hill, to work on theoretical models of male and mutual mate choice. The applicant will be expected to develop an independent research project(s) in addition to collaborating with the PI on theoretical projects. Prior experience with theoretical modeling techniques, a strong mathematical background, and programming skills is preferred. A Ph.D. and a strong background in evolution is required.

Research in the Servedio lab concentrates developing mathematical models of speciation and mate choice. Please see <http://www.bio.unc.edu/Faculty/Servedio/Lab/Home.html> or contact Maria Servedio (servedio@email.unc.edu) for more information on projects ongoing in the lab.

The appointment is for 1-2 years starting preferably in the summer of 2011 (start date flexible). Send applications including a CV, description of research experience and interests, brief description of background in theory and related skills, and names and addresses of three references to Maria Servedio at servedio@email.unc.edu

Informal inquiries are welcome as well. Review of applications will begin on Feb 15 and continue until the position is filled.

servedio@email.unc.edu

UOslo Avian Evolutionary Genomics

Centre for Ecological and Evolutionary Synthesis (CEES)

Position as post doc/researcher in evolutionary biology, ref. no. 2011/2183

A 3-year position as post doc or researcher is available from April 1st 2011 on the project "On the evolutionary genomics and behavioral ecology of homoploid hybrid speciation in Passer sparrows".

The candidate will be part of a project funded by The Norwegian Research Council. The CEES is a centre of excellence for integrative biological research and is well-funded. It provides a stimulating research environment, situated at the Department of Biology, with many young international and Norwegian scientists working on a variety of theoretical and empirical topics within ecology, evolution, population genetics, genomics, phylogenetics, molecular biology, and statistical methodology. The CEES is chaired by Professor Nils Chr. Stenseth and currently employs 16 faculty members, 43 postdocs/researchers, 32 PhD students and 30 MSc students. Information about the centre can be found at <http://www.cees.uio.no> Job description We seek to employ a post doc candidate/researcher on the project: "On the evolutionary genomics and behavioral ecology of homoploid hybrid speciation in Passer sparrows." The successful candidate will work in a research team that works on evolutionary processes related to speciation. The specific project focuses on different species of sparrows and in particular the Italian sparrow (*Passer italiae*) that appears to be a stabilized hybrid form between the house sparrow (*P. domesticus*) and the Spanish sparrow (*P. hispaniolensis*). The project includes "comparative genomics using 454-technology" "analysis of genetic variation across transects through hybrid zones" "phylogeographic studies of the species complex" "association studies of traits affecting reproductive barriers using a candidate gene approach" "ecological and behavioural studies related to assortative mating in aviaries and in the field" "breeding experiments in aviaries to investigate the inheritance of mate preferences and potential genetic incompatibilities between the species.

The successful candidate will be involved in 3-4 of these subprojects pending on qualifications and interests.

Requirements Applicants must hold a equivalent to a Norwegian PHD degree and we search for a candidate with a strong background in evolutionary biology. Experience with evolutionary genetic/genomic research and/or evolutionary ecological or behavioural studies of wild or captive animals are required. Candidates that are interested in, and able to combine genetic and ecological approaches are particularly attractive for the position.

The position requires good skills in writing and speaking English.

The main purpose of post-doctoral research fellowships is to qualify researchers for work in top academic positions within their disciplines. No one can be appointed for more than one period at the same institution. Please also refer to the regulations pertaining to the conditions of employment for post-doctoral fellowship positions.

Salary Postdoctoral Research Fellow (SKO, 1352)/ researcher (SKO 1109), pay grade: 57 - 64 (NOK 448 200 - 510 000 depending on qualifications and seniority).

The application must include: "Application letter including a statement of interest, summarizing the applicant's scientific work and interests and describing how she/he fits the description of the person we seek" "CV (summarizing education, positions, pedagogical experience, administrative experience and other qualifying activity), including a list of published and unpublished works" "Copies of educational certificates, transcript of records, letters of recommendation" "A complete list of publications and up to 5 academic work that applicant wishes to be considered by the evaluation committee" "Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number)

To apply for the position, see <https://uio.easycruit.com/vacancy/application/-bd3c765e4dd0bb5ff004c91082fb7f86/514022/-64421?iso=gb> Foreign applicants are advised to attach an explanation of their University's grading system. Please remember that all documents should be in English or a Scandinavian language.

The University of Oslo has an agreement for all employees, aiming to secure rights to research results a.o. <http://www.uio.no/english/for-employees/-employment/position/intellectual-rights/> In accordance with the University of Oslo's equal opportunities policy, we invite applications from all interested individuals regardless of gender or ethnicity.

Address: Oslo

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>

UOxford PlantEvolution

Department of Plant Sciences, University of Oxford,
Independent Research Fellows Event 2011

The Plant Sciences Department, University of Oxford, is an internationally leading centre of excellence in plant sciences, ranked equal third of 52 UK Biological Sciences research institutions in RAE 2008 and based in the central multidisciplinary science area of Oxford. We seek applications from outstanding researchers who would like to be Independent Research Fellows within our department.

Those already holding or intending to apply for such fellowships may apply to attend a two-day departmental Independent Research Fellows Event on 10th and 11th May 2011. If invited to this event, you will be asked to present a talk about your proposed area of research and have the opportunity to discuss in depth your proposals, the future development of your group and your future career plans with senior departmental academic staff. Following the event, selected candidates will be mentored in the writing of fellowship applications and/or offered the opportunity to move existing fellowships to the Department of Plant Sciences.

Further details are available on the Department of Plant Sciences website www.plants.ox.ac.uk. Please email a two-page summary of your research plan and your CV and arrange for two letters of recommendation to be emailed to debbie.reeves@plants.ox.ac.uk by noon on Friday 18th March.

Debbie Reeves <debbie.reeves@plants.ox.ac.uk>

UOxford PlantEvolution 2

Department of Plant Sciences, University of Oxford,
Independent Research Fellows Event 2011

Event: 11- 12 May. Deadline for applications: 18 March.

The Department of Plant Sciences seeks applications from outstanding researchers who would like to be Independent Research Fellows within our department.

The Department of Plant Sciences, University of Oxford, is an internationally leading centre of excellence in plant sciences, ranked equal third of 52 UK Biological Sciences research institutions in the national Research Assessment Exercise 2008. Based in the vibrant central multidisciplinary science area of Oxford University, it encompasses the full spectrum of contemporary plant science research and teaching. Annually, UK and international research bodies fund several prestigious fellowships to enable up-and-coming research leaders to start conducting independent research, and the Department of Plant Sciences seeks to work with the best scientists to secure such fellowships in basic and applied plant biology.

Those already holding or intending to apply for such fellowships may apply to attend a two-day departmental Independent Research Fellows Event on 11th and 12th May 2011. If invited to this event, you will be asked to present a talk about your proposed area of research, and discuss in depth with senior departmental academic staff your research proposals, the future development of your group and your future career plans. Following the event, selected candidates will be mentored in the writing of fellowship applications and/or offered the opportunity to move existing fellowships to the Department.

To apply to attend the event, please email a two-page summary of your research plan and your CV and arrange for two letters of recommendation to be emailed to debbie.reeves@plants.ox.ac.uk by noon on Friday 18th March.

Further details are available on the Department of Plant Sciences website www.plants.ox.ac.uk. Debbie Reeves <debbie.reeves@plants.ox.ac.uk>

UppsalaU EvolutionaryBiology

11 PhD AND POST-DOC POSITIONS IN EVOLUTIONARY BIOLOGY AND GENOMICS AT THE EVOLUTIONARY BIOLOGY CENTRE, UPPSALA UNIVERSITY

A Centre of Excellence in the interface of evolutionary biology and genomics has been established at the Dept of Evolutionary Biology of the Evolutionary Bi-

ology Centre (EBC) of Uppsala University. The environment consists of several relatively young research groups (Urban Friberg, Anders Gotherstrom, Simone Immler, Mattias Jakobsson Hanna Johannesson, Tanja Slotte and Jochen Wolf) with Hans Ellegren being Head of the unit. Currently, there are about 20 PhD students, 15 post-docs and some bioinformaticians working within these groups, with the great majority having a background from international universities. Thanks to a number of competitive grants recently obtained, the environment will now significantly expand by recruiting several new PhD students and post-docs.

An overview of the research activities in the environment can be found at our web pages (<http://www.ebc.uu.se/Research/IEG/evbiol/>). A common theme is that we address key questions in evolutionary biology, like speciation, local adaptation, life history evolution, and molecular evolution, using genomic approaches. Study organisms include natural bird and plant populations, Neurospora, Drosophila, zebra fish, domestic animals and humans. We have tight connections with several other research programs at the Evolutionary Biology Centre (see <http://www.ebc.uu.se/Research/IEG/> and a centre-wide graduate school "The genomics of phenotypic diversity in natural populations" (<http://www.ebc.uu.se/education/postgrad/gradschool/>) is organized from here.

Below are brief descriptions of the positions currently open. Further details about each of these, including necessary qualifications, are available at http://www.ebc.uu.se/Research/IEG/evbiol/open_positions/ or can be obtained from the named group leader. Informal inquiries and applications should be sent to the respective supervisor. Common to all positions is that we ask applicants to provide a CV, a statement of research interests and the name and contact details of at least two references. The positions remain open until filled.

1. PhD position: Haploid selection in animals Sexual reproduction in eukaryotic organisms entails the existence of two sexes (males and females) and two life phases (haploid and diploid). Selection acting differently in the two sexes and the two phases causes conflicts, which affect evolutionary processes. This PhD project aims to address questions about the causes and consequences of sexual selection across ploidy levels in animals. Experimental work using the zebrafish *Danio rerio* as a model system will bring answers to these questions. For more information please see our web pages or contact Simone Immler (Simone.Immler@ebc.uu.se).

2. PhD position: Natural selection on gene regulation Changes in gene regulation have long been hypothe-

sized to underlie adaptive phenotypic evolution. In this project, we aim to test this hypothesis and quantify the long-term impact of selection on regulatory sequences. The project will involve the use of genomic methods to study sequence and gene expression variation in the emerging plant model system *Capsella*. For more information please see our web pages or contact Tanja Slotte (Tanja.Slotte@ebc.uu.se).

3. PhD position: Whole-genome analysis of microsatellite evolution Next-generation sequencing (NGS) allows gathering a wealth of information on microsatellite variability both within and between species. Using recently assembled whole-genome sequences from multiple avian and mammalian species, this project aims to increase our understanding of the evolution of microsatellites and polymorphism at these loci. Moreover, this project also aims at using NGS microsatellite data to identify genomic regions subject to strong selective sweeps in natural populations of ecological model organisms, using microsatellites. For more information please see our web pages or contact Hans Ellegren (Hans.Ellegren@ebc.uu.se).

4. PhD position: Speciation genomics in a famous avian hybrid zone The hybrid zone between carrion and hooded crows (*Corvus [corone] corone / cornix*) is a text book example of incipient speciation that is well characterized from an ecological and behavioural perspective. We investigate its genetic architecture with a set of genomic tools currently including genome assembly, re-sequencing of several European populations and RNAseq-based transcriptome analyses. For more information please see our web pages or contact Jochen Wolf (Jochen.Wolf@ebc.uu.se).

5. PhD position: Sex differences in aging

— / —

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>

UppsalaU GeneticDiversity

*Post-doc project in genetic diversity and population resource use***

UppsalaUniversity is currently recruiting a postdoc for a project dealing with the importance of genetic diversity for population abundances and population wide

resource use. Zooplankton of the genus *Daphnia* and fish species will be used as model systems. The aim is to investigate:

1. The importance of genetic variation for plasticity and population wide resource use
2. The importance of genetic variation for variation in population densities

AFLP will be used to assess the genetic variation of populations and stable isotopes to study resource use. The project is planned to be conducted both in field and experimental studies.

The successful candidate should have a PhD in a related field. It is required that the candidate has documented experience of AFLP or some similar molecular genetic method. An experience of research associated with the interaction between ecology and population genetics is preferable. Previous work on *Daphnia* or fishes, or use of stable isotopes is an advantage.

The postdoc is intended to start no later than May 2011. The funding is a scholarship of 240 000 SEK/year (? EUR 24 000/year and non-taxable), and currently given for one year, but there are possibilities for a prolongation up to two years.

The project will be conducted at Department of Ecology and Genetics at Uppsala University, Sweden, more precisely in the subdepartment of Population Biology. The department has a strong focus on molecular ecology. This department is located at the Evolutionary Biology Centre housing about 400 researchers with a strong profile in ecology, evolution and systematic.

The applicant should send in a personal letter describing yourself and a CV including publication list by email (see below) no later than 20 Feb. For more information contact: Örjan Östman, +46 (0)18-471 26 80, orjan.ostman@ebc.uu.se Homepage: <http://www.iee.uu.se/popbiol/default.php?type=personalpage&lang=en&id=130> orjan.ostman@ebc.uu.se

UppsalaU HoneybeeGenomics

Please post the following message:

A post-doctoral position is available immediately at Uppsala University to work on next-generation sequence analysis of honeybee populations.

We have initiated a project to survey genetic variation across the genome in a number of subspecies and lines of

honeybee using next-generation sequencing on the AB SOLiD system. These include natural races sampled from around the world and experimental lines subjected to artificial selection. The main aim of the project is to identify signatures of selection in these data in order to understand the nature of genetic adaptation and find genetic variants responsible for traits of interest. The main duty of the postdoc will be bioinformatic analysis of the data generated.

The project is led by Matthew Webster at Uppsala University (UU) in collaboration with the honeybee research group in the Swedish University of Agricultural Sciences (SLU) led by Ingemar Fries and the Uppsala Genome Centre. It will also benefit from interactions with the groups of Leif Andersson (UU and SLU) and Kerstin Lindblad-Toh (UU and Broad Inst.), both involved in similar analyses in other species.

Uppsala is the fourth largest city in Sweden situated in pleasant surroundings close to Stockholm.

The ideal candidate should have: A PhD in bioinformatics, evolutionary/population genetics or related area. Experience in analysis of data from next-generation sequencing platforms. Skill in scripting (e.g. perl) and statistical data analysis (e.g. R).

The duration of the position will be at least 2 years.

Please address informal inquiries by email to Matthew Webster, who will send details of how to apply.

Matthew Webster matthew.webster@imbim.uu.se
Dept. of Medical Biochemistry and Microbiology, Uppsala University www.imbim.uu.se
matthew.webster@imbim.uu.se

UQueensland ConservationPlanning

Post-Doctoral Research Fellow in Landscape Genetics School of Geography, Planning and Environmental Management University of Queensland (Brisbane, Australia)

Excellent opportunity for an early career researcher to work in a stimulating and challenging research team environment. The School of Geography, Planning and Environmental Management is one of the largest Schools of this type in Australia with 34 full-time academic staff who are widely published internationally and have extensive research backgrounds. It is a vibrant, multidisciplinary School with extensive teaching and research

programs. The School has a strong international research profile with active Research Centres across its fields of expertises.

The role: Applications are invited for an 18 month fixed-term Post-Doctoral Research Fellow position to work on an ARC funded project involving the following collaborators: the University of Queensland, the Queensland Museum, Redland City Council, Moreton Bay Regional Council, Logan City Council, Gold Coast City Council and the Queensland Department of Environment and Resource Management. The aim of the project is to integrate genetic information into models of species distributions and apply these new models to systematic conservation planning.

The person: Applicants should have completed a PhD in a relevant discipline and have a strong desire to develop a successful and productive research career. They should have expert knowledge in the area of landscape genetics and have strong quantitative skills, preferably in the area of spatial analysis and statistics. Genetics laboratory experience, including DNA sequencing and microsatellite genotyping, is also essential, as well as evidence of successful publication of peer-reviewed research articles.

Remuneration: The remuneration package will be in the range \$67,958 - \$72,949 p.a., plus employer superannuation contributions of 17% (total package will be in the range \$79,511 - \$85,351 p.a.). This is a full-time, fixed term appointment for 18 months at Academic level A.

Application details: The position description and selection criteria can be found at: <http://www.uq.edu.au/jobs/index.html?page=151866&pid=11217> OR <http://www.seek.com.au/Job/post-doctoral-research-fellow-in-landscape-genetics/in/brisbane/19085224>

Contact: To discuss the role contact Dr Jonathan Rhodes, email j.rhodes@uq.edu.au or Dr Jessica Worthington Wilmer, email jessicaww@qm.qld.gov.au

Send applications to Human Resources, School of Geography, Planning and Environmental Management, The University of Queensland, St Lucia, Qld 4072, or email hr@gpem.uq.edu.au.

Applications close 4 March 2011. Reference No . 3012628

jessica.wilmer@qm.qld.gov.au

UReading ExperimentalEvolution

A postdoctoral position is available in the lab of Louise Johnson in the School of Biological Sciences at the University of Reading, UK. The project involves engineering bacterial strains to reassign stop codons, and using experimental evolution and whole genome resequencing to investigate the evolutionary and genomic consequences of genetic code change.

This 3 year project is in collaboration with Michael Brockhurst (University of Liverpool) and Robert Jackson (University of Reading), and funded by the Leverhulme Trust. Candidates should have a PhD and laboratory experience in microbiology or molecular biology; experience of mathematical modelling and programming are preferred but not essential. The closing date for applications is 28th March 2011 and interviews will be held on the 7th April.

For further information and a job description please see the following link:

https://www.reading.ac.uk/about/jobs/-tlive.webrecruitment/wrd/run/ETREC107GF.open?VACANCY_ID%3d0940743KV5%1BUSESSION%25A39CF70&WVID%2593791XsD&LANG=USA
<https://www.reading.ac.uk/about/jobs/-tlive.webrecruitment/wrd/run/ETREC107GF.open?VACANCY_ID%3d0940743KV5%1BUSESSION%25A39CF70&WVID%2593791XsD&LANG=USA>

The University of Reading is a leading research university in the UK, situated in the town of Reading 40 miles to the west of London. Information about the School of Biological Sciences is available via its website <http://www.reading.ac.uk/biologicalsciences/-biosci-index.aspx> .

Informal enquiries are welcome - please contact me at the email address below.

Louise

Dr Louise Johnson RCUK Fellow, School of Biological Sciences Room 302a Lyle Building University of Reading, RG6 6BX, UK Phone +44 118 378 4432

l.j.johnson@reading.ac.uk

USheffield 2 EvolutionBehaviour

I have a couple of postdoc positions open on human behavioural ecology at the University of Sheffield, and because I am hoping to find candidates with a degree on evolutionary biology and strong background on e.g.

quantitative genetics.

Two postdoc positions on human behavioural ecology at the Department of Animal and Plant Sciences, University of Sheffield

We are looking for two post-doctoral research associates to work at the interface between evolutionary biology, epidemiology, demography and anthropology on the genetic, ecological and demographic factors influencing life-history patterns and senescence rate in humans. The overall aim of the project is to understand the evolutionary ecology of human reproductive behavior across the large demographic and social changes occurring during the past 200 years, and how natural selection has affected human populations at different periods. The post-holder will be in charge of managing and analysing a large pedigree database on the demography of historical Finnish families spanning the time since early 1700s until the end of 1900s. More information about the research group is available at <http://www.huli.group.shef.ac.uk/>. The successful candidate will have a PhD in evolutionary biology or related topic and a good track record of publishing in leading specialist or multidisciplinary journals. Strong statistical skills are essential. The post is fixed-term with a start date of 1st April 2011 (or as soon as possible thereafter) and an end date of 31st March 2013 with a possibility of an extension subject to funding. The work will be performed at the Department of Animal and Plant Sciences, University of Sheffield - one of the largest departments in the UK devoted to the study of whole organism biology. We are ranked joint 3rd in the UK for biology research and 70% of our research activity has been judged to be "world-leading" or internationally excellent (RAE 2008). The position is funded by the European Research Council (ERC). Closing date: 14.3. 2011.

For all on-line application system queries and support, contact: e-Recruitment@sheffield.ac.uk

For informal enquiries about this job and department, contact: Dr Virpi Lummaa v.lummaa@sheffield.ac.uk or +44 (0)114 2220051

– Dr. Virpi Lummaa Department of Animal and Plant Sciences University of Sheffield Western Bank, Sheffield S10 2TN United Kingdom

tel. +44 (0)114 222 0051 fax. +44 (0)114 222 0002 email. v.lummaa@sheffield.ac.uk <http://www.huli.group.shef.ac.uk/> <http://www.shef.ac.uk/-aps/staff/acadstaff/lummaa.html> Virpi Lummaa <V.Lummaa@sheffield.ac.uk>

UTexas MDAnderson StatisticalGenetics

Postdoctoral Research Position in Statistical Genetics

A postdoctoral position in statistical genetics is available in the lab of Dr. Paul Scheet at the University of Texas M. D. Anderson Cancer Center in Houston. The focus of the lab is the development of statistical methods to analyze genetic and genomic data, with applications to human disease mapping and inference.

The lab provides an excellent environment for studying statistical and computational genomics, with close proximity to collaborators across the Texas Medical Center and a strong statistical genetics group in the Department of Epidemiology. Dr. Scheet has NIH-funded projects for statistical methods development and for collaborations at multiple institutions, including St. Jude Children's Research Hospital (PI: Mary Relling). There are opportunities for collaborative mentorship from colleagues Gary Rosner (Johns Hopkins) and Yongtao Guan (Baylor College of Medicine).

M. D. Anderson has topped U.S. News & World Report's list for cancer care ("America's Best Hospitals") 7 of the last 9 years and is located in the Texas Medical Center (TMC), the world's largest. The proximity of the TMC to Rice University and the Museum District, light rail connections to world-class performing arts and professional sporting venues, and a large and modern Chinatown make accessible a uniquely cosmopolitan and affordable city.

The applicant should be working towards or have received a Ph.D. (or equivalent) in statistics, biostatistics, bioinformatics, computer science, quantitative biology or genetics/genomics, or a related field with strong computational background.

To apply, send a cover letter with information about research experience and interests, a CV, and the names and contact information for 3 references to: pascheet@mdanderson.org. Please visit <http://epi.mdanderson.org/scheet> for more information.

PAScheet@mdanderson.org

UToronto Evolutionary Biol 2

Reminder: Review of applications for the Postdoctoral Fellowship in the Department of Ecology and Evolutionary Biology at the University of Toronto will begin on Feb. 1, 2011

The Department of Ecology and Evolutionary Biology < www.eeb.utoronto.ca > at the University of Toronto invites applications for Departmental Postdoctoral Fellowships in the areas of Ecology and Evolutionary Biology, broadly defined. One position is available this year, and we expect that another will become available next year through an ongoing EEB Postdoctoral Fellowship Program. Positions may continue for two years, subject to review after one year, and can begin as early as July 1, 2011. The salary starts at \$40,000 per year, with research expenses covered by the Postdoctoral Advisor.

The Fellow will be a fully participating member in the Department. Candidates must identify and communicate with a potential advisor (or advisors) in advance of the application process. All full-time faculty members at the St. George (downtown) campus of the University of Toronto are eligible to serve as advisors (see www.eeb.utoronto.ca/postdoc/ for a list of potential supervisors). Opportunities for teaching in an upper level course may be available, if the candidate wishes to teach.

To apply, applicants should first contact and obtain the agreement of a faculty advisor (or co-advisors). Afterwards, applicants should submit a cover letter clearly indicating the proposed faculty advisor(s), a curriculum vitae, copies of 2 publications, and a short (1-3 pages) description of past research accomplishments and future research plans. Applicants should include names and e-mail addresses of two potential referees. Applicants should also indicate the date they will be available to begin the position. All application materials must be submitted as PDF's in a single email to: Elizabeth Rentzelos <chairsec.eeb@utoronto.ca> <<mailto:chairsec.eeb@utoronto.ca>>. Review of applications will begin on Feb. 1, 2011.

The University of Toronto is a leading academic institution in Canada with over 60 faculty members specializing in ecology and evolution. Strong links exist between the Department of Ecology and Evolutionary Biology and the Royal Ontario Museum, the Centre for Global Change, the Centre for Environment, and

the Faculty of Forestry. The University owns a nearby field station dedicated to ecological research (the Kofler Scientific Reserve, ksr.utoronto.ca). The department also has a partnership with the Ontario Ministry of Natural Resources that helps provide access to infrastructure, including lab facilities in Algonquin Provincial Park (www.harkness.ca), funding, and long-term data sets. Genomic analyses are supported by the Centre for the Analysis of Genome Evolution and Function (www.cagef.utoronto.ca).

– Megan Frederickson Assistant Professor Department of Ecology and Evolutionary Biology University of Toronto 25 Harbord Street Toronto, Ontario, M5S 3G5, Canada Email: m.frederickson@utoronto.ca Web: labs.eeb.utoronto.ca/frederickson

Megan Frederickson <m.frederickson@utoronto.ca>

UTurku Stickleback Evolutionary Genomics

Postdoc in Evolutionary Genomics/Bioinformatics-threespine sticklebacks

A post-doctoral position is available to study phenotypic evolution in threespine stickleback in Erica Lederäs research group at the University of Turku, Finland (<http://users.utu.fi/eriled>). This position is part of an Academy of Finland funded project which aims to use a systems biology approach to identify the molecular mechanisms responsible for the evolution of sexual dimorphism as well as various adaptive phenotypic traits.

Requirements: Candidates are expected to have a PhD in biology or a related field and a strong background in molecular biology and genetics and/or bioinformatics. Researchers with previous experience (in any organism) in evolutionary genomics or molecular biology, in particular involving microarray analysis, next-generation sequencing, and/or bioinformatics are welcome to apply. The candidate is expected to be able to express him/herself fluently in English (written and spoken), be able to work both independently and as a member of a team, both nationally and internationally, and contribute to the supervision of PhD and MSc students.

To apply: Please send a letter describing your research interests and qualifications, a CV (including publication list), and contact information for three references (who will provide a letter of reference) to Erica Leder

(erica.leder@utu.fi).

Review of applications will commence on February 28 with the preferred starting date being April 2011. The position is initially available for 2 years, but an extension may be possible. The salary range is 3000 - 3800 EUR per month, depending on the previous post-doctoral experience of the candidate. Informal inquiries should also be addressed to Erica Leder.

Research Environment: The successful applicant will be part of an active research climate in the field of evolutionary genomics including interaction and collaboration with Professors: Craig Primmer, Juha Merilä, and Michael Bell. We are part of the Systems Biology Research Group at the Turku Centre for Biotechnology and core facilities for microarray analysis, next-generation sequencing, and proteomics are available through this affiliation. Turku, Finland is the 5th largest city (176 000 people), is located in the South-Western part of 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 the City of Turku was ranked third in the most recent classification of medium-sized European "Smart Cities" (<http://www.smart-cities.eu>)

Background/Example Publications: Leder EH, JM Cano, T Leinonen, RB O'Hara, M Nikinmaa, CR Primmer, and J Merilä. (2010) Concentration of female-biased expression on the X chromosome as an intermediate step in the evolution of sex chromosomes. *Molecular Biology and Evolution* 27: 1495-1503

Papakostas, S, LA VÅllestad, CR Primmer & EH Leder. 2010. Proteomic Profiling of Early Life Stages of European Grayling (*Thymallus thymallus*). *Journal of Proteome Research*, 9:4790-4800.

Leder EH, Merilä J, & Primmer CR. (2009) A flexible whole-genome microarray for transcriptomics in three-spine sticklebacks. *BMC Genomics* 10: 426

Erica Leder, PhD Academy Research Fellow Division of Genetics and Physiology Dept of Biology (Vesilinnantie 5) 20014 University of Turku Finland

mobile +358 50 3398204 tel. +358 2 3337086 fax. +358 2 3336680

Erica Leder <eriled@utu.fi>

Utah Solanaceae Systematics

Postdoctoral Position in Solanaceae Systematics. A postdoctoral position at the University of Utah is available in the area of Solanaceae systematics. Several projects are underway, including one to produce a global monograph of the genus *Solanum* (Solanaceae). *Solanum* includes between 1000 and 2000 species and is one of the largest genera of angiosperms. The species level taxonomy, including images, keys and specimen data, are being made available over the Internet on the Solanaceae Source webpage at www.solanaceaesource.org. Other projects include systematic and phylogenetic studies of other genera in the Solanaceae. Responsibilities include monographic taxonomy of selected groups of Solanaceae; specimen and image databasing and manipulation; field work for the collection of herbarium, seed and silica gel samples; generation of molecular data for phylogeny reconstruction (mainly sequences of chloroplast and nuclear genes); maintenance and analysis of living greenhouse collections of Solanaceae; data analysis, presentation, and publication; training and supervision of undergraduate lab assistants; and oversight of routine lab activities. Candidates should have a Ph.D. and experience in plant systematics, field work and with working in a team; experience with Solanaceae is preferred but not required, as is experience with molecular systematics and a variety of methods of data analysis. The position is available for one year beginning in April 2011 and extendable for up to several years as long as funds are available and satisfactory progress is demonstrated.

Electronic submission of applications is encouraged.

Review of applications will begin immediately and continue until a suitable candidate is chosen. Applicants should submit a statement of interest and description of past experience, a curriculum vitae, and contact information (names, email addresses, and phone numbers) of three references to:

Lynn Bohs Department of Biology 257 South 1400 East University of Utah Salt Lake City, UT 84112 USA
E-mail: bohs@biology.utah.edu Phone: [1] (801) 585-0380 Bohs lab - <http://biologylabs.utah.edu/bohs/>-
Solanaceae Source - www.solanaceaesource.org Information on the Biology Department at the University of Utah is available at www.biology.utah.edu The University of Utah is an Equal Opportunity Employer.

Lynn Bohs <bohs@biology.utah.edu>

UWisconsin Madison EvolutionaryGeneticsGenomics

Postdoctoral Position in Evolutionary Genetics/Genomics

A postdoctoral position is available immediately (one year, renewable) in the Laboratory of Professor Carol Lee in the Center of Rapid Evolution (CORE) at the University of Wisconsin, Madison to work on a project in collaboration with Joana Silva at the Institute for Genome Sciences. The research focuses on the evolutionary genetics and genomics of invasive populations. We are exploring the systematic and functional composition of microbial communities associated with an invading host, the copepod *Eurytemora affinis*, and how microbial-host interactions shift following habitat invasions. The project will make extensive use of microbiome and metagenome methodologies to study the microbiota, and of transcriptome sequencing and analyses to characterize metabolic shifts within the copepod host.

Requirements for this position include a Ph.D., a strong background in molecular biology/genomics and strong analytical and quantitative skills. Relevant training and experience include research in metagenomics, culturing of bacteria from environmental samples, transcriptomics, and genomic data analysis.

Applicants should email a cover letter, CV, a brief statement of research interests and experience, and up to three representative publications to: carollee@wisc.edu. Applicants should also arrange for three letters of recommendation to be sent by email. Any questions regarding this position are welcome. Application Deadline: March 30, 2010.

The University of Wisconsin, Madison provides an intellectually vibrant research environment, with ~37 biology departments and ~800 biology faculty, including a strong community of evolutionary biologists and geneticists. The University of Wisconsin is an Equal Opportunity/Affirmative Action Employer.

Carol Eunmi Lee, Ph.D. Associate Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

<https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html> carollee@wisc.edu

Vienna PopGenetics

Statistical genetics and population genetics in Vienna

Several postdoctoral positions in statistical genetics and population genetics are immediately available in the Nordborg group at the Gregor Mendel Institute. Major projects include genome-wide association mapping and systems genetics using 1,001 fully sequenced lines of *A. thaliana*, speciation genetics in a variety of plant species, and population genetics of vervet monkeys. More information is available at <http://www.gmi.oeaw.ac.at/research-groups/-magnus-nordborg>. Applicants are expected to have completed (or be close to completing) a PhD in a closely related field, to have published (or be close to publishing) in major international journals, and have experience with genomic data (e.g., next-generation sequencing data) as well as strong quantitative training (including programming). Please send an e-mail describing your background and interest in our projects, accompanied by a CV and the names of three referees to Dr. Magnus Nordborg.

Applications are open now and will be considered until positions are filled.

Cheers,

MN

Magnus Nordborg, Scientific Director Gregor Mendel Institute Dr. Bohr-Gasse 3 1030 Vienna, Austria
T: +43 1 79044-9000 F: +43 1 79044-9001 magnus.nordborg@gmi.oeaw.ac.at

<http://www.gmi.oeaw.ac.at> iChat A/V: nordborg@mac.com

“Nordborg, Magnus” <magnus.nordborg@gmi.oeaw.ac.at>

WorkshopsCourses

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Dear Colleagues, we still have a few places available at this workshop, please bring it to the attention of potential participants. Tad Kawecki

Evolutionary Biology Workshop in the Alps

26 June- 2 July 2011 Arolla, Switzerland

3 ETSC credit points

Faculty: John Pannell (University of Oxford, UK)
Mike Ritchie (University of St. Andrews, UK) Jerome
Goudet (University of Lausanne, Switzerland) Tadeusz
Kawecki (University of Lausanne, Switzerland)

Target participants: PhD students, advanced master students This workshop, based on a concept developed by Steve Stearns and John Maynard Smith, takes place in a small Alpine village (Arolla), which will allow you to focus while being able to enjoy the landscape and the Alpine flora. The main goals of this course are to develop the following skills: - developing your scientific ideas through discussions in groups - thinking critically and expressing oneself clearly - turning a general idea into a research project - writing a research proposal and defending it It is you, the students, who will be in charge in this course. You will be divided in groups of 4-5 students. In those groups, you will work on your

ideas. You, as a group, will decide what the important questions in broadly defined evolutionary biology are, you will choose one, and attempt to develop a proposal for a research project that will address it. The faculty will visit the groups during the discussions to answer your questions, provide coaching and give you feedback on your projects, but they will generally take the back seat. Additionally, the faculty will give informal talks about their research and be available for informal discussion with individual students. At the end you will present your projects to other participants, and we will party.

Costs: CHF 430.- for room and board.

More information under <http://biologie.euso.ch/-ecologie-evolution/activities/detail-activity/item/-courses/evolutionary-biology-workshop-in-the-alps-1/>

To apply, send a single file (pdf or rtf) containing a short motivation letter, a cv and the name of your scientific advisor to tadeusz.kawecki@unil.ch.

Deadline for application: 28 February 2011.

– Tadeusz J. Kawecki Associate Professor Department of Ecology and Evolution University of Lausanne Biophore CH 1015 Lausanne, Switzerland

tadeusz.kawecki@unil.ch

FortCollins Colorado ComparativeGenomics Jul10-23

Workshop on Comparative Genomics, North America
2011

Fort Collins, Colorado, USA

10 - 23 July 2011

Application Deadline: 15 May is the preferred application deadline, after which time people will be admitted to the course following review of applications by the admissions committee. However, later applications will certainly be accepted.

<http://www.molecularevolution.org/workshops/WCG>
Scott A. Handley, Michael Cummings and Kendra Nightingale, Co-Directors

The Workshop on Comparative Genomics consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of comparative genomics focusing on next-generation sequencing data. Faculty are chosen exclusively for their effectiveness in teaching theory and practice in comparative genomics. Included among the faculty are developers and other experts in the use of computer programs and packages such as ABySS, bowtie, velvet, bioperl, Scripture, GMOD, Gbrowse, Galaxy, PyCogent, QIIME who provide demonstrations and consultations. The course is designed for established investigators, post-doctoral scholars, and advanced graduate students. Scientists with strong interests in the uses of short-read sequence data, analytical methods, comparative structure of genomes, metagenomics, genome visualization tools and related areas are encouraged to apply for admission. Lectures and computer laboratories total ~90 hours of scheduled instruction. Admission is limited. No programming experience is required, however, detailed instruction suitable for the novice will be provided during the early days of the Workshop on the use of the command line, editing tools and basic scripting.

Topics to be covered include: - Linux command line usage and scripting for next-generation sequence analysis - Sequencing technologies and study design - Sequence data quality control - Assembly and alignment - Functional annotation - Transcriptomics - Metagenomic analysis - Evolutionary genomics - Population genomics

2011 Fee: 1800 USD does not include other meals or housing. Special discounted housing and meals are available on the campus of Colorado State University.

For more information and online application see the Workshop web site -

<http://www.molecularevolution.org/workshops/WCG>
and for housing and payment information see -

<https://regstg.com/Registration/RegForm.aspx?rid=-3Dd41e4a6a-bf9f-40f0-8b0a-74fba75088b4&action=add>

The Workshop on Molecular Evolution is also being offered immediately after the Workshop on Comparative Genomics.

<http://www.molecularevolution.org/workshops/WME>
mike@umiacs.umd.edu

FortCollins Colorado MolEvol Jul24-Aug6

Workshop on Molecular Evolution, North America 2011

Fort Collins, Colorado, USA

24 July - 6 August 2011

Application Deadline: 15 May was the preferred application deadline, after which time people will be admitted to the course following review of applications by the admissions committee. However, later applications are accepted.

<http://www.molecularevolution.org/workshops/WME>
Michael P. Cummings, Scott A. Handley and Kendra Nightingale, Co-Directors

The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. Faculty are chosen exclusively for their effectiveness in teaching theory and practice in molecular evolution. Included among the faculty are developers and other experts in the use of computer programs and packages such as BEAST, *BEAST, DataMonkey, FigTree, Genealogical Sorting Index, GARLI, HyPhy, LAMARC, MAFFT, MrBayes, and SeaView who provide demonstrations and consultations.

The course is designed for established investigators, postdoctoral scholars, and advanced graduate students with prior experience in molecular evolution and related fields. Scientists with strong interests in molecular evolution, phylogenetics, population genetics, and related

fields are encouraged to apply for admission. Scheduled lectures and computer laboratories total ~90 hours of instruction. Admission is limited and highly competitive.

Topics to be covered include:

- Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis; hypothesis testing - Maximum likelihood and Bayesian theory and practice in phylogenetics and population genetics: coalescent theory; estimation of population genetic parameters - Detecting positive selection: theory and practice; codon models - Dating phylogenies: theory and practice - Coalescent species trees

2011 Fee: 1100 USD does not include other meals or housing. Special discounted housing and meals are available on the campus of Colorado State University.

For more information and online application see the Workshop web site -

<http://www.molecularevolution.org/workshops/WME> and for housing and payment information see -

<https://regstg.com/Registration/RegForm.aspx?rid=-3D76c8770d-9b70-44e5-9d1d-804beeceb915&action=add> The Workshop on Comparative Genomics is also being offered immediately before the Workshop on Molecular Evolution, see <http://www.molecularevolution.org/workshops/WCG> mike@umiacs.umd.edu

Frauenchiemsee Phylogenetics Aug7-12

To whom it may concern,

the Master's programme "Ecology, Evolution and Systematics" is holding its annual Summer School 2011 on "Phylogenetics: new applications, pitfalls and challenges" from the 7th to the 12th of August, 2011, at the Frauenchiemsee, Germany.

As I wasn't quite sure how to send the information, please see below or attachment for the information that is to be posted.

If you have any questions, please don't hesitate to contact me.

Regards, Alice Edler

for website:

Dear all,

the Ludwig-Maximilian-University of Munich's Master's programme in Evolution, Ecology and Systematics (EES) is hosting its annual summer school from 7 - 12 August, 2011, on "Phylogenetics: new applications, pitfalls and challenges". We invite PhD students and advanced Master's students to join us at Frauenchiemsee!

Application deadline is May 31st, 2011. Please send a full CV, a statement about your research interests/current projects (max. half page), a statement about why you want to attend the summer school - explicitly addressing how you expect to benefit and what you can contribute (max. half page). Please send your application by email, preferably as a single PDF file to Dr. Alice Edler (ees@bio.lmu.de).

Invited speakers: Prof. Dr. Olaf Bininda-Emonds (University of Oldenburg, Germany), Prof. Dr. Nicholas Lartillot (University of Montreal, Canada), Prof. Dr. John Wiens (Stony Brook University, USA).

Organisers: Prof. Dr. Dirk Metzler LMU BioCenter Grosshaderner Str. 2 82152 Planegg-Martinsried Phone: +49 89 2180 74108 Fax: +49 2180 74104 Email: metzler@biologie.uni-muenchen.de Website: http://evol.bio.lmu.de/_statgen/ Dr. Alice Edler EES Program Coordinator Graduate Program in Evolution, Ecology & Systematics, University of Munich (LMU) Biozentrum - Department Biologie II Grosshaderner Str. 2 D-82152 Planegg-Martinsried, Germany Phone: 49 (0)89-2180-74234 Email: ees@biologie.uni-muenchen.de

For further information on the summer school, feel free to contact the organisers or see the summer school website (<http://www.eeslmu.de/eeswiki/-Summer.school.2011>).

Dr. Alice Edler EES Program Coordinator Graduate Program in Evolution, Ecology & Systematics, University of Munich (LMU) Biozentrum - Department Biologie II Grosshaderner Str. 2 D-82152 Planegg-Martinsried, Germany Phone: 49 (0)89-2180-74234

ees@biologie.uni-muenchen.de

Guarda Switzerland EvolBiol Jun18-25

Workshop in evolutionary biology for master students and first or second year PhD students.

It is my pleasure to announce this years Guarda workshop in Evolutionary Biology. The main aim of this 1 week course is to develop the skills to produce an independent research project in evolutionary biology. The course is for students with a keen interest in evolutionary biology.

The course takes place 18.-25. June 2011 in the Swiss mountain village Guarda. Faculty includes Richard Lenski, Peter and Rosemary Grant, Sebastian Bonhoeffer and Dieter Ebert (organizer).

The course is intended for master (Diploma) students and early PhD students. For the course 3 ECTS credit points are awarded.

The web page with all the details can be found under:

<http://www.evolution.unibas.ch/teaching/guarda/-index.htm> Please communicate this information to interested students.

dieter ebert

<http://evolution.unibas.ch/> Universität Basel, Zoologisches Institut, Vesalgasse 1 4051 Basel, Switzerland
Tel. +41-(0)61-267 03 60

dieter.ebert@unibas.ch

Hungary NicheTheorySpeciation Aug29-31

Workshop announcement

Niche theory & speciation workshop

August 29-31, 2011

Keszthely (Lake Balaton), Hungary

<http://nichews.elte.hu> Framework : ESF Research Networking Programme Frontiers of speciation research (FroSpects)

<http://www.iiasa.ac.at/Research/EEP/FroSpects/-index.html> Generation and maintenance of species diversity used to be distinct subjects of evolutionary genetics and ecology. During the workshop we shall discuss as many connections as possible between these strongly related facets of biological diversity. Over the last decade robust empirical evidence has been accumulating on the mechanisms maintaining species coexistence and on frequency-dependent selection,

ecological divergence as well as on sympatric speciation. The invited participants work on empirical and theoretical problems of the evolution of niche segregation and genetics of speciation that provide a unique opportunity to relate the ecological and genetic approaches to speciation.

The Darwinian idea for the origin of species connects divergence to weakening struggle for existence. It is inherently related to Darwin's view on reduced competition between species with different roles in the economy of nature. In modern terms, Darwinian speciation is based on niche segregation. In particular, adaptation to different environmental conditions ("habitats") and to different regulating factors ("resources") can be seen as complementary ways of reducing competition. Selection for reduced competition leads to robust coexistence. The idea of Darwinian speciation requires a Darwinian approach also to ecology where the various ways of population regulation are in the focus of interest.

Both empirical and theoretical contributions to these issues are welcome.

If you would like to attend and contribute please write an email to Géza Meszéna, geza.meszena@elte.hu subject=NicheWorkshop-LakeBalaton2011, at your earliest convenience, but not later than 7 March 2011.

Géza Meszéna, main organizer

Department of Biological Physics, Eötvös University

Pázmány Péter sétány 1A, H-1117 Budapest, Hungary

Phone:

+36 1 372 2786

E.mail:

Geza.Meszena@elte.hu

Other organizers:

Ake Branstrom, Ulf Dieckmann,

Liz Pásztor, András Szilágyi

Confirmed participants so far:

Peter Abrams (Toronto, Canada)

Joel Brown (Chicago, USA)

Daniel Dykhuizen (Stony Brook, USA)

Éva Kisdi (Helsinki, Finland)

Olof Leimar (Stockholm, Sweden)

Andrew Hendry (Montreal, Canada)

Joachim Hermisson (Vienna, Austria)

Robert D. Holt (Gainesville, USA)

Jim Mallet (London, UK)

Axel Meyer (Konstanz, Germany)

Ole Seehausen (Dübendorf, Switzerland)

Jonathan Silvertown (London, UK)

Jorge Soberon (Lawrance, USA)

Géza Meszéna, PhD Associate Professor Department of Biological Physics Eötvös University Pázmány 1A, H-1118 Budapest Hungary Phone: +36 1 372-2786 Mobile: +36 20 973-9204 Fax: +36 1 372-2757 Email: geza.meszena@elte.hu Web: <http://evol.elte.hu/~geza> geza.meszena@elte.hu

Financial support to cover room and board and help defray transportation costs is available. Let us know if this is not necessary. Academic credit, if desired, is available at appropriate MSU rates. Let us know if this is desired.

For more info see < <http://www.kbs.msu.edu/-education/elme> > or email elme2011@kbs.msu.edu.

Christopher Klausmeier Kellogg Biological Station Department of Plant Biology Michigan State University Hickory Corners MI 49060

Web: <http://preston.kbs.msu.edu/> Email: klausme1@msu.edu

Christopher Klausmeier <klausme1@msu.edu>

KelloggBiolStation EvolEcol Jun6-24

ELME is a summer educational program at Michigan State University's Kellogg Biological Station devoted to Enhancing Linkages between Mathematics and Ecology.

ELME 2011 will focus on evolutionary ecology, particularly game theory and Adaptive Dynamics (Geritz et al. 1998). In this hands-on three-week course, students will learn the basics of Adaptive Dynamics and apply their knowledge to independent modeling projects using the computer program Mathematica.

Dates: June 6-24, 2011

Hours: Mon-Fri 9-5

Instructors: Stefan Geritz (University of Helsinki) & Christopher Klausmeier (Michigan State University)

Target audience: 12-18 graduate students and post-docs; exceptional undergraduates will be considered

Prerequisites: At least one semester experience in theoretical ecology/evolution. Previous exposure to AD and Mathematica useful but not required.

Format: A mixture of lecture, guided computer labs, and independent/team projects

To apply, email elme2011@kbs.msu.edu the following:

- your CV - a statement of research interests and why you'd benefit from the course - a statement of relevant educational/research experience, including related coursework - the name of a reference who you've asked to email a letter of support

Deadline for applications: March 15, 2011

Montreal PopulationGenomics GeneticEpidemiology May30-Jun3

Montreal Spring School of Population Genomics and Genetic Epidemiology

May 30 - " June 3, 2011

See www.montrealspringschool.ca for details

Day 0 -" May 30th (Optional for those who need a review

(Concurrent Sessions)

Review of Genetics

Instructors: Camille Malouf and Mathieu Bourgey
Time: 8:00am -" 12:00pm

Â Mendel's Laws of Genetics The chromosome theory of heredity Linkage and genetic recombination >From genes to genotype

Â Population Genetics Genetic Variability Assessing the genetic diversity of populations Main evolutionary forces Applications of population genetics

Review of Epidemiology

Instructor: Ellen Freeman

Time: 8:00am -" 12:00pm

This lecture will review basic concepts in Epidemiology, including measures of disease frequency, study designs, and measures of association. We will also discuss principles of causal inference including recognizing and controlling for bias and confounding and detecting interactions. Examples from genetic epidemiology will

be presented and attendants will be asked to read and discuss an article from this field.

Review of Biostatistics

Instructor: Nathalie Malo

Time: 1:00 - "5:00pm

The lecture will review concepts in probability and statistics. Topics will include sample space and event, union and intersection, conditional probability and independence, Bayes- Theorem, common probability distributions, and the concept of likelihood. Statistical inference methods will be discussed, including maximum likelihood estimation, confidence intervals, and hypothesis testing (large sample tests, exact and permutation tests).

The related computer lab will illustrate the use of some of these biostatistical tools using the R software. Attendants will also be given practice exercises with R.

Day 1 -" May 31st (note that exact hours will be adjusted to fit lunch and coffee breaks etc.)

Introductory Concepts in Human Populations and Medical Genomics

Instructor: Laurent Excoffier

Time: 8:00am -" 12:00pm

Principles of population genetics: This lecture will cover some of the major concepts in human population genetics including random genetic drift and the derivation and properties of the basic coalescence model. (Laurent Excoffier 8:00am -" 10:30am).

1. Random Genetic Drift

- 1.1. The Hardy-Weinberg equilibrium law
- 1.2. The Wright-Fisher Model of random genetic drift
- 1.3. Effective population size

2. Gene trees and the basic coalescence model

- 2.1. Coalescence under different demographic scenarios (e.g., population growth)

Introductory Concepts in Genetic Epidemiology

Instructor: Alexandre Alca~s

Time: 1:00pm -" 4:15pm

We will first briefly introduce concepts and designs to study familial aggregation followed by basic principles of linkage and association analysis for qualitative traits. Topics covered will include designs and analytical methods used to study genetic linkage. Both parametric and non-parametric linkage analysis will be covered. Presentation of the concepts will be followed by a computer

lab application using real data and currently available software such as MLB.

Invited Lecture

Speaker: Andrew Clark

Time: 4:15 -" 5:00pm

Day 2 -" June 1st

Introductory Concepts in Human Populations and Medical Genomics

Instructors: Luis Barreiro and Lluís Quintana-Murci

Time: 8:00am -" 12:00pm

Human population genomics: This lecture will introduce the students to the most recent genomic datasets on human genome diversity. We will discuss the contribution of HapMap and the 1000 genomes project to the better understanding of human evolution and the development of genome-wide association studies. The following concepts will be presented:

Mutation and recombination

Recombination at pedigree level -" concept of linkage disequilibrium (LD)

Measures of LD and its decay

Tagging SNPs

Population mutation parameter, population recombination rate

lab will introduce methods of analyzing data from the HapMap project.

Demography of human populations: This lecture will introduce the different models to explain human evolution. It will give an overview of the most recent genetic data explaining the human origins and migration patterns. It will concentrate on phylogeographic studies, mostly concerning uniparentally-inherited genomes. (Lluís Quintana-Murci 10:30am -" 12:00pm).

Introductory Concepts in Genetic Epidemiology

Instructors: Alexandre Alca~s and HÃ©lÃ©ne VÃ©zina

Time: 1:00pm -" 5:00pm

This lecture will cover designs and analytic methods for genetic association studies. Methods to investigate direct (candidate locus) and indirect (linkage disequilibrium mapping) associations with human disease will be introduced. Both family-based and population based designs will be presented.

Presentation of the concepts will be followed by a computer lab

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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>

NESCent WEBS Evolutionary Biol Nov6-9

Dear Colleagues,

We are writing to introduce you to WEBS (Women Evolving Biological Sciences), an annual three-day symposium aimed at addressing the retention of female scientists and issues related to the transition of women from early career stages to tenure track positions and leadership roles in academic and research settings. Past WEBS symposium in 2007, 2008, and 2010 were huge successes. Early career participants as well as our senior scientist panelists reported feeling inspired and equipped with new connections and tools that they expect will help them in their career in the years to come. We would appreciate your assistance in passing along this information to any of your colleagues who you think will be interested in our program.

WEBS will target early career women in the Biological Sciences with an emphasis on ecology and evolutionary biology. In particular, it will focus on women who have earned their doctoral degrees within the past two to eight years and who do not have tenure in order to address the critical transition period from graduate studies and post-doctoral positions to permanent research and teaching positions. The symposium will provide a forum for professional development, including awareness and improvement of academic leadership skills; opportunities to establish mentoring relationships; and resources for developing professional networks. The 2011 symposium will be held at NESCent (National Evolutionary Synthesis Center) in Durham, NC, November 6-9, 2011.

Please visit our website (<http://www.webs.washington.edu>) for details and application materials. Feel free to contact us with any questions you might have (websinfo@u.washington.edu). Applications open March 1, 2011 and will be due on April 15, 2011.

Sincerely, Samantha Forde, Ph.D. Claire Horner-Devine, Ph.D. Joyce Yen, Ph.D.

Samantha E. Forde Assistant Professor, adjunct Ecology and Evolutionary Biology Cal Teach Development and Outreach University of California 831-459-1541
forde@ucsc.edu

Okinawa Comparative Genomics May16-Jun3

Dear Colleagues,

We are now soliciting applications for the Quantitative Evolutionary and Comparative Genomics workshop at the Okinawa Institute of Science and Technology. This is the second year we are offering this workshop. Last year's was a great success, and we would like to see the same high-level applicants in Okinawa this summer. We already have an excellent pool of lecturers (see below). I hope you can either apply to participate in the workshop, or bring this opportunity to the attention of talented graduate students, post-doctoral fellows and advanced undergraduates.

Yours, Alexander Mikheyev

<http://www.oist.jp/qecg2011/May> 16 - June 3, 2011.
OIST covers accommodation and travel expenses for all participants. Application deadline March 15, 2011.

Confirmed Lecturers: < <http://www.oist.jp/qecg2011/doku.php?id=3DPeople> >

- Dan Andersson, *Uppsala Universitet*, *Gene amplification and adaptation in bacteria* - Philip Hastings, *Baylor College of Medicine*, *Mechanisms of CNV* - Joachim Hermisson, *University of Vienna*, *Population genetic models of adaptation* - Takehiko Kobayashi, *National Institute of Genetics, Japan*, *Repetitive genes & concerted evolution* - Thomas Lenormand, Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier, *Molecular basis of adaptation in mosquitoes* - Michael Lynch, *Indiana University*, *Recombination* - Gilean McVean, *Oxford*, *TBD* - Simon Myers, *Oxford*, *Genealogical methods for detecting selection and inference of admixture history* - Molly Przeworski, *University of Chicago*, *Distinguishing hitchhiking from background selection* - David Romero, *Centro de Ciencias Genómicas, UNAM*, *Gene conversion and the migrating Holliday junction* - Susan Rosenberg, *Baylor College of Medicine*, *DNA repair mechanisms* - Mikkel Schierup, *Aarhus University*, *Reconstructing pre-speciation recombination events* - Guy Sella, *Hebrew

University of Jerusalem*, *Signatures of adaptation* - Yun Song, *UC Berkeley*, *Conditional sampling distributions in population genetics with recombination* - Joel Stavans, *Weizmann Institute of Science*, *Optical probes of recombination* - Clifford Zeyl, *Wake Forest University*, *Looking at the benefits of sex using experimental evolution approaches*

OIST Summer School and Workshop: Quantitative Evolutionary and Comparative Genomics 2011

The loosely defined theme of the 2011 Summer School is the linkage and recombination in genome sequences, which will be explored from a quantitative and multidisciplinary perspective, and connections forged with parts of biology outside of genomics. The format of the summer school consists of a three-hour presentation in the morning, with coffee breaks, followed by an discussion in the afternoon, as well as group projects led by tutors. The summer school is aimed primarily at introducing approximately forty students and post-docs with quantitative backgrounds - not necessarily in biology - to the cutting edge of contemporary comparative and evolutionary genomics research. As such, tutorials will be offered to get participants with less-developed quantitative skills or sparse biological background up to speed insofar as possible; however, we hope that presentations will be intense and self-contained.

We are looking for a set of students with a broad range of backgrounds, experimentalist and theorist: for example, biology, chemistry, computer science, ecology, engineering, evolution, genomics, mathematics, medicine, or physics. The essential prerequisite is an enthusiasm to overcome traditional boundaries of your own field of specialization. A small number of researchers at later stages of their careers may be invited to participate, particularly if we believe they can contribute to mediating the interdisciplinary dialog; such applicants should be certain to address this explicitly in their applications. *OIST is strongly committed to the advancement of women in the sciences, and women are especially encouraged to apply.*

Okinawa is a subtropical divers' paradise of diverse ecology and distinctive beauty and cultural flavor.

OIST provides summer school students with accommodation at Seaside House and financial support for their travel. Students will be selected competitively based upon their completed applications, submitted by March 15, 2011 on our web site < <http://www.oist.jp/qecg2011/doku.php?id=3DApplication> >. We also request that the applicants submit a recommendation letter from their advisor (see web site for details).

mikheyev@gmail.com

OxfordU ComputationalBiol Jul11-Aug20

Oxford Summer Projects in Computational Biology

>From July 11th until August 20th 2011, a project-based summer school in computational biology will take place in Oxford in The Department of Plant Sciences. The ideal student is strong in maths/stats/compsci/phys/chem, has studied 2-3 years of an undergraduate degree, and has an interest in moving into computational biology. However, we have also successfully had students from a pure biology background, as well as students in the process of doing their PhD. The instructors/teachers/project designers are: James Anderson, Luke Cartey, Tom Cavalier-Smith, David Gavaghan, Jotun Hein, Joe Herman, Nick Jones, Steve Kelly, Rune Lyngsø, Thomas Mailund, Istvan Miklos, Adam Novak, Bela Novak, Joe Pitt-Francis, Gail Preston, Miltos Tsiantis.

The presently planned projects are:

* Metabolic Random Fields * Correlated Alignment
* Phylogenomic Analysis of Algae * Stochastic Models Combining Alignment and Annotation * Advanced Software Design for Statistical Alignment * Evolving Dynamical Systems: the Cell Cycle as test case * Inverse RNA Folding Algorithms * Stochastic Models of Leaf Shape Evolution * Comparison of Parallel Solution Techniques for the Eikonal equation

More detailed descriptions of these can be found on this page can be found here and earlier project reports here. Students will work in groups of three with daily discussion with the instructors. There will be three presentations by each group and there should be a final report describing the work. Participation has in general been experienced as very demanding by students. There are no official credits for participation, but participation has been experienced as very rewarding as a research experience and in creating relationships with students/researchers in other countries.

In the work days in the above period, each day will start with a one hour lecture and we will hope to have given an overview of computational biology by the end of the period. But, the course will strongly focus on learning 'by doing'. There will also be one lecture describing how to enter an Oxford DPhil program. The present plan is:

* Week 1: Introduction to summer school, Introduction to computational biology, Alignment of a pair of sequences, Alignment of a set of sequences, Student Presentations.

* Week 2: Models of substitution I, Models of substitution II, Models of substitution III, Phylogenies I, Phylogenies II

* Week 3: Statistical alignment I, Statistical alignment II, Genetic mapping I, Genetic mapping II, Networks I

* Week 4: Networks II, Networks III, Integrative genomics I, Integrative genomics II, Student Presentations.

* Week 5: Genome annotation I: protein genes. Genome annotation II: RNA genes, Genome annotation III: signals by machine learning, Genome annotation IV: signals by evolutionary models, Patterns in biology

* Week 6: Modelling molecular reactions I, Modelling molecular reactions II, Predicting protein structure, Doing a DPhil in Oxford, Final Student Presentations.

There are a number of scholarships to cover housing and food, but more might be available dependent on applications under review. The deadline for applications is 1st March by email to Madeline Mitchell (mitchell@stats.ox.ac.uk). A CV with university grades and two people who can be contacted for references are needed. If possible, please apply as soon as possible as there are a series of alternative possibilities of funding for named students

Madeline Mitchell <mitchell@stats.ox.ac.uk>

OxfordU ComputationalBiol Jul11-Aug20 2

Oxford Summer Projects in Computational Biology 2011

>From July 11th until August 20th 2011, a project-based summer school in computational biology will take place in Oxford in The Department of Plant Sciences. The ideal student is strong in maths/stats/compsci/phys/chem, has studied 2-3 years of an undergraduate degree, and has an interest in moving into computational biology. However, we have also successfully had students from a pure biology background, as well as students in the process of doing their PhD.

The instructors/teachers/lecturers/project designers are: James Anderson, Phil Biggin, Phil Blunsom, Luke Cartey, Tom Cavalier-Smith, Elspeth Garman, David Gavaghan, Jotun Hein, Joe Herman, Wim Hordijk, Nick Jones, Steve Kelly, Rune Lyngsø, Thomas Mailund, Gil McVean, Istvan Miklos, Richard Mott, Adam Novak, Bela Novak, Joe Pitt-Francis, Gail Preston, Miltos Tsiantis.

The presently planned projects will be taken from the list below. People are encouraged to propose their own projects, which has happened, as long as it is well-worked through. So the list might grow if somebody has a good idea.

* Metabolic Random Fields * Correlated Alignment * Phylogenomic Analysis of Algae * Stochastic Models Combining Alignment and Annotation * Advanced Software Design for Statistical Alignment * Evolving Dynamical Systems: the Cell Cycle as test case * Inverse RNA Folding Algorithms * Stochastic Models of Leaf Shape Evolution * Network Combinatorics * Approximate Genealogies in Population Genomics * Evolutionary Docking * Comparison of Parallel Solution Techniques for the Eikonal Equation * Ab initio Detection of Regulatory Nucleotide Elements

More detailed descriptions of these can be found on this page can be found here and earlier project reports here. The projects should introduce a topic, meaningful progress should be possible in the 6 weeks and could also serve as an introduction to a research question that could be pursued in a DPhil.

Students will work in groups of three with daily discussion with the instructors. There will be three presentations by each group and there should be a final report describing the work. Participation has in general been experienced as very demanding by students. There are no official credits for participation, but participation has been experienced as very rewarding as a research experience and in creating relationships with students/researchers in other countries.

In the work days in the above period, each day will start with a one hour lecture and we will hope to have given an overview of computational biology by the end of the period. But, the course will strongly focus on learning 'by doing'. There will also be one lecture describing how to enter Oxford DPhil programs. Both lectures and projects will be updated before summer. Each week is attempted to have two general teaching lectures and two research topic lectures, with the week ending with student presentations, Oxford Introduction on Fridays.

The present plan is below, but it will be modified to

suit the students and chosen projects and accommodate time constraints of the lecturers:

Week 1: Introduction to summer school and computational biology, Alignment, Phylogenomics of Algae, Imprinting in Mice, Student Presentations.

Week 2: Models of substitution, Phylogenies I, Molecular Dynamics and Function, Leaves and their evolution, The 1000 Genomes Project.

Week 3: Phylogenies II Statistical alignment, Grammars and Biological Sequences, Genetic mapping, Dynamics Models of the Cell Cycle,

Week 4: Networks , Integrative genomics, Bacterial genomes and metabolism, Network Inference, Student Presentations.

Week 5: Annotating genomes for protein genes. RNA secondary structure, Finding signals, Computer comparison of languages and automatic translation, Doing a DPhil in Oxford,

Week 6: Comparative biology, Genome Rearrangement, Origin of Metabolism, Analysing protein structure, Final Student Presentations.

There are a number of scholarships to cover housing and food, but more might be available dependent on applications under review. The deadline for applications is 1st March by email to Madeline Mitchell (mitchell@stats.ox.ac.uk). A CV with university grades and two people who can be contacted for references are needed. If possible, please apply as soon as possible as there are a series of alternative possibilities of funding for named students.

Madeline Mitchell <mitchell@stats.ox.ac.uk>

Panama Tropical Evolution Apr11-May25 Panama Tropical Evolution Apr11-May25

Tropical Behavioral Ecology and Evolution Course in Panama

This course will provide an overview of the patterns and processes that determine tropical biodiversity and of the evolutionary biology of key invertebrate model systems. It is designed for graduate students at all levels beginning with proposal preparation, research implementation, and scientific manuscript preparation. The course will begin three weeks prior to arriving in

Panama (April 11-29th) and then continue with the field component (May 1-25th). Please see the following links for more details:

[http://www1.bio.ku.dk/forskning/oe/cse/kurser/-STRI_Course_Flier29Jan11Final.pdf/](http://www1.bio.ku.dk/forskning/oe/cse/kurser/-STRI_Course_Flier29Jan11Final.pdf) <http://www1.bio.ku.dk/english/research/oe/cse/kurser/>
or email Rachele Adams: RAdams@bio.ku.dk or rmmadams@gmail.com

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Rachele M.M. Adams PhD Marie-Curie International Incoming Fellow Centre for Social Evolution Department of Biology University of Copenhagen Universitetsparken 15 DK-2100 Copenhagen, Denmark

Smithsonian Institution Research Collaborator Department of Entomology Smithsonian Institution PO Box 37012 NHB, MRC 188, Rm. CE-518 Washington, DC 20013-7012 Tel.: 202-633-1002 (Office) Website:<http://entomology.si.edu/StaffPages/AdamsRMM.html> e-mail: RAdams@bio.dk.edu or rmmadams@gmail.com

Rachele Adams <RAdams@bio.ku.dk>

Phyloseminar Comparative Diversity Feb25

Please come to a free online seminar this coming Friday:

Luke Harmon speaks Friday, February 25th at 10am PST on “New Frontiers for the Comparative Analysis of Diversification”.

Abstract: We’re building the tree of life, but what can we do with it? It seems clear that there is a wealth of information about evolution in the structure of this tree. There are some methods that can use phylogenetic trees to test macroevolutionary models, but the range of models that we can test is still severely limited. In some cases, such as the estimation of extinction rates from phylogenetic trees, current methods have proven controversial. We are now beginning to develop and implement methods that use tree-of-life scale data to answer key questions in evolution. I will review three new approaches developed in my lab for analyzing comparative datasets: MECCA, fossil-Medusa, and reversible-jump MCMC. I argue that these methods represent the next generation of comparative methods that will open the door to analyzing a much broader range of models with large datasets.

Japan 03:00 (03:00 AM) on Saturday, February 26 New

Zealand 07:00 (07:00 AM) on Saturday, February 26
 West Coast USA 10:00 (10:00 AM) on Friday, February 25
 East Coast USA 13:00 (01:00 PM) on Friday, February 25
 England 18:00 (06:00 PM) on Friday, February 25
 France 19:00 (07:00 PM) on Friday, February 25

For more information on how to attend this and other seminars, visit phyloseminar.org.

ematsen@gmail.com

Roscoff France Marine Evolutionary Genomics May 15-28

Summer course on marine genomics at the Marine Biological Station of Roscoff (F)

>From May 15th - May 28th, 2011 the 7th Summer Course on Marine Evolutionary & Ecological Genomics will take place at the Station Biologique de Roscoff, France.

The course consists of lectures, tutorials and computer based exercises in the following subjects. Phylogeny & tree of life- sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies Population genetics - structure, connectivity and gene flow, assignment, effective size and population dynamics, case studies Genomics - next generation sequencing, database searching, basic skills in data handling and bioinformatics Functional genomics - genome structure, molecular evolution at the functional level Comparative genomics - whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, co-evolution Environmental genomics - methods for detecting diversity; detecting adaptive variation; NGS: why and how; case studies. Applications in aquaculture, blue biotech, conservation, fisheries, metagenomics, nutrigenomics and the like will be discussed.

Target group PhD students (at least in their second year) and post docs with a solid knowledge in phylogenetics and/or population genetics. Students with an applied background (e.g. aquaculture, blue biotech, fisheries, nutrigenomics) are encouraged to apply.

Application and contact To apply please fill in the application form and send to Jonas Collén ([collen@sb-](mailto:collen@sb-roscoff.fr)

roscoff.fr) together with a 2-page CV before April 10th 2011.

16 participants will be selected on the following criteria:

1. Relevance of the course for their PhD or post-doc project
2. Background and experience of applicant
3. We will aim at mixing people with different research backgrounds; probably not more than one person per institute will be considered. We will also aim at an equal gender distribution.

The selected persons will be notified at the end of April and have to confirm within 7 days. We will have a waiting list in case of non- confirmations and cancellations.

Confirmed teachers Sandie Baldauf, U. Uppsala, SE Jonas Collén, U Paris 6, FR Simon Creer, U Bangor, UK Yves Desdevises, CNRS Banyuls, FR J Jakob Hemmer-Hansen, DTU-Aqua, DK Galice Hoarau, U Bodø, NO Jeanine Olsen, U Groningen, NL Frédéric Partensky, SB-Roscoff, FR Heroen Verbruggen, U Gent, BE Filip Volckaert, KULeuven, BE Mathias Wegner, ETH Zurich, SW

Organizing committee Claudie Perron, SB-Roscoff, FR Jeanine Olsen, Univ Groningen, NL Jonas Collén, SB-Roscoff, FR Filip Volckaert, KULeuven, BE

For information and application forms: Jonas Collén Station Biologique de Roscoff BP 74, F-29680 ROSCOFF CEDEX France Phone: +(33)2 98 29 23 23 Fax: +(33)2 98 29 23 24 Email: collen@sb-roscoff.fr [URL: will be launched on 15 March 2011]

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

UCD Dublin MastersEvolBiol Sep

We are reminding you of the approaching first deadline for the “Masters in Evolutionary Biology” at UCD Dublin, Ireland. This is a full-time, 12-month course on the nature, relevance and far-reaching implications of evolutionary theory. The course features an outstanding diversity of topics and approaches in current evolutionary research (both organism-based and theoretical), and innovative educational approaches, including field-work, critical discussion, museum and laboratory training, data analysis and modelling.

Further information can be found at the following link: <http://www.ucd.ie/bioenvsci/graduatestudents/-postgraduatetaughtdegreesdiplomas/-mncevolutionbiology/> The first deadline is March

14th. We intend to offer a maximum of 10 placements, and approach successful candidates by the end of April 2011. The course will start early September 2011.

Please feel free to circulate this to potentially interested prospective students.

Masters in Evolutionary Biology UCD School of Biology & Environmental Science <http://www.ucd.ie/-bioenvsci/research/evolution.htm> evolution@ucd.ie

evolution@ucd.ie

UPadova EvoDevo

Summer School on Evolutionary Developmental Biology Conceptual and Methodological Foundations

2nd Edition: From Gene Networks to Organismal Systems Venice, 19-22 September 2011

Organizers: Alessandro Minelli, Gerd B. Müller and Giuseppe Fusco School director: Johannes Jaeger

School sponsors: Istituto Veneto di Scienze, Lettere ed Arti, Venice and Konrad Lorenz Institute for Evolution and Cognition Research, Vienna. Location: Istituto Veneto di Scienze, Lettere ed Arti, Palazzo Franchetti, Venice

Taching panel: J. Jaeger (School Director, CRG Barcelona), P. Beldade (Gulbenkian Institute, Lisbon), C. Braendle (CNRS and Université de Nice Sophia Antipolis), G. E. Budd (University of Uppsala), G. Fusco (University of Padova), A. Hejnol (Sars International Center for Marine Molecular Biology, Bergen), R. Jenner (Natural History Museum, London), A. Minelli (University of Padova), G. B. Müller (Konrad Lorenz Institute, Vienna), S. A. Newman (New York Medical College)

Deadline for applications: May 30th 2011.

For details, visit <http://www.istitutoveneto.it/-EDB2011/> Giuseppe Fusco Department of Biology University of Padova Via U. Bassi 58/B I-35131 Padova Italy tel. +39.049.827.6238 fax +39.049.827.6230 e-mail giuseppe.fusco@unipd.it webpage <http://dept.bio.unipd.it/fusco>

Giuseppe Fusco <giuseppe.fusco@unipd.it>

UppsalaU QTLmapping Apr5-7

Workshop on quantitative trait locus (QTL) mapping 5-7 April 2011 Evolutionary Biology Centre, Uppsala University

Speakers: Dario Beraldi (University of Edinburgh), Örjan Carlborg (Uppsala University), Hans Ellegren (Uppsala University), Martien Groenen (Wageningen University), Bengt Hansson (Lund University), Åsa Johansson, (Uppsala University), Arne Nolte (Max Planck Institute for Evolutionary Biology Plön), Kees van Oers (Netherlands Institute of Ecology Heteren), Josephine Pemberton (University of Edinburgh), Erik Postma, (University of Zürich), Holger Schielzeth (Uppsala University), John Willis (Duke University), Dominic Wright (Linköping University), Jon Ågren (Uppsala University)

Venue: Ekmansalen, Evolutionary Biology Centre, Norbyvägen 14, Uppsala

Contact persons and registration: Arild Husby (arild.husby@ebc.uu.se) and Holger Schielzeth (holger.schielzeth@ebc.uu.se)

Aim: The workshop will cover different approaches to QTL mapping in natural and domestic populations of plants and animals. It will also cover part of the pipeline from marker discovery and genotyping. Presentations will be given by experts on the respective fields. The workshop will focus on applications and will also include practical sessions.

Audience: Graduate students, postdocs and faculty members. The workshop is open to external participants, but priority will be given to members of the Uppsala Graduate School on Genomes and Phenotypes.

Note: There will be an open slot for a presentation on QTL mapping. Please contact us, if you are interested in presenting your own case study.

For more details see: <http://www.ebc.uu.se/-digitalAssets/45/45211-QTLmappingWorkshop.pdf> holger.schielzeth@ebc.uu.se

UWashington StatisticalGenetics Jun13-Jul1

16th Annual Summer Institute in Statistical Genetics (SISG 2011) will be held at the University of Washington, Seattle, WA, June 13 through July 1, 2010. Website: <http://sisg.biostat.washington.edu>. 3rd Annual Summer Institute in Statistics and Modeling in Infectious Diseases (SISMID 2011) will be held at the University of Washington, Seattle, WA, June 13-29, 2010. Website: <http://depts.washington.edu/sismid/>
Thanks!

Sandra

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Sandra Coke <sjcoke@u.washington.edu>

Valencia Spain MEPPA 2011 May30-Jun3

FIRST ANNOUNCE

DEADLINE FOR APPLICATIONS: April 29th, 2011

Dear mailing list member,

Registration is now open for:

MEPPA11 - Molecular Evolution, Phylogenetics, Phylogenomics, and Adaptation

Please visit the Course website for details:

<http://bioinfo.cipf.es/courses/mol.evol.phylo.6ed/>

This course is likely to be very competitive for seats. Our maximum capacity is 25 seats. Early application is recommended!

Instructors: Hernan Dopazo, Toni Gabaldon, François Serra, Jaime Huerta- Cepas, and Salvador Capella

Invited Instructors: David Posada, University of Vigo (Spain) and Rafael Zardoya, MNCN-CSIC (Madrid, Spain)

Duration: 5 days. May 30 to June 03, 2011

Course Fee: Eur 380, include meals. A limited number of grants will be available.

Place: Centro de Investigacion Principe Felipe. Valencia. Spain. <http://www.cipf.es/> Course description:

Currently, the simplest Bioinformatics analysis uses species comparisons in order to hypothesise the function of a novel biological sequence. Moreover, in most Molecular Biology labs, evolutionary and phylogenetic concepts are constantly being used with more or less formality: homology, similarity, evolutionary rates, long branch attraction, rooted and unrooted trees, monophyletic group, molecular clock, adaptation, lineage effects, neutralism, cladograms, phylograms, etc. The course aims to provide the necessary background to understand the basic concepts from comparative and evolutionary biology that are frequently used in molecular biology and bioinformatics analyses. The course consists in five full-day sessions with an adequate balance between theory and computer practice, oriented to solve frequent problems and hypothesis testing. The program covers the basic and advanced analysis of Phylogenetic reconstruction, Phylogenomic analysis of genomes and Maximum likelihood tests for molecular adaptation. The software resources that will be used in the practical sessions include: Phylip, MrBayes, PAML, Modeltest-Protest, Jmodeltest and the Phylemon 2.0 web server. (phylemon.bioinfo.cipf.es)

Please feel free to pass this information to colleagues in your community.

Co-ordinators: Hernan Dopazo and François Serra

Hernán J. Dopazo, PhD Head of the Evolutionary Genomics Unit Bioinformatics & Genomics Department Centro de Investigación Príncipe Felipe c/ ep Avda. Autopista del Saler 16 (Junto al Oceanográfico) 46012, Valencia, España Tfn: (34) 96 328 96 80 ext: 1008 Fax: (34) 96 328 97 01 hdopazo@cipf.es <http://hdopazo.bioinfo.cipf.es/> Hernan Dopazo <hdopazo@cipf.es>

Vienna Austria NGSworkshop May23-27

Next Generation Sequencing Workshop

The Vienna Graduate School of Population Genetics is hosting a next generation sequencing (NGS) workshop. The participants are provided hands-on training

on NGS data analysis and covers mapping NGS reads on a reference genome, SNP and indel discovery, sequence analysis of pooled data (Pool-Seq), de novo assembly and RNA-Seq. The workshop is designed for PhD-students and post-docs working on projects that involve NGS analysis. A basic knowledge of UNIX would be beneficial.

Date: May 23-27 Location: Vetmeduni Vienna, Austria
Application deadline: March 10 (9:00 a.m. CET)

Being supported by the Thermadapt program of the European Science Foundation, there is no course fee

and all participants are provided with free accommodation. Furthermore, up to five travel fellowships will be awarded. For more information including the application procedure, please visit: <http://www.popgen-vienna.at/training/ngs-workshop.html>

Daniel K. Fabian

daniel.fabian@vetmeduni.ac.at Vienna Graduate School of Population Genetics University of Veterinary Medicine Vienna Veterinärplatz 1 1210 Wien Austria/Europe <http://www.popgen-vienna.at>
el.dansch@gmail.com

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as \LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be 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.