EvolDir

March 1, 2008

Month in Review

Forward

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

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

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

—— / ——

Conferences

Arlington ParasiteEvolutionSymposia Jun27-30

Dear Colleagues,

It is my pleasure to announce the 83rd Annual meeting of the American Society of Parasitologists (ASP) in Arlington, Texas (June 27-30, 2008). This year there are three symposia that address the evolutionary biology of parasites (see below). Thus, I would like to invite all who are interested in the ecology, evolution, and phylogenetics of parasites to attend and participate (oral or poster presentations). Please see the ASP web site (http://asp.unl.edu/) for meeting details and the call for papers. Abstracts are due March 7, 2008.

I would also like to invite those interested in the evolutionary biology and ecology of parasites to become members of ASP. ASP has a long history of supporting and advocating research in the fields of ecology, evolution, and phylogenetics. For more details on becoming a member, please visit the web site (http://asp.unl.edu/).

Symposia ASP President's Symposium: "Lessons from the tree of life: Illuminating macro-parasite biology through molecular phylogenetic frameworks" organized by Steve Nadler and George Cain. Speakers: James G. Baldwin (Nematodes) Martï¿½n Garcï¿½a (Acanthocephalans) Peter D. Olson (Platyhelminthes).

Special Symposium: "Evolutionary Ecology of Host-Ecto-Parasite Interactions" organized by Dale Clayton and Sarah Bush. Speakers: Michal Polak on behavioral ecology on how mites physically block copulation of their host flies Mark R. Forbes on host-parasite interactions between damselflies and Mites 1 TBA.

Special Symposium: "Population genetics of parasites: from geography to genes" organized by Charles

Criscione. Speakers: Noah Whiteman (geographic scale): Comparative geographic structures of ectoparasites: using parasite life history characters to predict genetic structure among host populations Charles Criscione (within host population): Molecular epidemiology and landscape genetics of Ascaris: elucidating transmission dynamics with molecular markers Michelle Steinauer (within individual hosts): Parentage analyses/mating dynamics of Schistosoma mansoni within hosts; Tim Anderson (population genetics of parasite genes): Loci under selection in malaria.

I hope to see you in Arlington.

Sincerely,

Charles D. Criscione, Postdoctoral Scientist Department of Genetics Southwest Foundation for Biomedical Research P.O. Box 760549 San Antonio, Texas 78245-0549 Phone: (210)-258-9722 Fax: (210)-258-9796 CV and pdf reprints: www.geocities.com/cooch2000/ Web page: www.sfbr.org/pages/genetics_cv.php?u9

Shipping Address Department of Genetics Southwest Foundation for Biomedical Research 7620 NW Loop 410 San Antonio, Texas 78227-5301

ccriscio@sfbrgenetics.org

Barcelona SMBE 2008 Jun5-8 2

Dear SMBE members,

The Organizing Committee is pleased to invite you to attend the 2008 annual meeting of the Society for Molecular Biology and Evolution (SMBE) that will be held on June 5-8, in Barcelona, Spain.

Conference registration and abstract submission is now available online at the SMBE 2008 website (http://www.smbe2008.com/). The site also contains additional information on accommodation and travel, confirmed speakers, as well as the Walter M. Fitch Prize competition for young investigators, postdocs and graduate student travel awards, and the Undergraduate Diversity Mentoring Program awards.

IMPORTANT DATES

Abstract Submission Deadline: March 3 Early Registration From January 17 to March 10. Walter Fitch Prize Deadline: March 3 Undergraduate Diversity Mentoring Program Awards Deadline: February 15

SYMPOSIUM TOPICS

Animal domestication genomics Animal molecular Evo-Devo Beyond scans for selection: Studying the phenotypes Bioinformatics for molecular evolution Dating divergence: The Tower of Babel of geneticists and paleontologists? Drosophila population genomics Evolution of gene regulation Evolutionary comparative genomics Evolutionary genomics of human and pathogen interactions Evolutionary radiations and molecular phylogeny Genetics and molecular biology of speciation Genome variation: Lessons from the human genomes Genomic evidence for natural selection and implications Genomics for crop evolution and improvement Models of genome evolution and phylogenomics Molecular and evolutionary epidemiology Molecular phylogeography and population genetics Network evolution and systems biology Popgen in space! Theory and inference in spatial population genetics RNA world: Emergence of life on earth Spontaneous mutations and their evolutionary consequences The ancestral eukaryotic cell The crossroads between prokaryotic genomics, ecology and adaptation The X - an eXceptional chromosome! Transposable elements: diversity, dynamics and evolutionary impact on host genomes What would/should we do with a million DNA barcodes?

ORGANIZING COMMITTEE

Chairs Carmen Segarra (Universitat de Barcelona) Julio Rozas (Universitat de Barcelona)

Members Montserrat Aguade (Universitat de Barcelona) Pere Are (Institut de Recerca i Tecnologia Agroalimenteries) Jaume Bertranpetit (Universitat Pompeu Fabra) Jose Castresana (Consejo Superior de Investigaciones Cienteficas) Roderic Guige (Universitat Pompeu Fabra) Elvira Juan (Universitat de Barcelona) Marta Riutort (Universitat de Barcelona) Alfredo Ruiz (Universitat Autonoma de Barcelona) Mauro Santos (Universitat Autonoma de Barcelona) Lluis Serra (Universitat de Barcelona)

Julio Rozas Carmen Segarra www.smbe2008.com SMBE <info@smbe.org>

Barcelona SMBE 2008 Jun5-8 BarcodeSymposia

Barcelona, SMBE2008 Conference June5-8 What would/should we do with a million DNA barcodes?

Dear Evoldir Members,

We would like to invite you to submit your abstracts (talks and posters) for the symposium What would/should we do with a million DNA barcodes?± at the 2008 annual meeting of the Society for Molecular Biology and Evolution (SMBE) in Barcelona, Spain.

Symposium description: The number of formally described species that have been DNA barcoded and added to the BOLD database now exceeds 30,000. In this fast moving field it is now indispensable to propose an update. The aim of this symposium would be to clarify the current progress and limitation of barcoding and its methodologies. The symposium would attempt to answer: What is the power of barcoding? What are its limits? What are the best methods to analyse barcoding? How could the concept be improved? What would/should we do with a million DNA barcodes?

Confirmed Main Speakers: Eldredge Bermingham (Smithsonian Tropical Research Institute, USA); Timothy Barraclough (Imperial College London, UK)

Details of the conference: SMBE2008 runs from the 5th-8th June 2008. Details of the conference, including online abstract submission can be found here: http://www.smbe2008.com/ Abstract submission deadline: March 3, 2008

Symposium organisers: Axel Meyer (University of Konstanz, Germany) Stphane Hemmerter (University of Technology, Sydney; The Institute for the Biotechnology of Infectious Diseases, Australia)

stephane hemmerter <hemmerter@yahoo.fr>

Barcelona SMBE 2008 Jun5-8 CallForAbstracts

SMBE 2008, Barcelona. Annual Meeting of the Society for Molecular Biology and Evolution

Just a friendly reminder that the deadline to submit your abstracts (talks and posters) to the Barcelona SMBE2008 meeting is March 3, 2008.

MEETING INFORMATION www.smbe2008.com IMPORTANT DATES Deadline for the Abstract Submission (talk and posters): MARCH 3. Deadline for applying to the Walter Fitch Prize: MARCH 3.

SYMPOSIUM TOPICS Animal domestication genomics Animal molecular Evo-Devo Beyond scans for selection: Studying the phenotypes Bioinformatics for molecular evolution Dating divergence: The Tower of Babel of geneticists and paleontologists? Drosophila population genomics Evolution of gene regulation Evolutionary comparative genomics Evolutionary genomics of human and pathogen interactions Evolutionary radiations and molecular phylogeny Genetics and molecular biology of speciation Genome variation: Lessons from the human genomes Genomic evidence for natural selection and implications Genomics for crop evolution and improvement Models of genome evolution and phylogenomics Molecular and evolutionary epidemiology Molecular phylogeography and population genetics Network evolution and systems biology Popgen in space! Theory and inference in spatial population genetics RNA world: Emergence of life on earth Spontaneous mutations and their evolutionary consequences The ancestral eukaryotic cell The crossroads between prokaryotic genomics, ecology and adaptation The X - an eXceptional chromosome! Transposable elements: diversity, dynamics and evolutionary impact on host genomes What would/should we do with a million DNA barcodes?

Julio Rozas Carmen Segarra www.smbe2008.com jrozas@ub.edu jrozas@ub.edu

---

Barcelona SMBE 2008 Jun5-8 NetworkEvolutionSymposium

Dear Evoldir readers,

We invite submissions of abstracts for the Network Evolution and Systems Biology symposium at the SMBE2008 Conference June 5-8 in Barcelona. A description of the symposium follows. Please note our special encouragement of paired talks by collaborating theoreticians and experimentalists.

SMBE2008 Conference June 5-8, Barcelona Network Evolution and Systems Biology

A central aim of molecular evolutionary biology is to understand the molecular changes underlying the evolution of complex traits. Complex traits, by their nature, are the products of networks of interacting factors. It is therefore necessary to understand how variation in these networks produces phenotypic variation, and how evolutionary forces acting on phenotypic variation in turn shape the underlying molecular networks. Recent advances in genomics and systems theory are beginning to contribute to this understanding. It is therefore an excellent time to showcase leading research, to evaluate the challenges that remain, and to encourage the wider community of molecular evolutionary biologists to incorporate network thinking into their work.

Questions to be considered include (but are not limited to): What are the causes and consequences of robustness in regulatory networks? How much variation do regulatory networks harbor? Does cryptic genetic variation contribute to phenotypic divergence? Does network topology constrain evolutionary divergence? Do evolutionary forces constrain network topology? Does phenotypic invariance imply network conservation?

These questions require both empirical and theoretical investigation, and the proposed symposium will feature talks from both experimentalists and theoreticians. Because it is often extremely valuable, yet difficult, for "wet" and "dry" scientists to collaborate, priority will be given to work that integrates theory and experiment. Indeed, a novel aspect of our proposed symposium is that we will welcome paired talks, in which two collaborating scientists (e.g., a modeler and a molecular biologist) will be allocated adjacent timeslots, with titles clearly emphasizing their link.

Invited Speaker: Marie-Anne Félix (Institut Jacques Monod), "Robustness and evolution of the Caenorhabditis vulval intercellular signaling network"

Co-organizers: Mark Siegal (New York University), Joanna Masel (University of Arizona)

Abstract deadline: March 3, 2008

Conference website: http://www.smbe2008.com/

Barcelona SMBE 2008 Jun5-8 UndergradDiversityProgram

DEADLINE–FEBRUARY 15

SMBE Undergraduate Diversity Mentoring Program Awards

Program Outline

The Society for Molecular Biology and Evolution (SMBE) is pleased to make available 10 awards for undergraduate students from underrepresented groups to participate in a Diversity Mentoring Program. The goals of this program are: (1) to promote diversity at the SMBE annual meeting, (2) to provide students with the opportunity to experience the excitement of attending and presenting at an international scientific conference, and (3) to foster enthusiasm for molecular biology and evolution as well as a possible career in this field.

To achieve these goals, each recipient of an SMBE Undergraduate Diversity Mentoring Program Award will be paired with two mentors, one a senior graduate student and the other a postdoctoral fellow or faculty member (who may or may not be the student's current advisor).

Specific mentoring activities will include:

* Attending conference sessions with the student, answering questions about the basic concepts being presented, and, more generally, explaining the goings-on at a multi-day scientific conference. * Interacting with the student during some mealtimes, coffee breaks and other social gatherings. * Introducing the student to other undergraduates, graduate students, postdoctoral fellows and faculty members as a way of facilitating connections with potential future graduate supervisors and colleagues. * Attending the poster session and SBME Undergraduate Diversity Program Award reception with the student in order to minimize/overcome the anxiety often felt by first-time conference attendees. * Serving as a contact point for the student to help resolve any issues surrounding conference registration, travel and accommodation.

Eligibility

Candidates must currently be enrolled as undergraduate students (Bachelor's level degree) or have graduated within the last 6 months at the time of application and be from groups underrepresented in our scientific discipline.

Meeting Participation

Recipients of an SMBE Undergraduate Diversity Mentoring Program Award will be invited to present their research at a special reception / poster session on Friday, June 6, attended by their mentors, supervisors and other interested conference participants.

Award

10 awards will be handed out. Awards recipients will receive a travel award to cover the cost of airfare, accommodation, and Meeting registration expenses. The travel award amount will not exceed US $1,000 for within-Europe contestants and $1,500 for all other contestants. Each participant will also receive an online student membership to the Society journal, Molecular Biology and Evolution, for the year of 2009.

Application

1. Faculty members may nominate undergraduates by sending a brief letter/email of recommendation to Laura Katz (Lkatz[at]email.smith.edu) and John

Archibald (john.archibald[at]dal.ca). The letter should outline the student's eligibility for the award and confirm their current academic status. Also indicate if your student would be able to present a poster.

OR

2. Students may apply for the award themselves by providing information on their background, academic status and an email address for their current supervisor. Students should also indicate whether they are able to present a poster.

The deadline for receipt of nominations/applications is February, 15.

John M. Archibald, Ph.D. Assistant Professor and Associate Graduate Coordinator Scholar, CIFAR Program in Integrated Microbial Biodiversity Department of Biochemistry & Molecular Biology Dalhousie University Sir Charles Tupper Medical Building 5850 College Street, Halifax, Nova Scotia B3H 1X5, Canada

Phone: (902) 494-2536 Fax: (902) 494-1355 Webpage: http://myweb.dal.ca/jmarchib/ Nirenberg's second reading in Moscow electrified the audience, Crick later wrote. (Whereupon, in the interest of historical accuracy, Seymour Benzer, who had been in Moscow too, mailed Crick a photograph taken of that audience, in which several people appeared to be asleep.)

Horace Freeland Judson, The Eighth Day of Creation

John Archibald <jmarchib@dal.ca>

Barcelona SMBE Jun5-8 WalterFitchPrize

Barcelona, SMBE 2008 Meeting

Beginning with the first annual meeting of the Society for Molecular Biology & Evolution (SMBE) in 1993, the Walter M. Fitch Symposium has provided a forum for young investigators (students and Postdocs) to showcase their exemplary research. The selection committee will nominate 8 individuals to enter the competition on the basis of the abstracts submitted.

This year, the winner will receive a US $1,000 gift check. In addition, all selected contestants will receive a travel award to cover the cost of airfare, accommodations, and meeting registration expenses. The travel award amount will not exceed US $1,000 for within-Europe contestants and $1,500 for all other contestants.

Each selected participant will also receive an online student/postdoc MBE membership for the year of 2009.

More information: SMBE 2008 website (http://www.smbe2008.com/).

IMPORTANT DATES Walter Fitch Prize Deadline: March 3 SMBE Abstract Submission Deadline: March 3 Early Registration From January 17 to March 10. Undergraduate Diversity Mentoring Program Awards Deadline: February 15

Julio Rozas Carmen Segarra www.smbe2008.com jrozas@ub.edu jrozas@ub.edu

---

ColdSpringHarbor PlantBioinformatics Apr7-10

Thank you for letting everyone know about this meeting!

The iPlant Collaborative inaugural conference "Bringing Plant and Computing Scientists Together to Solve Plant Biology's Grand Challenges" will be held at Cold Spring Harbor Lab, NY, from the evening of April 7 to noon April 10. The purpose of this conference is: 1) to explain the nature of the project and 2) to promote and facilitate community discussion of grand challenges, relevant data and computation tools, and cyberinfrastructure development necessary to solve such grand challenges. The conference will be webcast live to allow for interactive participation by viewers not present in person at the conference (and will be archived at < http://www.iplantcollaborative.org/ >. Additional webcasts, podcasts, etc. will also be conducted (and archived at < http://www.iplantcollaborative.org/ >) to introduce the community to the project and to explain how to participate in it. Community-organized Grand Challenge Workshops will follow later in 2008 for more in-depth discussion and debate of which Grand Challenges are the most compelling and most tractable.

To participate in the conference in person, please pre-register at < http://www.iplantcollaborative.org/meetings/ipc/register-042008 >. Participation will be balanced among disciplines, both across the plant sciences and the computing sciences, as well as by type of institution, geography, etc., and must ensure participation by underrepresented minorities (which is why we need to have a pre-registration process). Participants will be selected with Board of Directors oversight to ensure broad representation. Registration and logistics will be handled by Cold Spring Harbor Meetings and Courses.

The plant and computing sciences community, through the external Board of Directors (Chair, Robert Last, MSU), will choose several grand challenges by late 2008/early 2009 towards which Collaborative resources will be directed (i.e., the BoD will make all such major decisions, NOT project PI's. See < http://www.iplantcollaborative.org/ > for more details on the process.)

A draft of the conference program is as follows:

Bringing Plant and Computing Scientists Together

to Solve Plant Biology's Grand Challenges

@

Cold Spring Harbor Laboratory

April 7-10, 2008

Organized by

The iPlant Collaborative:

a cyberinfrastructure-centered community

for a new plant biology

Monday evening (April 7) Dinner 5:30PM 7PM Introduction and Project Overview 8PM Francine Berman, Director San Diego Supercomputer Center, <http://www.sdsc.edu/about/Director.html < http://www.sdsc.edu/about/Director.html > > "Opportunities and Challenges in Cyberinfrastructure Development" Confirmed 9PM Kathleen Carley, Director of the Center for Computational Analysis of Social and Organizational Systems (CASOS) Tentative

Tuesday morning (9-12:30) I. Nature and function of networks and systems: from single cell to complex organism, and from metabolism to ecosystem Elliott Meyerowitz, CalTech Confirmed Eric Mjolsness, UC Irvine Confirmed Noel (Missy) Holbrook, Harvard Tentative Dennis Shasha, NYU Confirmed

12:30-2 Lunch

Tuesday afternoon (2-4:30pm) 2 PM Break-out groups on Data and Algorithms: (1) systems and networks: transcriptome, proteome and metabolome data (e.g., microarrays vs. new sequencing approaches)

(2) development, differentiation, morphology, anatomy: phenotypic (morphological and developmental) data (3) organismal biology, physiological ecology and ecosystems: environmental (abiotic) and biotic interaction data 3:30 Reports of breakout groups and discussion by conf participants

4:30 Wine and cheese in foyer of Grace Auditorium 6PM Dinner

Tuesday evening session (7:30 - 10pm) II. Software development and architecture, data management, systems analysis and design 7:30 co-PIs Lincoln Stein and Sudha Ram: iPlant's Integrated Solutions Team and the community's Grand Challenge Teams: a collaboration to build prototype cyberinfrastructures (aka Discovery Environments) to solve the community's most compelling grand challenges in the plant sciences

Wednesday morning session (9-12:30) III. Gene to protein to phenotype; genotype-phenotype relationships A. Genetic and evolutionary diversity: population genetics, systematics and phylogenomics Magnus Nordborg, USC Invited Speaker TBD B. Protein modeling: prediction of function and interactions David Baker, U. Washington <http://depts.washington.edu/bakerpg/

— / —

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

---

Ghent Euro-Evo-Devo Jul29-Aug1

Euro-Evo-Devo *Ghent, 29 July-1 August 2008*

Call to participate You are invited to participate in, and contribute to, the Second Meeting of the European Society for Evolutionary Developmental Biology in Ghent, 29 July-1 August 2008. The scientific program will consist of plenary sessions, symposia, contributed talks and a poster session, see our website: *_http:// evodevo.eu/_*

Call for abstracts You are invited to submit an abstract for a constributed talk or poster. Online submission will begin on February 19, 2008. Please submit your abstract before *April 15, 2008*

*Keynote speakers * - *Walter** **Gehring* /(Basel, Switzerland) /- The history of Hox - *J**ane Langdale* /(Oxford, U.K.) /- Evolution of meristems and leaves - *Angela Nieto* /(Alicante, Spain) /- The Snail gene family in development and evolution - *Kevin Peterson* /(Dartmouth, USA) /- Molecular palaeobiology - *Sabine Zachgo* /(Kï¿½ln, Germany) - The evolution of bilateral symmetry in flowers/

Symposia: *-Development as bridge between micro- and macroevolution *Organizer(s): Jukka Jernvall

(Helsinki) *-**Nodes for change: the molecular systems underlying developmental evolution *Organizer(s): Claudio Alonso (Cambridge) and Miltos Tsiantis (Oxford) *-Origin and diversification of seeds and flowers *Organizer(s): Gï¿½nter Theiï¿½en (Jena) *-Fossilized ontogenies** *Organizer(s): Marcelo Sï¿½nchez-Villagra (Zï¿½rich) *-History of Evo-Devo** *Organizer(s): Scott Gilbert (Swarthmore) *-Evolutionary Developmental Genomics** *Organizer(s): David Ferrier (St. Andrews), Pedro Martinez (Barcelona) *-Theoretical contributions of evo-devo to evolutionary theory** *Organizer(s): Isaac Salazar-Ciudad (Helsinki) and Gerd B. Mï¿½ller (Vienna) *-Evolution of plant form** *Organizer(s): Paula Rudall (Kew), Rolf Rutishauser (Zï¿½rich) *-Evolution of axis formation and axial patterning in basal metazoans** *Organizer(s): Gï¿½nter Plickert (Kï¿½ln), Yulia Kraus (Moscow) *-Bioinformatics** *Organizer(s): Didier Casane (Paris) *-Evolution of head and brain (the arthropod head problem) *Organizer(s): Gregor Bucher (Gï¿½ttingen) *-Canalization, robustness and developmental stability *Organizer(s): Vincent Debat (MNHN Paris), Tom Van Dooren (Leiden) *-Mesenchymal development and evolution of the vertebrate head *Organizer(s): Shigeru Kuratani *-Multi-level modeling of morphogenesis *Organizer(s): Pauline Hogeweg and Stan Marï¿½e (Utrecht) *-Human Evo-Devo** *Organizer(s): Christian Klingenberg (Manchester), Neus Martinez (Barcelona) *-Saltation** *Organizer(s): Richard Bateman (Kew), Jean Deutsch, (Paris) *-From polyphenism to complex life cycles** *Organizer(s): Alessandro Minelli, Giuseppe Fusco (Padua) *-Evolution and development of segmentation** *Organizer(s): Wim Damen (Kï¿½ln) *-Adaptive Developmental Plasticity** *Organizer(s): Caspar J. Breuker (Oxford), Melanie Gibbs ((Louvain-la-Neuve) *-Stem cells, regeneration and cancer** *Organizer(s): Ram Resheff (Haifa), John Nagy (Scottsdale), Eckhard Witten (Sunndalsï¿½ra), Ann Huysseune (Ghent)

The International Tribolium Meeting will again be held as a satellite meeting of the EED meeting, on 29 July 2008 in Ghent and it is organized by Sue Brown, Martin Klingler and Ernst Wimmer (information: klingler@biologie.uni-erlangen.de <mailto:klingler@biologie.uni-erlangen.de>).

Registration Online registration will begin 19th February 2008 and the deadline for early fee registration is 15 April 2008: *_http:// evodevo.eu/._*

The all-in fee is 230 Euro for students and 270 Euro for non-students (including post-docs) and 80 Euro for accompanying persons. The late fee will be 100 Euro more expensive for students and non-students. The fee includes a welcome party (29/7), three lunches (30/7, 31/7, 1/8), two dinners (30/7, 31/7) and the membership fee for the society for two years (20 Euro for two years). The conference dinner (1/8) is not included. The price for the conference dinner which will be held in an old monastery is 40 Euro.

Lodging Student rooms are available as package for four nights at a first come first serve basis. The price for the four night package including breakfast is 140 Euro (35 Euro per night). Hotels have reasonable prices, most are around 100 to 110 Euro (tax and breakfast included), but there are also some cheaper and some more expensive ones.

*Further information will become available from the Society website: * *_http:// evodevo.eu/_*

We look forward to seeing you in Ghent!

*Executive committee EED * *Philip Donoghue* Frietson Galis *G*ï¿½*nter Theissen* *Eckhard Witten** **__*

— / —

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

GlasgowU TextMining Feb21-22

Event on 21st-22nd February - in Glasgow

The Scottish Bioinformatics Forum will be hosting a two-day event on Thursday 21st-22nd February

Location: Kelvin Gallery, Hunterian Museum, Glasgow University

Title: Finding Hidden Knowledge: Text Mining for Biology and Medicine

Two days of talks by leading international speakers from academia and industry (backgrounds to include biology, medicine, pharmaceuticals, bioinformatics, ontologies and text mining).

Poster/demo sessions for participants to present recent work and specific information needs

Ample time for informal discussion nad networking inclding a reception with wine and food

More information can be found http://www.sbforum.org/events.php Please book this event to help us gauge numbers for the catering http://www.sbforum.org/eregister.php?e_id3 We look forward to seeing you on Thursday 21st/22nd February.

Sandra Borthwick, Executive Assistant Scottish Bioinformatics Forum The Royal Society of Edinburgh 22-26 George Street Edinburgh EH2 2PQ

Tel: +44 (0)131 240 2783 Fax: +44 (0)131 240 2786 email: sandra.borthwick@sbforum.org www.sbforum.org

Sandra Borthwick <sandra.borthwick@sbforum.org>

Jean EarlyMetazoanEvolution Oct17-20

International symposium: NONBILATERIAN ANIMAL MODEL ORGANISMS 2008 www.namo2008.de October 17-20, Altes Schloss Dornburg/Saale, Jena, Germany

1. Circular

SYMPOSIUM RATIONALE: Study of the early evolution of multicellular animals (Metazoa) holds the key to some of the most important questions in Evolutionary Biology. In recent decades gene and genome data have strongly influenced our understanding about the phylogenetic relationship of the main metazoan clades and of their developmental biology, but other fields such as comparative morphology and physiology have also provided new insight into animal organization. The use of model organisms has greatly contributed to our expanding knowledge of animal body plans, but the most widely used model organisms (Caenorhabditis, Drosophila, Danio, Xenopus, Mus and Gallus) are all representatives of bilaterian animals; there is a serious absence of models to use for understanding early metazoan evolution. The need for new widely available nonbilaterian model organisms has become pronounced, and while some models have been identified for Cnidaria, none exist for the Porifera. The fully sponsored NAMO2008 symposium (final funding commitment pending) aims at catalyzing the process of choosing models for research on early evolution of metazoan organization. Recent progress but also the most important questions, tasks and the first steps that nonbilaterian animal research should take will be addressed. NAMO 2008 will bring together scientists from various disciplines who are all specialized in different nonbilaterian animal groups and catalyze the process of establishing new nonbilaterian animal model organisms that can be studied in detail by every lab worldwide. We also aim at input from existing bilaterian model organism communities (e.g. the Caenorhabditis elegans community).

VENUE: The symposium venue, the 1000 year-old castle Altes Schloss Dornburg near Jena, will help to create an exclusive working environment for a unique, interdisciplinary team of experts. The castle provides the ideal retreat for exchange of ideas across disciplines and for fostering new alliances and pathways. Two days of combined presentations (invited perspectives) and workshops (discussion and exchange of ideas) will result in a synopsis of the current questions and proposed new directions for future research. In addition NAMO2008 will put together recommendations concerning the selection of new animal models as well as mechanisms to promote use of these experimental models world-wide.

PARTICIPANTS: The symposium will be open for a limited number of participants: 21 invited contributors and 45 assorted participants representing graduate students, postdoctoral researchers and senior scientists, who will be chosen by their excellence of research and expression of interest plus an abstract.

FURTHER INFORMATION: visit www.namo2008.de for further information and our symposium poster.

MAILING LIST: You will be able to register for our mailing list to make sure you will not miss the 2nd Circular and the opening of the registration.

COVERED PERSPECTIVES & KEYNOTE SPEAKERS: ORIGIN OF MULTICELLULAR ANIMALS Claus Nielsen, Denmark THE NEED FOR NEW MODEL ORGANISMS Ronald A. Jenner, Great Britain PALEONTOLOGY OF NONBILATERIAN ANIMAL GROUPS Andrew H. Knoll, USA SELECTED TOPICS: PORIFERA Maja Adamska, Norway Noriko Funayama, Japan April Hill, USA Sally P. Leys, Canada Michael Nickel, Germany Gert Wörheide, Germany SELECTED TOPICS: CNIDARIA & CTENOPHORA Thomas Bosch, Germany Allen G. Collins, USA Mark Martindale, USA Katja Seipel, Great Britain Uli Technau, Austria SELECTED TOPICS: PLACOZOA Ana Signorovitch, USA GENOMICS OF NON-BILATERIAN ANIMALS Claire Larroux, Australia John R. Finnerty, USA Dennis Lavrov, USA LESSONS FROM BILATERIAN MODEL ORGANISMS David C. Hall, USA Peter Ladurner, Austria Sheldon McKay, USA

SCIENTICIF COMMITTEE: Maja Adamska, Sars Centre, Bergen, Norway Dennis Lavrov, Iowa State

University, Ames, USA Sally Leys, University of Alberta, Edmonton, Canada Michael Nickel, Friedrich-Schiller-Universität Jena, Germany Gert Wörheide, Georg-August-Universität Göttingen, Germany

LOCAL ORGANIZER: Michael Nickel Friedrich-Schiller-Universität Jena Institut für Spezielle Zoologie und Evolutionsbiologie Erbertstr. 1 07743 Jena Germany Email contact via webpage form at www.namo2008.de

m.nickel@uni-jena.de m.nickel@uni-jena.de

KansasCity ArthropodGenomics Apr11-13 Deadline

SYMPOSIUM: NEW INSIGHTS FROM ARTHROPOD GENOMES April 11-13, 2008, in Kansas City

This is a friendly reminder that Friday, February 29, is an important deadline for submitting a poster abstract for presentation at the 2nd Annual Arthropod Genomics Symposium. Abstract Guidelines can be found at www.ksu.edu/agc/symposium.shtml. February 29 is also the deadline to receive discounted early registration fees. After February 29, we will continue to welcome your registration to attend the Symposium at a slightly higher cost. A brochure and complete information with links for registration and hotel reservations can be downloaded at www.ksu.edu/agc/-symposium.shtml.

SYMPOSIUM PROGRAM: The main symposium sessions will take place on Friday-Saturday, April 11-12. Speakers will present new insights from genomic approaches in arthropods and describe the development of tools for genomic analysis. Optional workshops are scheduled for Thursday and Friday evenings. An evening of jazz and KC barbeque is planned for Saturday night. On Sunday morning, participate in a roundtable discussion with the ArthropodBase Consortium. Activities will conclude by noon on Sunday.

FEATURED SPEAKERS: John Kenneth Colbourne, Indiana University, Preservation, expansion and invention of crustacean genes with reference to insect genomes. Christine G. Elsik, Georgetown University, Unusual base composition of the honey bee genome. Sarjeet S. Gill, University of California, Riverside, Mosquito midgut interactions with bacterial toxins. Catherine A. Hill, Purdue University, Tick genome organization and evolution. Thomas Kaufman, Indiana University, The latest news from CNN: What the 12 sequenced Drosophila genomes have told us about rapidly evolving genes and positive selection. J. Robert Manak, University of Iowa, Empirical annotation of arthropod genomes using tiled genomic microarrays. Subbaratnam Muthukrishnan, Kansas State University, Functional genomics of insect chitin metabolism. Hugh M. Robertson, University of Illinois at Urbana-Champaign, What we've learned about the insect chemoreceptors from arthropod genome projects. Bruce R. Schatz, University of Illinois at Urbana-Champaign, BeeSpace: Interactive functional analysis of arthropod genomic data. Jeff Stuart, Purdue University, Avirulence, sex determination, and a physical map of the Hessian fly genome. Judy Willis, University of Georgia, Insect cuticular proteins: Annotation, proteomics, expression, evolution. Evgeny Zdobnov, University of Geneva, Medical School, Switzerland, A comparative perspective on insect genomes.

POSTER SESSIONS: There will be two poster sessions, limited to first 150 abstracts received before Friday, February 29. A few platform presentations will be chosen from submitted poster abstracts.

WORKSHOPS AND ROUNDTABLE DISCUSSION: On Thursday evening, a workshop on "Community Contributions to Genome Annotation" will feature a presentation on use of the Apollo Genome Annotation Curation Tool by Dr. Chris Elsik (BeeBase). On Friday evening, Dave Clements (NESCent) and Scott Cain (CSHL) will lead a workshop, "Chado Databases and Integration with GMOD Tools." Throughout the meeting, arthropod genome database and bioinformatics tool developers will be available for individual training. On Sunday morning, participate in a roundtable discussion led by members of the ArthropodBase Consortium regarding the generation of integrated arthropod genome databases and tools for genome analysis, and community curation. Symposium attendees are invited to participate in these additional events.

VENUE: The symposium will take place at the historic Muehlebach Hotel (operated by Marriott) in downtown Kansas City.

KANSAS CITY JAZZ AND BARBEQUE: Participants are encouraged to stay Saturday night for an optional evening of jazz and KC barbeque in the historic 18th and Vine district.

REGISTRATION: The registration fee will be $275 ($150 for graduate and undergraduate students), and will include a welcome reception Thursday evening, breakfast and lunch on Friday and Saturday, and light refreshments at the Friday poster session. Additional fees apply for the Apollo Workshop Thursday evening and Saturday night dinner.

INFORMATION: Contact Doris Merrill at dmerrill@k-state.edu or 785-532-3482. To receive future Symposium announcements, send your contact information to dmerrill@k-state.edu.

SYMPOSIUM WEBSITE: www.k-state.edu/agc/-symposium.shtml

DEADLINES: February 29, 2008 - Poster abstracts (limited to first 150 received) February 29, 2008 - Early registration March 20, 2008 or until room block is filled - Hotel reservations

Please share this announcement with colleagues and students!

Susan J. Brown, Professor Director, Center for Genomic Studies on

— / —

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

---

KoenigMuseum Biodiversity May19-30

The Convention on Biological Diversity will have its ninth Confernece of the Parties (COP 9) in Bonn, Germany, from 19 to 30 May 2008. There will be an associated scientific meeting “Biodiversity Research - Safeguarding the Future” at the Museum Koenig, Bonn, Germany, from May 12 - 16, 2008.

Further Information please visit www.preCOP9.org .

Swen Renner

– Dr. Swen C Renner Phone: +49 711 8936 172 Fax: +49 711 8936 100

Staatliches Museum fur Naturkunde Stuttgart National Focal Point for the Global Taxonomic Initiative (GTI) of the Convention on Biological Diversity (CBD) Rosenstein 1, 70191 Stuttgart, GERMANY www.gti-kontaktstelle.de renner.smns@naturkundemuseum-bw.de

---

Marseilles EvolBiology Sep24-26 movies

Dear all,

We are pleased to inform you that the first movies of the oral presentations of the 11th Evolutionary Biology Meeting at Marseilles are now available on the web site: http://sites.univ-provence.fr/webtv (select channel 2)

Please note also that the next edition of the Evolutionary Biology Meeting at Marseilles will take place on 24th 25th 26th September 2008. The following subjects will be discussed: - Evolutionary biology concepts and modelisations for biological annotation; - Biodiversity and Systematics; - Comparative genomics and post-genomics (at all taxonomic levels); - Functional phylogeny; - Environment and biological evolution; - Origin of Life and exobiology; - Non-adaptative versus adaptative evolution.

Please, do not hesitate to visit our website to find more information http://sites.univ-provence.fr/evol-cgr

Yours sincerely,

Axelle Pontarotti

Egee@univ-provence.fr

Myshkin Russia RodentEvolution Jul24-28

Dear Colleagues,

It is a great pleasure for us to invite you to participate in the 11th International Conference on Rodent Biology (Rodens et Spatium), which will be held at the end of July (approximately 24-28 July), 2008 in Myshkin,Russia.

The Conference will be hosted by A.N.Severtsov Institute of Ecology and Evolution of the Russian Academy of Sciences, Russian Theriological Community and Myshkin Municipal District Administration. The three most recent Rodent Conferences have been held in Belgium (2002), Poland (2004) and Italy (2006), with 130-150 ’rodentologists’ from 25-30 countries in attendance at each.

The aims of the Conference are to bring together scientists studying rodents from all over the world, to associate mammalogists from East and West for future collaboration and to exchange scientific information and experiences through the discussion of various issues. It's for the first time the Conference takes place in Russia and we'll be pleased to acquaint you with our country, its people, history and nature.

Myshkin is a tiny old town in the historical region of old Russia (Yaroslavl region, 250 km North of Moscow). Its name can be translated as "Little Mouse Town" and it was proclaimed by its citizens as "The World Capital of Mice". Despite being among the smallest towns in Russia (6000 inhabitants), it possesses 10 museums, including the world's only Mouse Museum. Many famous old cities and towns are near Myshkin, including Yaroslavl, Uglich, Rostov-the-Great, and Pereslavl-Zalessky. Myshkin is situated on the high bank of the Volga, the largest river of Europe, and surrounded by picturesque landscapes and untouched countryside.

The year 2008 is the Year of Mouse in the Oriental Calendar and it is declared to be a special Festival Year in Myshkin. Thus, it's a special place and time for those of us studying rodents to meet and discuss our researches.

Conference information can be obtained from the website www.sevin.ru/rodensetspatium/index.html or by contacting Olga Osipova (o_osipova@mail.ru) or Tatyana Chistova (tachi@mail.ru) of the Organizing Committee.

YOU ARE WELCOME TO PRELIMINARY REGISTRATION via website.

We would be grateful to you if you spread this information among your colleagues.

We look forward to seeing you in July 2008 and hope your stay in Myshkin,Russia will be both useful and enjoyable.

vdeffontaine@ulg.ac.be vdeffontaine@ulg.ac.be

NHM London Speciation Mar12-13 2

Speciation Symposium, London 12-13 March 2008

The third Natural History Museum Speciation Symposium will be held from 1pm (first talk 2pm)on 12 March to lunchtime on 13 March in the Museum's Flett Lecture Theatre, Exhibition Road, London.

The Keynote Address will be by Prof. Leo Beukeboom (Groningen) on 'Speciation in Nasonia wasps'.

Other speakers include Roger Thorpe (Bangor), James Cook (Reading), Benjamin Isambert and Harald Schneider (NHM), Albert Phillimore (Imperial), Philine Feulner and Juan Galindo (Sheffield), Magdalena Zarowiecki (NHM and Manchester).

Booking for participants is not necessary.

We will try to reserve a table for dinner on 12 March. If you wish to attend the meal, please email Roger Butlin (r.k.butlin@sheffield.ac.uk).

We will not be providing accommodation so you might like to look at London hotels now. For a list of hotels within easy reach of the Museum, please contact Ralph Harbach (reh@nhm.ac.uk).

Ralph Harbach and Roger Butlin

r.k.butlin@sheffield.ac.uk r.k.butlin@sheffield.ac.uk

PortTownsend Evo-WIBO Apr18-20

The 2008 meeting of "Evo-WIBO* evolutionary biologists in the Pacific Northwest" will take place April 18-20, 2008 at Ft. Worden State Park in Port Townsend, Washington. We averaged about 140 people attending the 2004 and 2006 meetings and have expanded our capacity for this year, but please register early to make sure that we have a slot for you. We have made every effort to keep costs down (registration covers all housing and food), and a simple goal of the meeting is to have a good time with friends, old and new.

Registration and general information is available at: http:// www.zoology.ubc.ca/evo-wibo The conference begins with a Friday night gala reception and ends by noon on Sunday. The meeting has no concurrent sessions, and talks and posters are presented by faculty, postdocs and students. The slate of talks will be chosen by the organizing committee. We strongly encourage faculty to nominate/encourage outstanding students and postdocs to give platform talks (send an email to Dick Gomulkiewicz, gomulki@wsu.edu, with suggestions). Dolph Schluter will be giving the plenary talk for the meeting Sunday morning.

*Evo-WIBO stands for Evolutionary Biologists from Washington, Idaho, British Columbia and Oregon, although we draw much more widely than that, including

Alaska, Alberta, California, and Montana.

– Richard Gomulkiewicz gomulki@wsu.edu PHONE: (509) 335-2527 FAX: (509) 335-3184 http://www.wsu.edu/~gomulki/ Department of Mathematics; P.O. Box 643113 or School of Biological Sciences; P.O. Box 644236 Washington State University Pullman, WA 99164 USA

gomulki@wsu.edu gomulki@wsu.edu

QuebecCity PopConservGenetics IUFRO Aug24-29

INTERNATIONAL IUFRO-CTIA 2008 JOINT CONFERENCE < http://www.iufro-ctia2008.ca >www.iufro-ctia2008.ca

The Executive Committee is pleased to invite you to attend the 2008 Joint Conference of the IUFRO Working Groups 2.04.01 (Population, ecological and conservation genetics) and 2.04.10 (Genomics), along with the Canadian Tree Improvement Association (CTIA) that will be held in Quebec City, August 24-29, 2008, including satellites activities and workshops. It will be hosted by Laval University and its partners, under the theme Adaptation, Breeding and Conservation in the Era of Forest Tree Genomics and Environmental Change.

The conference venue (Loews Le Concorde) is located near the beautiful Battle Fields, the St-Lawrence River and the historical city.

CONFIRMED KEYNOTE SPEAKERS include David Neale (USA) and Antoine Kremer (France); other confirmed invited speakers are Thomas Byram (USA), Yousry El-Kassaby (Canada), Matias Kirst (USA), and Antje Rohde (Belgium). More to come...

The IUFRO-CTIA main conference event will be held from Monday, August 25 to Thursday, August 28. The CTIA Working Groups on Tree Seeds and Wood Quality will hold their workshops on Monday, August 25. The first Arborea-Treenomix Joint Workshop on spruce genomics will be held on Monday, August 25. The 2nd CONFORGEN Conference will be held on Friday, August 29.

CONFERENCE REGISTRATION AND CALL FOR PAPERS ARE NOW AVAILABLE ONLINE at the IUFRO-CTIA 2008 website (< http://www.iufro-ctia2008.ca >http://www.iufro-ctia2008.ca).

The site also provides additional information on accommodation, on-line room booking, main conference program, workshops and field trips.

IMPORTANT DATES: *CALL FOR PAPERS SUBMISSION DEADLINE: APRIL 15, 2008. * EARLY REGISTRATION DEADLINE: APRIL 15, 2008.

Looking forward to see you in Quebec City next summer,

The Executive Committee,

Jean BOUSQUET, Laval University Jean BEAULIEU, Canadian Forest Service Andre RAINVILLE, Ministere des Ressources Naturelles et de la Faune du Quebec John MACKAY, Laval University

< http://www.iufro-ctia2008.ca >www.iufro-ctia2008.ca

info@iufro-ctia2008.ca info@iufro-ctia2008.ca

RaleighNC BehaviorEvolution Jun4-7

2008 Annual Meeting, American Genetic Association 2008, June 4-7, 2008. “Genetics and Genomics of Behavior.” Key Lecturer: Mariana Wolfner.

This conference will explore current status and future trends in the genetic architecture of behavior, neurogenetic mechanisms of behavior, and evolution of behavior. In addition to a stellar group of invited speakers, there will be an opportunity for platform presentations from participants who submit abstracts.

Competitive scholarships for travel and registration will be available for students and postdoctoral fellows.

Details and registration at www.agasymposium2008.org agajoh@oregonstate.edu agajoh@oregonstate.edu

Rostock CrustaceanPhylogenetics Oct7-11

Advances in Crustacean Phylogenetics

1st International Symposium to be held in Rostock, Germany, 7-11 October 2008

2nd CIRCULAR

Dear Colleagues, We would like to invite you to the first international symposium on Advances in Crustacean Phylogenetics. The symposium will take place from 7 - 11 October 2008 in Rostock. We are pleased to announce that 25 high profile international speakers have affirmed their attendance. They will provide us with a broad overview of the following topics: (1) the place of crustaceans within arthropods, (2) the phylogeny of single sub-taxa and (3) the contribution of certain character complexes to the phylogeny of Crustacea. These talks are scheduled to take 30 mins, plus 10 mins discussion per talk, spread over the four days. In addition, the conference is open for posters on all aspects of crustacean phylogeny! The best student posters will be awarded by The Crustacean Society! Alongside the stimulating scientific program, there will be space and time for individual discussions and social events. On Wednesday evening there will be a river cruise to the Baltic Sea, including an excellent fish buffet. On Thursday afternoon a general poster session will be held which will be preluded by a public lecture. On Friday there will be an excursion to the newly built Ozeaneum in Stralsund, followed by a visit to a site near Stralsund where thousands of Eurasian cranes rest on their migration South. We hope the program will tempt you to come to the historic city of Rostock to hear about and discuss with us recent Advances in Crustacean Phylogenetics.

Organizers and Venue Stefan Richter, Christian Wirkner, Ole Sten Moller Universitat Rostock, Allgemeine & Spezielle Zoologie Universitatsplatz 2, D-18055 Rostock, Germany Phone +49 (0)381 498-6261 FAX +49 (0)381 498-6262 Please visit our home page for further information http://www.biologie.uni-rostock.de/zoologie/acp_home.html

On behalf of the ACP 2008 organizers: Prof. Stefan Richter Dr. Christian Wirkner Dr. Ole S. Moller

—

Dr. Ole S. Moller

Wissenschaftlicher Mitarbeiter Allgemeine und Spezielle Zoologie Institut fur Biowissenschaften, Universitat Rostock Universitatsplatz 2 D-18055 Rostock

Tel: (+49) 381 498 6279 Funk: (+49) 0177 5155354

Fax: (+49) 381 498 6262

ole.moeller@uni-rostock.de

http://www.biologie.uni-rostock.de/zoologie/moeller.htm osmoller@snm.ku.dk

---

Rostock CrustaceanPhylogenetics Oct7-11 correction

A small but important typo rendered the link to the ACP homepage non-functional; Below you will find the correct one! Sorry about that :-)

Advances in Crustacean Phylogenetics

1st International Symposium to be held in Rostock, Germany, 7-11 October 2008

2nd CIRCULAR

Dear Colleagues, We would like to invite you to the first international symposium on Advances in Crustacean Phylogenetics. The symposium will take place from 7 - 11 October 2008 in Rostock. We are pleased to announce that 25 high profile international speakers have affirmed their attendance. They will provide us with a broad overview of the following topics: (1) the place of crustaceans within arthropods, (2) the phylogeny of single sub-taxa and (3) the contribution of certain character complexes to the phylogeny of Crustacea. These talks are scheduled to take 30 mins, plus 10 mins discussion per talk, spread over the four days. In addition, the conference is open for posters on all aspects of crustacean phylogeny! The best student posters will be awarded by The Crustacean Society! Alongside the stimulating scientific program, there will be space and time for individual discussions and social events. On Wednesday evening there will be a river cruise to the Baltic Sea, including an excellent fish buffet. On Thursday afternoon a general poster session will be held which will be preluded by a public lecture. On Friday there will be an excursion to the newly built Ozeaneum in Stralsund, followed by a visit to a site near Stralsund where thousands of Eurasian cranes rest on their migration South. We hope the program will tempt you to come to the historic city of Rostock to hear about and discuss with us recent Advances in Crustacean Phylogenetics.

Organizers and Venue Stefan Richter, Christian Wirkner, Ole Sten Moller Universitat Rostock, Allgemeine & Spezielle Zoologie Universitatsplatz 2, D-18055 Rostock, Germany Phone +49 (0)381 498-6261 FAX +49 (0)381 498-6262 Please visit our home page for further information http://www.biologie.uni-rostock.de/zoologie/acp_home.htm On behalf of the ACP 2008 organizers: Prof. Stefan Richter Dr. Christian Wirkner

Dr. Ole S. Moller

—

Dr. Ole S. Moller

Wissenschaftlicher Mitarbeiter Allgemeine und Spezielle Zoologie Institut fur Biowissenschaften, Universitat Rostock Universitatsplatz 2 D-18055 Rostock

Tel: (+49) 381 498 6279 Funk: (+49) 0177 5155354

Fax: (+49) 381 498 6262

ole.moeller@uni-rostock.de

http://www.biologie.uni-rostock.de/zoologie/moeller.htm osmoller@snm.ku.dk

StMalo France TE evolution Apr20-23

Dear All,

The French Society of Genetics and the French Transposition Community (CNRS) are happy to announce an International Congress on Transposable genetic elements. Transposable elements are at the heart of biology. Since their discovery in the 1940's, they have been shown to contribute significantly to genome structure, evolution and function. Their study aims at understanding their biological success and to characterize their contribution to fundamental biological functions. The increasing interest in these elements is strongly linked to our recent knowledge of genome organization and function. They are major players of phenotypic diversity but they are also involved in diverse human pathologies. Transposable element studies cover a broad spectrum of organisms and a large variety of biological processes and methodologies. The aim of this international congress, a "premiere" in Europe, is to integrate recent knowledge to design new concepts and to identify future orientations of research. Several topics will be covered such as, the evolution and activity of transposable elements, their dynamics within genomes and populations, their mechanisms of transposition and control and their impact on genomes. The congress will be held on April 20-23, 2008 at "Palais du Grand Large", St Malo, France. (" EUDORA="AUTOURL"http://www.pgl-congres.com/index.aspx?VersionId=2 http://www.pgl-congres.com/index.aspx?VersionId=2). The preliminary program, the registration form and the website can be found at the following address: http://www.icte2008.com/ The deadline to register to ICTE2008 with preferential rates and to submit an abstract for an oral or a poster presentation has been postponed to February 10, 2008. Deadline for abstract submission (oral and poster presentations): February 10, 2008. Deadline for preferential rate: February 10, 2008. Do not wait for the last minute. The web site of the International Congress on Transposable Elements (ICTE) that will be held in France is open at the following address. http://www.icte2008.com/ We would be grateful if you could distribute this as widely as possible.

Best wishes, The organising committee Pierre Capy Abdelkader Ainouche Dominique Anxolabéhère Alain Bucheton Mick Chandler Pascale Lesage François Mallet Didier Mazel Chantal Vaury

M. L. AINOUCHE Evolution des Genomes et Speciation, Equipe MOB (Mecanismes à l'Origine de la Biodiversite) UMR CNRS 6553 Ecobio, Universite de Rennes 1 Campus Scientifique de Beaulieu, Bat. 14A 35 042 Rennes Cedex France Ph. 33 (0)2 23 23 51 11 Fax 33 (0)2 23 23 50 47

Malika Ainouche <Malika.Ainouche@univ-rennes1.fr>

Tokyo TetrapodAdaptation Jun9-13

FIFTH CONFERENCE ON SECONDARY ADAPTATION OF TETRAPODS TO LIFE IN WATER

When: June 9-13, 2008 Where: National Museum of Science and Nature, Tokyo, Japan Abstracts due: End of February Conference Website/Email list: http://www.kahaku.go.jp/english/news/2007/secad08/ The tri-annual conference on the secondary adaptation of tetrapods to life in water brings together a highly interdisciplinary group of scientists who are interested in the processes of evolution and the change of form and function through the adaptation of terrestrial tetrapods to aquatic environments.

Following successful meetings in France (1996), Denmark (1999), New Zealand (2002) and the USA (2005), the 2008 conference will be held in Japan for the first time in Asia.

In addition to the open sessions, the 2008 conference will feature: Pre-symposium keynote lectures open to the public (with English-Japanese translation) Cetacean anatomy workshop with guided dissections by

Dr. T. K. Yamada (co-organizer) Exhibition of aquatic tetrapods newly opened at the National Museum of Nature and Science

padam@ucla.edu

Toulouse BehaviourEvolution Apr14-17

4th meeting in Ecology & Behaviour April 14-17, 2008 Toulouse

Meeting point : EcoleNationale de Formation Agronomique BP22687 2route de Narbonne 31326Castanet Tolosan cedex

The 4thmeeting in Ecology & Behaviour is mostly organised by and for PhD studentsand post-docs. It aims to gather young and senior researchers from diversebackgrounds extending from animal behaviour to ecology and evolutionarybiology. The five sessions will be introduced by established researchers and oral presentations will be given in English. In the first evening a plenary session will take place and a documentary film will be shown the night after. These 2 events will be open to the public and followed by a discussion. Half a day will be devoted to visit the Muse dHistoire Naturelle de Toulouse±.

Program :

Group-living, Conflicts and Cooperation - J. Krause Behaviour and Cognition - N. Clayton & M. Giurfa Foraging strategies - V. Fourcassi & J.-L. Hemptinne Habitat use, dipersal and reproductive strategies - J. Clobert & M. Hewison Signals and host/parasite interactions - P. Heeb & K. McCoy Plenary talk, scientific documentary film and discussion - P.-H. Gouyon, J. Orivel & B. Thierry

Participation :

To submit a talk or a poster, please complete the form available on the following website: http://www.uappu.org/serl/pmwiki.php. Save your file as: yourname_sessionname.doc and send it by email to serl08@uappu.org. Please put the name of the session in the subject of the message. Deadlineto submit summaries: February 20th, 2008. Summaries have to be written in English, with no more than 250 words. 10-minute-length talks will be given in English, with 3-5 minutes questions after it.

Registration is free of charges. Accommodation and meals are offered by our partners.

For more information: http://www.uappu.org/serl/pmwiki.php With the best wishes, The organizingcommittee serl08@uappu.org

Gabor Czirjak <czirjakgabor@yahoo.com>

UBritishColumbia EarlyCareer Female EvolutionaryBiologists May11 Registration

The Symposium for Women Entering Ecology and Evolution Today (SWEEET) is now open for registration for senior doctoral graduate students, post-docs, and early career scientists. The goal of this symposium is to address issues that influence the advancement of women from postgraduate degrees into academic and government positions in the fields of Ecology and Evolutionary Biology.

Canadian women scientists are significantly underrepresented in scientific positions at universities, government agencies and in industry. Interestingly, women are much better represented in the upper graduate level and postdoctoral programs leading to these careers than they are as professionals in the fields. One factor that may contribute this phenomenon is a lack of information specifically targeted at women as they endeavor to make the critical leap from their training to a career track. This symposium will to address this gap by identifying concrete tips and tools for getting an academic or government job, developing a research program, networking, mentoring, and establishing work-life balance.

When: Sunday May 11, 2008 in conjunction with the 3rd annual meeting of the Canadian Society for Ecology and Evolution (http://www.ecoevo.ca/ubc2008).

Where: Green College at the University of British Columbia, Vancouver, B.C. (www.greencollege.ubc.ca/)

Format: Series of presentations by senior scientists (including academic faculty, academic administration, government scientists), followed by roundtable discussions.

Cost: No charge

How to register: http://www.ecoevo.ca/ubc2008/SWEEET/registration.html Deadline for registration: March 15, 2008. Participants will be randomly selected from the applications, ensuring even geographic representation.

Suggested accommodations: (http://www.ecoevo.ca/-ubc2008/en/residences.htm)

Please see our website for more information (http://www.ecoevo.ca/ubc2008/SWEEET/-index.html) or contact the organizing committee (sweeet2008@gmail.com) with specific questions or comments.

We look forward to receiving your application and to meeting you in May!

Sincerely, SWEEET Organizing Committee

Dr. Risa Sargent UFA Assistant Professor, University of Ottawa

Dr. Carrie Holt Scientist, Fisheries and Oceans Canada

Dr. Katrina Dlugosch Postdoctoral Fellow, University of British Columbia

katrina.dlugosch@gmail.com

UEdinburgh ParasitoidGeneticsGenomics Jun5-6

Genetic and Genomic Approaches for Parasitoid Behavioural Ecology BEPAR workshop 5-6 June 2008 Institute of Evolutionary Biology, University of Edinburgh, U.K.

We are very pleased to invite you to Edinburgh this summer for an ESF-funded workshop under the BEPAR framework. The two-day workshop will explore the new tools becoming available to parasitoid behavioural ecologists, focusing in particular on novel genetic and genomic approaches. We will consider the ways in which advances in population genetics and genomic analysis can help us address questions old and new in parasitoid insects, including biological control, life history evolution, interspecific interactions and reproductive decision-making.

The workshop will mix invited expert speakers with research talks from delegates, with a focus on early-career researchers. Discussion sessions will also be a key feature. There will also be a poster session. For many species of parasitoid, the use of genetic approaches remains limited. We therefore expect spoken and poster presentations to vary in the approaches taken (including non-genetic studies), allowing us to explore to what extent emerging technologies can help address outstanding questions. Novel research areas, involving genetics are not, are therefore extremely welcome as well.

Researchers with no or little experience in genetics or genomics are especially encouraged to participate, as the workshop specifically aims to unlock the use of genetic information to a wide audience of parasitoid behavioural ecologists.

Confirmed keynote speakers for the workshop are: - John Werren (University of Rochester, NY, USA) - The Nasonia genome project: Implications to parasitoid genetics - Leo Beukeboom (University of Groningen, The Netherlands) - Sex determination and life history - Amy Toth (University of Illinois, Urbana-Champaign, USA) - TBA - Bart Pannebakker (University of Edinburgh, UK) - Genetics of sex allocation behaviour in Nasonia parasitoids - Hans Smid (Wageningen University, The Netherlands) - Ecology of learning in insect parasitoids: from genes to behaviour - Lex Kraaijeveld (University of Southampton, UK) - Evolutionary forces on defence and counter-defence in a host-parasite interaction - Saskya van Nouhuys (University of Helsinki, Finland, and Cornell University, Ithaca, NY, USA) - Host specialization by Cotesia parasitoids: Cryptic species groups and community structure

The workshop will have an all-inclusive registration fee of ï¿½120 (this includes accommodation, breakfasts and lunches). Accommodation is available for the nights of 4th and 5th June, with some rooms available (at no extra charge) for 6th June. Delegate number is limited to 80. The workshop and accommodation will be located at Pollock Halls, University of Edinburgh.

Registration and abstract submission is via our website http://www.biology.ed.ac.uk/bepar2008/Home.html. Registration will remain open until the workshop is fully occupied. The deadline for submission of spoken or poster presentations is Friday 2nd May 2008. Links with information about travel to and from Edinburgh and the workshop locations are available on the website. Further details concerning the scientific program will appear shortly. Until then, enquiries can be sent to David Shuker (david.shuker@ed.ac.uk).

We very much look forward to welcoming you to Edinburgh this June.

David Shuker, Leo Beukeboom, Jetske de Boer, Bart Pannebakker and Louis van de Zande (Universities of Edinburgh and Groningen) –

Bart Pannebakker Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Road Edinburgh EH9 3JT Scotland UK e-mail: Bart.Pannebakker@ed.ac.uk tel: +44

(0) 131 650 5553 fax: +44 (0) 131 650 6564 http://westgroup.biology.ed.ac.uk/BartP/BartP.html Bart.Pannebakker@ed.ac.uk

UIowa Evolution of Sex Jun16-19

[3]EVOLUTION OF SEX & RECOMBINATION: IN THEORY AND IN PRACTICE[2]

June 16-19, 2008, at the University of Iowa, Iowa City, USA.

http://ccg.biology.uiowa.edu/sexrec The Roy J. Carver Center for Comparative Genomics and the Department of Biology at the University of Iowa announces an international conference on the evolution of sex & recombination. This conference will immediately precede the 2008 Evolution meeting taking place in nearby Minneapolis, Minnesota (June 20-24).

Talks will be given by invited speakers at both the junior and senior level. There will also be opportunities for contributed talks and posters to be given by conference attendees at all levels of seniority. A number of travel awards (10-15) will be provided to deserving students and postdocs.

Topics will include: -Advantages of sexual reproduction -Experimental evolution of sex -Estimating recombination rates -Mating types & sex determination -Linkage, selection & population size -Sex chromosomes -Sex & pathogenesis -Sexual selection -Sexual conflict

Confirmed speakers include: Philip Awadalla University of Montreal Doris Bachtrog University of California, San Diego Graham Bell McGill University Rhona Borts University of Leicester Bernardo Carvalho Universidade Federal do Rio de Janeiro Andy Peters University of Wisconsin-Madison Brian Charlesworth University of Edinburgh Nick Colegrave University of Edinburgh Tim Cooper University of Houston Ursula Goodenough Washington University-St. Louis Joe Heitman Duke University Michael Hood Amherst College Alex Kondrashov University of Michigan Curt Lively Indiana University Stephanie Meirmans University of Bergen Bill Rice University of California, Santa Barbara Isa Schön Royal Belgian Institute of N.S. Marcy Uyenoyama Duke University Jerry Wilkinson University of Maryland Cliff Zeyl Wake Forest University

Check the conference website for details regarding registration, accommodation, etc.: http://ccg.biology.uiowa.edu/sexrec/registration.php A symposium issue to be published in Journal of Heredity is being planned.

All enquiries are encouraged (including potential sponsors) and should be directed to the organizers: sexrec@uiowa.edu

On behalf of the organizing committee,

John Logsdon –

John M. Logsdon, Jr., Ph.D. Associate Professor Director, Roy J. Carver Center for Comparative Genomics University of Iowa Department of Biological Sciences 319 335 1082 office 310 Biology Building 319 335 1083 lab Iowa City, IA 52242-1324 319 335 1069 FAX

email <john-logsdon@uiowa.edu> web < http://www.biology.uiowa.edu/ccg/ > < http://euplotes.biology.uiowa.edu >

john-logsdon@uiowa.edu john-logsdon@uiowa.edu

UMichigan EarlyCareerScientistsSymposium Mar15

Dear Colleagues,

On Saturday March 15, 2008, the Ecology and Evolutionary Biology Department at the University of Michigan will sponsor the fourth annual U-M Early Career Scientists Symposium. This one-day symposium is focused on the topic of NETWORKS IN ECOLOGY AND EVOLUTION. It is truly an international symposium with our 10 speakers coming from 5 different countries (i.e. USA, Spain, Switzerland, Canada, and Brazil).

PLEASE REGISTER (for free!) TODAY at http://lessons.ummu.umich.edu/2k/ yss/registration.

Additional information available at http://www.sitemaker.umich.edu/ yss2008/home.

The symposium includes keynote talks by ANDREAS WAGNER (University of Zurich) and JORDI BASCOMPTE (Biological Station of Doñana, Spanish Research Council).

Other speakers at the event are: Stefano Allesina National Center for Ecological Analysis and Synthesis, Santa Barbara, California Postdoctoral Associate

Paulo Guimarães Universidade Estadual de Campinas (UNICAMP), Brazil Postdoctoral Associate

Christian Landry University of Montreal, Quebec, Canada NSERC Postdoctoral Fellow, Department of Biochemistry

Sasha Levy New York University, New York Postdoctoral Fellow

Emily Stuart Minor University of Maryland Center for Environmental Science, Appalachian Laboratory, Frostburg, Maryland National Parks Ecological Research Postdoctoral Fellow

Kristi Montooth Indiana University, Bloomington Assistant Professor, Department of Biology

Samraat Pawar University of Texas at Austin Ph.D. candidate, Section of Integrative Biology

Steve Proulx Iowa State University, Ames Assistant Professor, Ecology, Evolution and Organismal Biology

Patricia J. Wittkopp, Ph.D. Assistant Professor Ecology and Evolutionary Biology Molecular, Cellular and Developmental Biology 1061 Natural Science Building University of Michigan Ann Arbor, MI 48109-1048 tel: 734.763.1548 (office); 734.647.5483 (lab) fax: 734.763.0544 www.umich.edu/ ˜ pwlab wittkopp@umich.edu wittkopp@umich.edu

UMinnesota Evolution 2008 Jun20-24

Online registration is now available for Evolution 2008, the annual meeting of the Society for the Study of Evolution, the Society of Systematic Biologists, and the American Society of Naturalists, to be held June 20-24, 2008 on the Minneapolis campus of the University of Minnesota.

Please visit http://www.evolution2008.org The deadline for receipt of presentation titles including posters and talks is April 1, 2008. Participant registration should be completed by May 2, 2008 to qualify for discounted rates. Evolution 2008 is the premier annual opportunity for sharing scientific research related to evolution. Symposia, concurrent talks, and posters will be presented by 1,200 expected participants. Related activities include exhibits, an opening reception, a picnic, a banquet, and two poster receptions.

The University of Minnesota venue is in the heart of Minneapolis, a vibrant metropolitan area of four million people that offers a diverse array of cultural, entertainment, dining, and sporting opportunities. It also a point of departure for pre- or post- meeting exploration of Minnesota; from its Boundary Waters Canoe Area, Lake Superior and the port of Duluth, the prairies of southwestern Minnesota, to the headwaters of the Mississippi River at Lake Itasca.

We look forward to welcoming you to Evolution 2008 and are eager to answer your questions to make your participation a productive and memorable experience. Questions may be directed questions to Heather Dorr (cceconf3@umn.edu).

On behalf of the societies, the organizing committees, and the University of Minnesota, thank you for your participation.

George Weiblen Evolution 2008 Program Chair Associate Professor, Department of Plant Biology Herbarium Curator, Bell Museum of Natural History

gweiblen <gweiblen@umn.edu>

UMinnesota Evolution 2008 Jun20-24 OnlineRegistration

Online registration is now available for Evolution 2008, the annual meeting of the Society for the Study of Evolution, the Society of Systematic Biologists, and the American Society of Naturalists, to be held June 20-24, 2008 on the Minneapolis campus of the University of Minnesota.

Please visit http://www.evolution2008.org SSB members should be sure to mark the box that identifies you as an SSB member because meeting proceeds (if any) will be divided among the three societies according to proportional representation. All SSB proceeds will as always be used for student awards. If your membership is not current, you can renew online now to receive the member discount: http://systbio.org/?q=node/6 The deadline for receipt of presentation titles including posters and talks is April 1, 2008. Participant registration should be completed by May 2, 2008 to qualify for discounted rates. Evolution 2008 is the premier annual opportunity for sharing scientific research related to evolution. Symposia, concurrent talks, and posters will be presented by 1,200 expected participants. Related activities include exhibits, an opening reception, a picnic, a banquet, and two poster receptions.

The University of Minnesota venue is in the heart of Minneapolis, a vibrant metropolitan area of four million people that offers a diverse array of cultural, entertainment, dining, and sporting opportunities. It is also a point of departure for pre- or post- meeting exploration of Minnesota; from its Boundary Waters Canoe Area, Lake Superior and the port of Duluth, the prairies of southwestern Minnesota, to the headwaters of the Mississippi River at Lake Itasca.

We look forward to welcoming you to Evolution 2008 and are eager to answer your questions to make your participation a productive and memorable experience. Questions may be directed to Heather Dorr (cceconf3@umn.edu).

On behalf of the societies, the organizing committees, and the University of Minnesota, thank you for your participation.

George Weiblen Evolution 2008 Program Chair Associate Professor, Department of Plant Biology Herbarium Curator, Bell Museum of Natural History

SSB <SSBMembership@BurkInc.com>

UMontpellier HumanEvolution Apr2-4

Reduced registration fees - Last 2 days

EHBE

European Human Behaviour and Evolution Conference

2-4 April 2008

University of Montpellier

< http://www.ehbe08.com/ >www.ehbe08.com

Charlotte Faurie & Michel Raymond Conference organizers European Human Behaviour and Evolution Conference (EHBE 2008) < http://www.ehbes.com/- >www.ehbes.com

Institut des Sciences de l'Evolution (CNRS UMR 5554) Universite Montpellier II - CC 065 Place Eugene Bataillon F-34095 Montpellier cedex 05 TEL: +33 (0)467 144 632 FAX: +33 (0)467 143 622

ehbe08@univ-montp2.fr

UOregon EvoDevo Apr4-6

UOregon.EvoDevo.Apr4-6

Hello Fellow Researchers,

On behalf of the NSF IGERT Trainees at the University of Oregon, I would like to remind EvolDir members about the 2008 NSF IGERT Symposium on Evolution, Development and Genomics entitled "From Patterns to Process: Bridging Micro- and Macro-evolutionary concepts through Evo-Devo".

The symposium will be held in Eugene, Oregon at the Valley River Inn from April 4 - 6, 2008.

Information on registration, speakers and poster submission can be found on the website:. http://evodevo.uoregon.edu/symposium.html The symposium has been organized by the IGERT-associated graduate students at the University of Oregon. We are very proud of the invited speakers and we look forward to an intellectually stimulating and enjoyable symposium. We hope that you can attend!

Please feel free to contact me with any questions.

Cheers, Conor O'Brien

Cresko Lab Center for Ecology & Evolutionary Biology University of Oregon cobrien1@uoregon.edu

cobrien1@uoregon.edu Center for Ecology & Evolutionary Biology University of Oregon Eugene, OR 97403

cobrien1@uoregon.edu

UOregon EvoDevo Symposium Apr4-6

UOregon.EvoDevo_Symposium.Apr4-6

This is a reminder that the registration deadline for the 2008 Evolution, Development and Genomics Symposium is March 1st!

WHERE: Eugene, Oregon at the Valley River Inn

WHEN: April 4 - 6, 2008.

KEYNOTE SPEAKERS: Jerry Coyne - University of Chicago Greg Wray - Duke University

SCHEDULED SPEAKERS: Detlev Arendt - European Molecular Biology Laboratory Bill Cresko - University of Oregon Bernie Degnan - University of Queensland Hopi Hoekstra - Harvard University Mark Martindale - University of Hawaii Daniel Meulemans - California Institute of Technology Leonie Moyle - Indiana University Fred Nijhout - Duke University Kevin Peterson - Dartmouth College Stephan Schneider - University of Oregon Mike Wade - Indiana University Deneen Wellik - University of Michigan

FURTHER INFORMATION: http://evodevo.uoregon.edu/symposium.html The symposium has been organized by the NSF IGERT-associated graduate students at the University of Oregon. We are very proud of the invited speakers and we look forward to an intellectually stimulating and enjoyable symposium. We hope that you can attend!

Please feel free to contact me with any questions.

Cheers, Conor O'Brien

Cresko Lab / Bradshaw-Holzapfel Lab Center for Ecology & Evolutionary Biology University of Oregon cobrien1@uoregon.edu

---

Valencia MarineBiodiversity Nov11-15

Dear all

There will be a *marine biogeography session* at the *World conference on marine biodiversity*, that will be held in Valencia(Spain), 11-15 november 2008.

We invite you to submit your proposals for oral presentations (15 minutes)and posters. Suggestions for invited speakers or name (and CV) of scientists from a developing country susceptible to be invited are welcome.

Abstracts for oral presentations, and poster titles are expected to be sent to me or Filipe by the 30 march 2008.

< http://www.marbef.org/worldconference/programme.php >

Marine biogeography and comparative phylogeography: joining paleontologists, taxonomists, ecologists and geneticists

This session aims at using the unique opportunityof an international marine biology congress to join scientists who usedistinct approaches for studying the geographical distribution of species and populations, in an ecological as well as a historical perspective. During the last ten years, an increasing number of studies of marine phylogeography were published. Data from molecular markers provide patterns which interpretation, in terms of historical anddemographical events, is now at the point of becoming extremely morepowerful. This is made possible by the availability of new analytical tools associated with the possibility of analysing multiple independent molecular markers for the same sample. However, without life history knowledge, ecological, taxonomical and paleontological/paleogeographical information, genetic data do not allow to assess the timing and causes of past dispersal, vicariance, expansion and extinction events. Joining these competences provides a powerful frame to predict the evolution of biodiversity in response to global change. The GeBIRM consortium (NoE MarBEF), joining marine phylogeography scientists studying several taxa across European seas, attempts to find patterns common across taxa. GeBIRM partners are strongly willing to exchange information with scientists from other fields.

Chairs_: Anne Chenuil <chenuil@univmed.fr> and Filipe Alberto <falberto@ualg.pt>

Thank you in advance for your contributions

Anne

– Anne CHENUIL

UMR 6540 CNRS DIMAR Centre d'Ocanologie de Marseille Station Marine d'Endoume Chemin de la Batterie des Lions 13007 MARSEILLE Tel.: +33 (0)4 91 04 16 17 Fax: +33 (0)4 91 04 16 35

<http://www.com.univ-mrs.fr/DIMAR/ >

Anne CHENUIL

PLEASE USE NOW MY NEW EMAIL ADDRESS : <anne.chenuil-maurel@univmed.fr> or <chenuil@univmed.fr>

THAT WILL REPLACE THE OLD ONE <chenuil@com.univ-mrs.fr>

UMR 6540 CNRS DIMAR Centre d'Ocanologie de Marseille Station Marine d'Endoume Chemin de la Batterie des Lions 13007 MARSEILLE Tel.: +33 (0)4 91 04 16 17 Fax: +33 (0)4 91 04 16 35

<http://www.com.univ-mrs.fr/DIMAR/ >

Anne CHENUIL <chenuil@com.univ-mrs.fr>

Valencia MarineBiodiversity Nov11-15 2

Dear all

'Feedback effects between the genetic components of biodiversity and ecosystem stability' will be one of the sessions proposed at the World conference on marine biodiversity in Valencia(Spain), 11-15 november 2008 (http://www.marbef.org/worldconference/).

Electronic submission of proposal are welcome for oral presentations(12 m. presentation + 3 m. discussion) and posters until April 1st (http://www.marbef.org/worldconference/registration.php).

If you have any question, please contact us (Sophie Arnaud-Haond <sarnaud@ifremer.fr> or Janine Olsen <j.l.olsen@rug.nl>)

Feedback effects between the genetic components of biodiversity and ecosystem stability

Chairs: Sophie Arnaud-Haond and Janine Olsen

Genetic diversity is one of three forms of biodiversity recognized by the IUCN as deserving conservation along with species and ecosystems. The genetic components of biodiversity substantially determine the ability of populations and species to adapt to environmental changes and are, in turn, affected by such change. The two parts of this circular interaction have to be understood: 1) How does genetic diversity influence, qualitatively and quantitatively, the ability of populations to adapt to sudden environmental changes; and 2) To what extent is the genetic architecture of populations and species modified by those processes?

Increasing human driven alteration of the environment and global change are the two main factors affecting ecosystem stability and resilience through species declines and distribution shifts. Using examples drawn from the intertidal, sub-tidal and pelagic biotas involving invertebrates, fish and macrophytes this symposium will gather presentations reporting results from in situ and manipulative field experiments that contrast stressed/non-stressed populations.

Some examples of invited aims: 1) genetic diversity and community diversity; 2) genetic diversity and population/community resistance or resilience; 3) rapid genetic adaptation to new environmental conditions; 4) genetic changes on impacted populations; 5) climate change and range shifts.

Sophie.Arnaud@ifremer.fr Sophie.Arnaud@ifremer.fr

YaleU Evolution in Health Feb21

The Yale Symposia on Evolution in Health and Disease will take place on February 21 and April 17, 2008, at the Yale School of Medicine, New Haven, Connecticut.

They will bring together leading researchers to discuss recent, exciting progress in applying evolutionary thinking to a broad range of issues in medical research and practice.

Please call this opportunity to the attention of faculty, postdoctoral fellows, graduate students, and advanced undergraduates by forwarding this email to them.

Those interested can get details and register at the symposium web site:

http://www.yale.edu/evomedsymposia Please note that there is a small fee for registration, payable online by credit card, and that this fee covers the costs of lunch and a reception that follows the talks in the evening, allowing the audience to meet and chat with the speakers. Your registering will give the organizers the accurate head count they need to order the food.

For the organizing committee,

Stephen C. Stearns Edward P. Bass Professor of Ecology and Evolutionary Biology

Other members of the organizing committee:

Durland Fish, Professor of Epidemiology and Public Health Charles Lockwood, Professor of Obstetrics, Gynecology, and Reproductive Sciences Stephen Malawista, Professor of Medicine Paul Turner, Associate Professor of Ecology and Evolutionary Biology

stephen.stearns@yale.edu stephen.stearns@yale.edu

GradStudentPositions

ImperialCollegeLondon EvolutionDiversity

NERC-funded PhD Project - Evolutionary dynamics in multi-species assemblages

Division of Biology, Imperial College London, Silwood Park Campus, UK Supervisor: Tim Barraclough

Environments change over a range of time-scales. Therefore, a key task for understanding the dynamics of living systems, and for predicting the impacts of human activity on those systems, is to understand how ecosystems respond to environmental change. However, most studies have considered ecological responses (changes in species abundance and distribution) and evolutionary responses (changing genotypes and adaptation) separately. For example, ecosystem studies normally assume that species attributes are fixed, under the assumption that evolution operates over much longer timescales than ecological processes. In contrast, evolutionary studies mostly consider single species or pairs of interacting species such as pathogens and hosts. Yet, most organisms live in species rich assemblages in which the characteristics and responses of co-occurring species could have a big impact on how each species in turn responds to a given environmental change.

This project will use theory, evolution experiments and field surveys of bacteria from the tree-holes of beech (1) to test key hypotheses concerning the interaction between evolutionary and ecological responses to environmental change. Does diversity inhibit evolution as predicted by recent theoretical models (2)? Can evolvability explain which species survive periods of environmental change? Do species coevolve according to Red Queen dynamics or is the abiotic environment a more important source of selection?

We're looking for a student with a good first degree and Masters degree (or equivalent experience). NERC funding is open to UK residents or EU nationals who have spent the last three years in the UK for education or employment (www.nerc.ac.uk/funding/-available/postgrad/eligibility.asp). We also invite applications from other students who have access to their own funding sources, for example scholarships through their home countries.

To apply, please reply by the 29th February, but preferably ASAP, sending a CV and a brief letter explaining why you are interested in this PhD to Tim Barraclough at t.barraclough@imperial.ac.uk.

References 1) Bell, T, JA Newman, BS Silverman, SL Turner, & AK Lilley.2005. The contribution of species richness and composition to bacterial services. Nature 436: 1157-1160 2) De Mazancourt C, E Johnson & TG Barraclough 2008. Biodiversity inhibits species' evolutionary responses to changing environments. Ecology Letters. In Press.

——— Dr. Timothy G. Barraclough, Reader in Evolutionary Biology, Imperial College London and Royal Botanic Gardens, Kew

——— Division of Biology Imperial College London Silwood Park Campus Ascot, Berkshire SL5 7PY, UK Telephone: +44 (0)20 7594 2247 Fax: +44 (0)20 7594 2339 Web-page: www.imperial.ac.uk/people/t.barraclough ——— **MSc course - Ecology, Evolution & Conservation** www3.imperial.ac.uk/naturalsciences/courses/pg/ls/ecology

———

t.barraclough@imperial.ac.uk

MacquarieU FishBrainEvolution

Evolution & Development of cerebral lateralisation: Fishes as model organisms

Macquarie University is offering a PhD scholarship to International or Australian student to work on the above research topic in the Department of Biological Sciences starting 2008. The research will be conducted under the supervision of Dr Culum Brown (http://www.bio.mq.edu.au/beef/) and will comprise a mixture of lab and field based experiments. The research is supported by the ARC.

The project: Cerebral lateralisation refers to the functional partitioning of information processing between the two hemispheres of the brain and is often overtly expressed as lateralised behavioural traits such as handedness. Previous research has focussed on the neural mechanisms behind cerebral lateralisation, yet surprisingly little is known about its function and the fitness benefits it may provide animals in their natural environments. This project will address these questions by examining the development and function of lateralisation using an evolutionary approach. The research will determine the relative costs and benefits associated with cerebral lateralisation in the day to day lives of fishes occupying a range of natural environments and, in doing so, identify its ecological correlates and phylogenetic constraints. This research will address fundamental questions pertaining to the evolution of cognition in vertebrates using Australian rainbowfish as a model.

The candidate: The student for this program of research will have a background in behavioural ecology or comparative psychology. Experience working with fishes is preferential. A first class honours degree (or equivalent) is required for enrolment in the PhD program at Macquarie University. Some evidence of publication is desirable.

Further reading: Brown et al (2007)Animal Behaviour, 74, 231-238. Brown (2005) Behavioural and Brain Sciences, 28(4), 591-592. Brown et al (2004) Proc. Roy. Soc. Lond. B (suppl), 271, S455-S457.

Contact: Dr Culum Brown cbrown@bio.mq.edu.au for more information

Culum Brown <culumbrown@yahoo.com>

MaxPlanckInst Ornithology EvolutionaryEcol

Max-Planck-Institute for Ornithology, Germany

We offer: PhD Position in Evolutionary and Physiological Ecology

Job description: We are looking for a PhD student (m/f) in evolutionary and physiological ecology. The PhD position is part of the project /Evolutionary consequences of an urbanizing world/ funded by the Volkswagen-Foundation within the research initiative /Evolutionary Biology/ (http://www.volkswagenstiftung.de/index.php?id=3&L=1 < http://www.volkswagenstiftung.de/index.php?id=3&L=1 >). In this project we study the urbanization of animals and its ecological and evolutionary consequences. The human impact in the global biosphere now controls many major facets of ecosystem function. One of the most striking man-made environmental changes is the existence and rapidly ongoing spread of urban areas. Human ecological impact has enormous evolutionary consequences as well and can greatly accelerate evolutionary change in the species around us. Anecdotal observations and recent studies suggest that urbanization does not only affect the overall species composition and certain aspects of the phenology but may change the behavior and physiology of individuals thriving in urban areas, as well. Using a combined field- and laboratory approach the aim of this PhD-project is to investigate whether urban life changes the general behavioral disposition (similar to the personality types in humans) and the underlying physiological coping mechanisms (e.g. stress physiology) of European blackbirds (/Turdus merula/). A common garden experiment will be used to examine the potential evolutionary consequences of the rapidly urbanizing world.

Requirements: We are looking for an enthusiastic person, who is interested in behavioral ecology, physiology (endocrinology) and evolution, with good organizational skills, able to work independently as well as in a team (field experience with birds is advantageous), who would like to take this unique opportunity to combine field with lab work at the well-equipped Max-Planck-Institute for Ornithology.

Appointment: Starting date is May 1 2008. The appointment will be on a temporary basis for a maximum of 4 years. The gross salary starts at approximately 1400,- per month depending on age and experience (TVöD 13/2, Stufe 1).

Information: Additional information about this appointment is available upon request from Jesko Partecke (partecke@orn.mpg.de <mailto:partecke@orn.mpg.de> or ++49-8152-373-117). More general information about the Max-Planck-Institute for Ornithology can be found on our website (http://orn.mpg.de/).

Application: Please send your application including complete curriculum vitae, a transcript of the university diplomas, a summary of the Master's (Diploma's) thesis and names of three referees to Dr. Jesko Partecke at the Dept. Behavioral Ecology and Evolutionary Genetics, Max-Planck-Institute for Ornithology, Von-der-Tannstr. 7, 82346 Andechs/Erling, Germany, or by email to partecke@orn.mpg.de <mailto:partecke@orn.mpg.de>. The closing date for application is March 31 2008, and the interviews will take place in the first week of April.

partecke@orn.mpg.de partecke@orn.mpg.de

MaxPlanck PlantMolEvol

Dear EvolDir members,

I have a 3 year PhD position opening this coming November. The work will be done in my group, the student will register at a German university to obtain the degree (the choice is open), and in addition the student will register with and follow the guidelines of the "International Max Planck Research School" in Jena (http://imprs.ice.mpg.de).

We are using population genetic approaches to understand the origin and evolution of apomixis (asexual reproduction through seed) in Boechera (wild relative of Arabidopsis) and in Hypericum perforatum (St John's Wort). We have recently finished a large project whereby we have identified over 6000 differentially expressed genes in the microdissected ovules of sexual and apomictic Boechera (using SuperSAGE and 454 sequencing), and we are performing similar experiments in Hypericum. As the projects in my group are all ongoing, the subject of the PhD work is thus not fixed and partially dependent on our present work.

If you are interested in applying for the position, please send me an email and we could discuss potential projects which also fall within your own interests. Experience with molecular biology methods (DNA and RNA work, microarrays, microsatellites, etc.) are not required, but would be an advantage.

I would also require a list of references (contacts) and CV so I can evaluate your application.

The IPK is a very well-equipped institute located about 2 hours Southwest of Berlin, in the foothills of the Harz mountains.

Best wishes, Tim

Dr. Tim Sharbel Apomixis Research Group Leader Dept. of Cytogenetics and Genome Analysis Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstraße 3, D-06466 Gatersleben Germany

Apomixis Group Webpage http://-www.ipk-gatersleben.de/Internet/Forschung/-CytogenetikGenomanalyse/Apo mixis

International Max Planck Research School (IMPRS) faculty member http://imprs.ice.mpg.de/people/-Faculty_Members.htm?mp=3D12 IPKWebpage www.ipk-gatersleben.de tel: +049 (0)39482 5608 fax: +049 (0)39482 5137

sharbel@ipk-gatersleben.de sharbel@ipk-gatersleben.de

NatlUIreland Geneflow

Highly motivated candidate sought for PhD position in Ireland.

Project title: Assessing the impact of stochastic geneflow events in potato crops.

The studentship will focus on investigating the impact of foraging pollinators and the spatial arrangement of plants on pollen flow between cultivated potato plots. Recent work by Teagasc Oak Park and NUI Maynooth has cast doubt on the accepted isolation distance for GM potato cultivars and highlighted the role both of foraging pollinators (particularly the pollen beetle M. aenus) and wind breaks in skewing expected inverse-exponential pollen and gene flow dispersal patterns between cultivar plots. Building on established molecular (microsatellite) and morphological marker protocols within the host research team, this project will utilise a variety of experimental planting strategies to investigate the dynamics of stochastic pollination events using conventional potato varieties. The project will combine molecular marker-based gene flow methods and spatial analysis of insect flight patterns.

The project will be supervised by Dr. Conor Meade at the Molecular Ecology Laboratory, NUI Maynooth in collaboration with Dr. Ewen Mullins, Teagasc Oak Park. The stipend for the position is 16,500 per annum, plus allowances for fees and travel. The start date for the position is June/July 2008. The National University of Ireland, Maynooth is located in a small university town 30km from Dublin and hosts one of the leading biological science clusters in Ireland. Applications, including a personal statement, an up to date CV, and the names and contact details of three academic referees should be sent to conor.v.meade at nuim.ie, or posted to:

Dr. Conor Meade Molecular Ecology Laboratory Department of Biology NUI Maynooth Co. Kildare, Ireland.

This project is funded by the Department of Agriculture and Food Research Stimulus Programme 2007-2010. NUI Maynooth is an equal opportunities employer.

Non-European Students: As this grant does not cover non-EU postgraduate fees unfortunately you must have access to your own funding to be considered for this position.

– Dr. Conor Meade Department of Biology National University of Ireland, Maynooth Co. Kildare, Ireland.

Tel. +353-1-708-6386 fax. +353-1-708-3845

http://www.may.ie/academic/biology/-cmgeneflow.shtml conor.v.meade@may.ie conor.v.meade@may.ie

Oslo 3 CenterEcolEvolSynthesis

3 Doctoral Research Fellow (PhD stipendiat)

3 POSITIONS AS DOCTORAL RESEARCH FELLOW (PhD stipendiat)

available at the Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo.

Candidates with background in molecular biology, organismal biology, theoretical biology and statistics are encouraged to apply.

The positions is available for a period of four years with 25% compulsory work.

The CEES is a centre for integrative biological research that has recently been awarded the status of a national centre of excellence by the Norwegian Research Council. The centre is an important part of the Department of Biology, and researchers at CEES collaborate with many of the faculty staff that are not directly connected to the centre. The purpose of the CEES is to combine competence from various fields of biology, molecular biology, bioinformatics and statistics in order to approach major, but still unresolved, scientific challenges. An overall goal is to achieve an increased understanding of how living organisms respond and adapt to environmental changes. The centre has funding to engage in cutting-edge research, it features a modern and well-equipped molecular lab facilitated for high-throughput sequencing, as well as a broad spectrum of field facilities. We are focusing both on development of new theoretical/ statistical methods/models and on diverse ecological and evolutionary questions in empirical systems ranging from microorganisms and plants to aquatic and terrestrial vertebrates. On-going research includes subjects such as gene flow and the early stages of diversification, selection and evolvability, evolutionary effects of human-altered ecological systems (e.g., harvesting and climate change) and genetic aspects of reproductive isolation. Read more about our research and possible research projects at http://www.cees.uio.no/about/vacancies/sff2008.html . We are looking for qualified and motivated individuals and offer broad training possibilities in biology and statistics within a stimulating academic environment.

The CEES provides an international and inspiring research environment. The centre is chaired by Nils Chr. Stenseth and currently employs 17 faculty members, 33 postdocs/researchers, 27 PhD students, 25 Master students, and 33 official collaborators. The PhD candidates will each have at least two supervisors and will be trained as part of a collaborative, inter-disciplinary research team.

A detailed plan for the dissertation work will be developed in collaboration with the supervisors within the first term of the program, 25% of the four years will be devoted to teaching-related duties. The fellowship period may be reduced within the framework of pertaining regulations based on previously held research fellowship positions. A good command of English is required of all students attending the University of Oslo. International students who are not native speakers of English must document their proficiency in English by taking one of the following internationally recognised tests: TOEFL - Test of English as a Foreign Language (test result of min. 600 PBT or 250 CTB or 100 IBT) or IELTS - International English Language Testing Service (test result of 7,0 or more)

Application for the PhD positions requires a Master's degree or equivalent experience.

The purpose of the fellowship is research training leading to the successful completion of a PhD degree.

Applicants should submit a letter of application describing their scientific experience and interests, a project description, at least 2 references/recommendation letters, curriculum vitae and four sets of copies of certificates.

Please consult our web page (http://www.cees.uio.no/about/vacancies/sff2008.html). and do not hesitate to contact any members or the centre leader Nils Chr. Stenseth (n.c.stenseth@bio.uio.no) for more information. When evaluating the application, emphasis will be given to the project description and the applicant's academic and personal prerequisites to carry out the project. Applicants may be called for an interview.

Appointment to a research fellowship is conditional upon admission to the Faculty's research training program. See the following URL for further details and guidelines for appointment to research fellowships at the University of Oslo: http://www.uio.no/admhb/reglhb/personal/tilsettingvitenskapelig/guidelinesresearchfellowship.xml Applications should be sent to the Faculty of Mathematics and Natural Sciences, (marked with the REF:NR.), Attn.: Senior Executive Officer Bente Schjoldager, P.O.Box 1032, 0315 OSLO, NORWAY.

— / —

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

StateUNewYorkAlbany EvolImmuneFunction

I am currently recruiting students to join my lab in the Department of Biological Sciences at the State University of New York at Albany. Highly motivated students interested in the evolutionary ecology of immune function and pathogen/host interactions are encouraged to apply. Experimental and genetic/genomic approaches are used in my lab to understand factors contributing to the evolutionary maintenance of disease susceptibility in Drosophila populations. Current projects include examining the causes and consequences of 'costs' of immunity, the evolution of cooperative virulence mechanisms, characterization and evolution of natural pathogens of Drosophila, and the evolution of sexual conflict, sex-biased gene expression, and implications for immune function. (See: http://www.albany.edu/faculty/kmckean/Site/McKean_Lab_Home.html)

U. Albany is committed to expanding graduate research opportunities in the evolutionary ecology of disease (EED). An interdisciplinary doctoral-research emphasis has recently been initiated, with participating faculty from the Department of Biological Sciences and the Department of Anthropology, as well as researchers from the Department of Biomedical Sciences at the Wadsworth School of Public Health. The EED program has sponsored seminar series, various journal clubs and discussion groups, as well as a formative curriculum relevant to this interesting and rapidly growing field of research. Information on this program and other participating faculty can be found here: http://www.albany.edu/biology/EED/index.html . U. Albany is located in Albany, the capitol of the state of New York. Centrally located between the Catskill and the Adirondack parks, the region provides abundant opportunities for outdoor recreation, and is also close to the metropolitan centers of New York City, Boston and Montreal.

Interested students should contact me directly (kmckean@albany.edu). More information concerning the application process can be found here: http://www.albany.edu/biology/gradprograms/index.html . Students accepted into the program are guaranteed support for 4 years. Review of applications will begin immediately for students starting in the Fall of 2008.

Please use the following links to find out more about: The Department: http://www.albany.edu/biology/ The Ecology and Evolutionary Biology Program: http://www.albany.edu/biology/gradprograms/EEB.html The University: http://www.albany.edu/ The City of Albany: http://www.albany.org/ Dr. Kurt A McKean Department of Biological Sciences 329BI SUNY at Albany 1400 Washington Ave. Albany, NY 12222 Phone (office): 518-442-4367 Fax: 518-442-4767 kmckean@albany.edu http://www.albany.edu/faculty/kmckean/Site/McKean_Lab_Home.html kmckean@albany.edu kmckean@albany.edu

TexasStateU FishEvolEcol

BEHAVIORAL ECOLOGY OF SAILFIN AND AMAZON MOLLIES

Teaching/Research Assistantship for M. S.

Applications are being sought for one student interested in pursuing an academic career studying various aspects of the behavior of sailfin and Amazon mollies starting no later than June 2008. Amazon mollies, Poecilia formosa, are a unisexual (all female) species of molly that are essentially sexual parasites as they require sperm from the closely related bisexual sailfin molly, P. latipinna but don^{1}t use it to fertilize their eggs. Conflict exists between male sailfin mollies that prefer to mate with conspecifics and the Amazon mollies that require matings with these males. We have three months of summer funding for a Research Assistant to work on some aspects of this system and can supply Instructional Assistant (teaching labs) for the fall and spring terms. See http://www.bio.txstate.edu/~gabor/gabor.htm for details about our lab and our research interests.

The Department of Biology offers a strong environment in evolutionary ecology as the basis for training in behavioral ecology. Students will benefit from interactions with other faculty interested in evolutionary questions such as: Jim Ott (Insect-plant interactions and ecological genetics), Noland Martin (Plant population genetics), and Chris Nice (Speciation in insects and phylogeography). We have both General Biology and Population and Conservation Biology MS programs available.

GRE (verbal and quantitative) scores of 1000 for MS, and a GPA of 2.75 are minimum requirements. For more information on admissions see http://www.bio.txstate.edu/grad/GradGuide.html . Please also see the Department of Biology (http://www.bio.txstate.edu/) and Texas State University (http://www.txstate.edu/) web sites for more information.

To apply for this job please send a statement of interest and a CV/resume of related research, coursework, GPA, GRE, and any other relevant experience by February 28, 2008 to Caitlin Gabor by email (gabor at txstate.edu). Reference letters for top candidates will be solicited at a later date. Applications will be reviewed as they come in, and may also be reviewed after the target date if the position has not been filled.

Caitlin Gabor <gabor@txstate.edu>

UCollegeLondon BiodiversitySpeciation

NERC-funded PhD studentship (available from Sept. 2008) - Biodiversity and speciation in African white-eyes (Aves: Zosterops)

Department of Biology, University College London. Supervisors: Drs Julia Day (UCL) and Robert Prys-Jones (CASE partner, Natural History Museum)

A prevalence of cryptic species in the tropics has recently been documented using DNA taxonomy (e.g. Hebert 2004). The genus Zosterops (white-eyes) is a species-rich lineage of birds, with high dispersal capabilities. Traditionally, species diagnosis has been based on colour and song, yet these birds have subtle plumage variation and as such are particularly cryptic. The African species complex is no exception, with recent mtDNA data (Warren et al. 2006) highlighting discordance between traditional taxonomy based on morphology and conclusions based on genetics. It currently remains unclear to what extent the numerous species and subspecies in mainland Africa are genetically distinct and how they are related to one another. The focus of this project will be to assess the overall biodiversity of mainland African Zosterops using a multigene phylogeny. The biogeographic history and diversification of this lineage will be examined through phylogenetic inference, with a strong focus on East African species, in order to test the influence of climate with regards to speciation (e.g. Kozack & Wiens 2007).

References: Kozak KH & Wiens JJ 2007. Proc. R. Soc. B. 274: 2995-3003; Hebert PND et al. 2004. PNAS: 101 14812-14817; Warren BH et al. 2006. Mol. Ecol. 15: 3769-3786.

Enquiries and applications (including covering letter, CV & contact details of two referees) to: Dr Julia Day: email: j.day@ucl.ac.uk. Ideally applicants will have a post-graduate qualification and will have a good understanding of molecular biology and phylogenetics. Applicants need to meet residency criteria of UK Research Councils. Closing date March 19th 2008.

Dr Julia J. Day Department of Biology University College London Darwin Building Gower Street London

WC1E 6BT

Tel: 0044 (0)20 7679 2660 - internal ext. 32660 Fax: +44 (0)20 7679 7096 Email j.day@ucl.ac.uk

Julia Day <j.day@ucl.ac.uk>

UCollegeLondon Evol of SexualTriats in Flies

Dear Evoldir members,

Please bring this advert to the attention of potential applicants.

Best wishes,

Kevin Fowler

Position available from Sept. 2008

BBSRC-funded PhD studentship - Molecular and cellular basis of sexual traits in stalk-eyed flies

Stalk-eyed fly research group, UCL (group leaders: Kevin Fowler, Hazel Smith & Andrew Pomiankowski)

In stalk-eyed flies the eyes are laterally displaced through expansion of the head capsule. Males of species such as Teleopsis dalmanni, have greatly exaggerated eyespan which is used as a sexual display. We are evaluating 'good genes' and 'direct benefit' models of sexual selection with particular focus on the relationships between male eyespan, male fertility and ejaculate quality.

Little is known about the molecular and cellular basis of sexual traits or the mechanisms by which correlations between them are generated. We have identified several genes expressed during the development of the eye-stalks and the male reproductive system. The student will characterise the developmental function and regulation of these genes. They will also exploit recently established transgenic protocols in T. dalmanni to perform functional studies using RNAi- mediated knockdown in transgenic flies.

Reference: Warren I & Smith H. 2007. Stalk-eyed flies (Diopsidae): modelling the evolution and development of an exaggerated sexual trait. BioEssays 29: 300-307. Additional background information available at http://www.ucl.ac.uk/stalkie/stalkie/research.html .

Enquiries and applications (including covering letter, CV & contact details of 2 referees) to: Dr Kevin Fowler: email: k.fowler@ucl.ac.uk. Applicants ought to have a good degree in a relevant subject. Interest and enthusiasm for evolutionary and developmental genetics would be beneficial. Applicants need to meet residency criteria of UK Research Councils. Closing date March 19th 2008.

ucbhkof@ucl.ac.uk

UEastAnglia LifeHistoryEvolution

NERC CASE PhD studentship, 2008

The making of a successful male: an integrated study of male reproductive success in a pest insect.

Start: October 2008.

Location: School of Biological Sciences, University of East Anglia, Norwich, NR47TJ and Oxitec Ltd, Abingdon, OX14 4RX.

Supervisors: Tracey Chapman, Matt Gage (http://www1.uea.ac.uk/cm/home/schools/sci/bio) and Luke Alphey (CASE partner) (http://www.oxitec.com/).

Aim: To take a broad approach to integrate the understanding of fundamental, evolutionarily-important traits in insect pest control.

Summary: Male reproductive success comprises pre- and post-mating components that are rarely subject to integrated study. This studentship will address this, and apply pure and applied research approaches to a pest of significant economic importance for which transgenic insect technology is well advanced. We have applied experimental evolution to the Mediterranean fruit fly (medfly) and now seek to determine reproductive fitness and divergence in male reproductive traits. We predict that males evolving under increased sexual competition will evolve more effective courtship and significantly higher post-mating competitiveness. This will reveal the traits that make a successful male medfly, and also whether pre- or post-mating traits are more strongly selected. The student will pursue this work at a novel molecular level by utilising the expertise of the CASE partner to conduct a targeted transcriptional analysis of important male reproductive proteins in the evolved lines. The project will extend into the applied domain by testing whether pre- and post-mating traits in evolved lines and in transgenics produced for a novel method of insect control, vary predictably in their response to the key environmental variable of nutritional status. The results will reveal potential trade-offs and the likely efficacy of the control strains under varying conditions.

Training: The student will join the Evolution, Ecology and Biodiversity Group at UEA (http://bioweb2.bio.uea.ac.uk/research/themes/-organismsenvironment/eeb.html). The School of Biological Sciences at UEA (http://www.uea.ac.uk/-bio/) provides an excellent Ph.D. research and training environment in a Grade 5 research department. The CASE partner Oxitec employs 24 research staff and is an exciting and challenging environment in which to work. It is at the forefront on a world-wide scale in the development of insect transgenesis. The link with Oxitec will therefore provide invaluable insight and experience for the student into work in the commercial world, and will offer technical expertise of the highest standard.

Eligibility: Applicants should have a strong degree in biological sciences or genetics. The full award is available only to residents of the UK, or those satisfying NERC eligibility requirements (http://www.nerc.ac.uk/funding/available/postgrad/-eligibility.asp). The award includes a standard NERC stipend supplemented by 1000GBP per annum by the CASE partner. The student will spend years 1 and 3 at UEA and year 2 with the CASE partner.

Applications: Informal enquiries to Tracey Chapman (tracey.chapman@uea.ac.uk). Formal applications should be made via the Faculty of Science Post-Graduate Office (scipg@uea.ac.uk), see http://-biobis.bio.uea.ac.uk/Resproject/how_to_apply.html for full details. There is no formal closing date and the position will remain open until filled.

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

UFlorida LifeHistoryEvolution

Are you interested in understanding the mechanisms underlying adaptive life history evolution and phenotypic plasticity? I am currently seeking graduate students to join our research group at the University of Florida. We take an integrative approach to understanding life history plasticity and life cycle evolution in insects that includes combining analyses of costs and benefits, organismal and cellular physiology, molecular genetics, and population genetics. Examples of possible projects include:

1) Mechanisms of phenotypic plasticity in insect hibernation/diapause (combining organismal biology, physiology, microarray genomics, and high-throughput proteomics)

2) Consequences of body size and nutrient storage on the costs and benefits of diapause.

3) Physiology of reproductive plasticity including identifying and testing candidate molecules and pathways for the control of reproductive timing and allotment and diapause.

4) Evolution of diapause strategies and the role of diapause strategies in diversification and speciation.

A possible project would be to study the physiological basis of adaptive shifts in life history timing in the apple maggot, Rhagoletis pomonella R. pomonella is a model system for studying the evolution of insect-host plant associations and sympatric speciation. (yes, the one from all the textbooks!) Historically, R. pomonella larvae fed on the fruits of hawthorns (Crataegus sp.) but radiated onto domesticated apple (Malus pumila) after its introduction to North America. In areas where both hosts occur, apple and hawthorn populations form genetically distinguishable host races. The timing and depth of diapause (overwintering dormancy) are critical life-history traits differentially adapting apple and hawthorn-infesting populations of R. pomonella to differences in the fruiting times of their respective hosts, generating reproductive isolation in the process. Physiological traits such as nutrient storage and metabolic rate affect diapause length and timing in other insects. We will test the hypothesis that adaptive differences in diapause length between the apple and hawthorn host races are mediated by energetics, particularly the accumulation of metabolic fuel prior to diapause and its utilization during diapause.

We will determine the functional importance of nutrient storage and metabolism to diapause length and timing for apple and hawthorn host races of R. pomonella in the field and lab; and then equate any observed difference in fuel storage, body size, and metabolic rate with allelic variation at loci that have diverged between the host races. Linking allele frequencies to diapause-associated nutrient storage and metabolism will provide the basis for our ultimate goal of identifying the specific physiological, biochemical, and genetic alterations underlying adaptive host plant-mediated life history evolution in the two R. pomonella host races.

Additional projects could include addressing similar questions about plasticity in diapause responses and the physiological basis of costs of diapause on reproduction and dispersal in flesh flies.

The student would join Dan Hahn's group in the Department of Entomology and Nematology at the University of Florida (http://danhahn.ifas.ufl.edu/) and will have significant interactions with Jeff Feder's group in the Department of Biological Sciences at Notre Dame (http://www.nd.edu/~biology/JeffreyFeder.shtml). Interdisciplinary training at UF could include coursework, research, and interactions across campus including the Department of Zoology, the USDA Center for Medical and Vetrinary Entomology, various departments in the medical school, and more. Tuition, health care, and a competitive salary are included.

Interested students please contact Dan Hahn (dahahn@ufl.edu) right away including a copy of your resume and a short statement of interests.

Daniel A. Hahn Assistant Professor Department of Entomology and Nematology The University of Florida P.O. Box 110620 Gainesville, Fl 32611-0620 dahahn@ifas.ufl.edu Phone: 352-392-1901x156 Fax: 352-392-0190

http://danhahn.ifas.ufl.edu/

dahahn@ufl.edu dahahn@ufl.edu

UGlasgow HostParasiteMetapopulation

PhD position: Host-parasite dynamics in a naturally fragmented landscape

Division of Environmental & Evolutionary Biology, University of Glasgow Supervisor: Roman Biek

The spatial and evolutionary dynamics of host-parasite systems are frequently discussed in the context of metapopulation theory. Yet, the applicability of metapopulation concepts to parasite dynamics in natural systems has rarely been demonstrated. This project will investigate the combined population dynamics of wild rodents and their diverse parasite community in a system of natural islands situated within Scotland's largest lake (Loch Lomond). Islands vary in size and in their degree of geographic isolation, providing an ideal situation to examine the effects of host population size and gene flow on parasite prevalence and distribution. The project will have a significant field component since multiple populations will need to be sampled by live-trapping several times a year.

How to apply: Applications are invited from students who either hold, or expect to obtain, a First or Upper Second class Honours degree, a Masters, or an equivalent degree in a relevant subject. Previous field experience would be highly advantageous. Please note that this studentship only covers fees for UK or EU students. The student will join a new and dynamic research group at the Division of Environmental & Evolutionary Biology at the Faculty of Biomedical and Life Science (http://www.gla.ac.uk:443/ibls/staff/staff.php?who=3DPeS~PA).

Please send a copy of your CV, together with a cover letter describing your interest in and suitability for this project, and the names and contact details of two academic referees to Dr. Roman Biek (from whom further details may be obtained): r.biek@bio.gla.ac.uk; Division of Environmental and Evolutionary Biology, Faculty of Biomedical and Life Sciences, Graham Kerr Building, University of Glasgow, Glasgow G12 8QQ. Emailed applications are encouraged.

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

r.biek@bio.gla.ac.uk r.biek@bio.gla.ac.uk

UGroningen EvolEcol

PhD position in climate change ecology for an evolutionary ecologist with firm field experience.

Climate change will have an enormous impact on ecosystems, leading to habitat changes and spectacular range shifts. For evolutionary ecologists it gives the exciting possibility to study evolutionary processes during a researchers lifetime. We have good evidence that birds so far adapted their breeding time insufficiently to climate change, resulting in some spectacular population declines. The crucial question is what individuals should do when they become locally maladapted.

In the Animal Ecology Group of the University of Groningen a four-year PhD-studentship is available to work on the effect of timing of avian breeding in relation to timing of food availability. The idea is that birds breeding in strongly seasonal habitats, like forests, should match their hatching date with the local peak in food availability. Due to climate change, this caterpillar food peak has advanced much stronger than the birds hatching date. Some bird species now raise their offspring too late to profit from the food peak, feeding their chicks apparently on a suboptimal diet. One interesting question is why some insects are so much better as food than other insects. Another important question is whether individuals V facing advanced spring phenology V would disperse to more northern areas, where the food peak is later. Such movements may speed up an evolutionary process because they may transport genes for earlier migration and earlier breeding to the north, on which selection can act. However, there may also be disadvantages of moving, because individuals may be locally adapted to their natal sites (food, parasites, etc.). The idea of this PhD project is that we address the seasonality of forest environments at different latitudes (including tree, insect and bird phenology), and how the birds exploit seasonality at these different sites. With an experimental translocation of birds to northern breeding latitudes, the candidate could experimentally test the fitness consequences of dispersal to more northern breeding areas. In an ongoing project we also aim to estimate long-distance dispersal over latitudes in response to climate change, with the use of stable isotopes.

For this project we are looking for a keen evolutionary ecologist with good field experience. The candidate is supposed to work both with birds and insects, so broad field ecological knowledge is a prerequisite. The candidate should be able to work independently in the field, but will be part of a highly collaborative group at the University of Groningen.

Conditions of employment

The University of Groningen offers a fellowship is for a period of four years which period should be finished with a Ph.D. examination. The stipend is £á 1583,- per month and will be adjusted to general price movements once a year. After one year, the performance of the candidate will be evaluated to decide whether there is sufficient progress to expect a successful completion of the PhD thesis within the remaining three years. A training programme is part of the agreement. You and your supervisor will make up a plan for the additional education and supervising that you specifically need.

The research will take place in the Ecology research group, being part of. the Centre for Ecological and Evolutionary Studies (CEES) The supervisor will be Dr. Christiaan Both. Applications should be done before 7 March 2008, and addressed to Christiaan Both by email. The appointment should start at 1 May 2008 to make use of the 2008 field season.

Information

Information about the position can be obtained from Christiaan Both (phone ++31)-50-3632235 or -3632040), c.both@rug.nl http://www.rug.nl/biologie/animalecol On CEES http://www.rug.nl/cees On the Faculty of Mathematics and Natural Sciences http://www.rug.nl/fwn C Both <c.both@rug.nl>

UHelsinki MathBiology

Postdoc and PhD positions in Mathematical Biology

The Mathematical Biology Group at the Department of Biological and Environmental Sciences, University of Helsinki, Finland (leader Dr. Otso Ovaskainen) is seeking outstanding, highly motivated candidates to join research projects at the interface between mathematics and ecology and evolutionary biology. Successful candidates may have their training either in mathematics or in biology, the main criteria being the potential to perform top-quality research. We anticipate hiring up to 4 postdoctoral researchers or Ph.D. students over the next 3 years. Research projects will be developed in conjunction with the interests of the successful candidates, focused on the following areas:

1. The roles of space and stochasticity in population dynamics
2. Metacommunity dynamics of wood-decaying fungi
3. Animal movement in heterogeneous environments
4. Bayesian approaches in evolutionary quantitative genetics

The PhD student positions are available for 4 years. The postdoc positions are for 1 year, with the possibility of a 2-year extension.

The Mathematical Biology group is part of the Metapopulation Research Group (leader prof. Ilkka Hanski), which is a Centre of Excellence in Research supported by the Academy of Finland. We offer an international research environment with excellent possibilities to cooperate with experts in mathematics, statistics, population biology, and evolutionary ecology. Salary and social benefits according to the University of Helsinki Salary system, around 2,300 /month for PhD students and 3,100 /month for post docs (the latter negotiable).

Applications including a short CV (max 3 pages), list of publications, and the e-mail addresses of two researchers willing to write a letter of reference should be sent to otso.ovaskainen@helsinki.fi with cc to tuuli.ojala@helsinki.fi; write either “postdoc position” or

" PhD student position" on the subject line. For more details on the research projects and on the application procedure, see http://www.helsinki.fi/science/-metapop/MBG/positions/index.htm Deadline for applications 14th March 2008, starting date 1st May 2008 (negotiable).

Otso Ovaskainen Academy Research Fellow Department of Biological and Environmental Sciences P.O. BOX 65 (Viikinkaari 1) 00014 University of Helsinki FINLAND

otso.ovaskainen@helsinki.fi otso.ovaskainen@helsinki.fi

UNottingham Evolution Vocal Communication

The following PhD research project is available in my group.

Vocal communication in goats (Capra hircus)

The research will examine vocal communication in this species from an evolutionary biology perspective. The work will largely be field-based and combine observations with recordings and playback experiments. Some experience of the equipment and software used in vocal communication research would be advantageous.

The deadline for applications is 05 February 2008. You should be available for interview in the UK during early March.

Unfortunately, full funding for this position is only available to UK citizens.

Please contact me via email if you are interested.

Alan

Dr. Alan McElligott The School of Biology Biology Building The University of Nottingham University Park Nottingham NG7 2RD UK amcellig1@yahoo.ie Tel + 44 (0) 115 951 3231 Fax + 44 (0) 115 951 3251 http://www.nottingham.ac.uk/biology/ Alan McElligott <amcellig1@yahoo.ie>

UOxford HumanPopGenetics

The Peopling of the Mediterranean: A Genetic Perspective

The studentship will focus on the investigation of the historical and pre-historical processes that have led to the human peopling of the Mediterranean region: the role played by the Last Glacial Maximum Refugia in the preservation of Palaeolithic diversity and the subsequent re-peopling of the continent; the demographic impact of the Neolithic revolution; the dissection of more recent historical events, as the Greek colonisation of Southern Italy and Sicily. The questions, defined within an archaeological and historical framework, will be investigated by the genetic analysis of populations living in the Mediterranean. Y chromosome and mtDNA data will be generated and analysed using a phylogeographic framework, to identify signatures of demographic changes and population admixture/migration. Data from uniparentally transmitted markers will be complemented by genome-scan analysis, to provide a refined picture of the specific demographic questions.

The studentship will combine molecular genetics techniques with population genetics analysis. In particular, the laboratory work will include STR analysis, sequencing and SNP genotyping. Data analysis will focus on phylogeoagraphy, lineage dating and population admixture.

To apply please complete the University application form (available from: www.admin.ox.ac.uk/gsp/) and include two references from

academic referees (follow procedure in Booklet A). Please submit two copies of the application forms and all supporting material to the Graduate Administrator, Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS (and NOT the address detailed on the application form). Closing date: 29 February 2008

The University of Oxford is an Equal Opportunities Employer.

Funding Notes: UK Research Council funded.

Competition Funded Project (European Students Only)

This research project is one of a number of projects at this institution. It is in competition for funding with one or more of these projects. Usually the project which receives the best applicant will be awarded the funding. The funding is available to citizens of a number of European countries (including the UK). In most cases this will include all EU nationals. However full funding may not be available to all applicants and you should read the full department and project details for further information.

Non-European Students: In most cases if you have the correct qualifications and access to your own funding, either from your home country or your own finances, your application to work with this supervisor will be considered.

Cristian Capelli <cristian.capelli@zoo.ox.ac.uk>

UppsalaU GenomeEvolution

PhD studentship in genome evolution

at the Department of Medical Biochemistry and Microbiology, Uppsala University. Available immediately.

We are looking for a highly motivated person interested in doing a PhD in comparative and population genomics. His/her project will focus on using computational approaches to study speciation and adaptation.

Summary: Newly sequenced genomes can allow us to answer longstanding questions about the genetic basis of speciation and adaptation. By using genomic comparisons between species, and analyzing patterns of genetic diversity within populations, we aim to understand how new species form, why some genes undergo accelerated evolution, and how genetic variation is affected by domestication.

We intend to develop new methods to compare variation in divergence time across two genomes, and to use them to study the timing and nature of the speciation process in humans and chimpanzees. We are also analyzing forces that cause rapid evolution of genes in humans, and whether genes with accelerated evolutionary rates could be implicated in human-specific adaptation. Finally, we are studying whether domestication has led to an accumulation of deleterious mutations in modern-day dogs.

The successful candidate will work on these projects under the supervision of Matthew Webster (Uppsala Univ.) and co-supervised by Kerstin Lindblad-Toh (Uppsala Univ. and Broad Institute of Harvard and MIT).

Qualifications: The person we are looking for ideally has a degree at Masters level (or equivalent) in biology, bioinformatics, mathematics, computer science or other relevant area. He/she should have strong interests in evolution, comparative genomics, population genetics, statistics and computer programming.

The main task of the student is to focus on his/her doctoral studies. Some additional work at the institution, involving teaching etc., can be part of the position (max 20%). Information on the PhD education programme in the department can be found at the following webpage: http://www.medfarm.uu.se/forskarutbildning/-index.shtml .

Further information: please contact Matthew Webster, matthew.webster@imbim.uu.se , tel: +46 18-471 4525. Union representatives are Anders Grundström, SACO-rådet, tel: +46 18-471 5380, Carin Söderhäll, TCO/ST, tel: +46 18-471 1996 and Stefan Djurström, SEKO, tel: +46 18-471 3315.

Please submit your application with a CV containing the names and email/phone numbers for two references and a one page personal letter where you describe yourself, your area of expertise and your interests, no later than March 20, 2008 to: Registrar, UFV-PA 2008/515, Box 256, 751 05 Uppsala, Sweden, fax +46 18-471 2000. If you apply by fax you will have to send the paper version as well at the latest a week after application deadline.

Matt Webster <matthew.webster@imbim.uu.se>

UStAndrews Bioinformatics

Dear all,

We are seeking applicants for a PhD position, as follows.

REGULATORY REGIONS IN THE HUMAN GENOME

Despite recent advances in genomics, our understanding of the processes regulating transcription remains poor. The project will use bioinformatic methods to predict transcription factor binding sites from sequence and microarray data. In collaboration with colleagues, predictions will be tested and refined by laboratory experiments. Joint-funded by the Biotechnology and Biological Sciences Research Council (BBSRC) and the Bute Medical School, University of St Andrews.

Supervisors:

Dr Daniel Barker, http://bio.st-andrews.ac.uk/staff/-db60.htm and Professor Richard Iggo, http://-medicine.st-andrews.ac.uk/staff/ri20.htm For further details (towards the bottom of the page) and application forms, see:

http://biology.st-andrews.ac.uk/-

projectSummaries.aspx?psry Important note on funding:

A successful candidate would receive funding to cover university fees and a stipend; some non-UK, EU applicants are only eligible for "fees-only" support. To be considered for financial support, applicants must meet the BBSRC residence requirements. Please see:

http://www.bbsrc.ac.uk/funding/studentships/-studentship_eligibility.pdf Applicants who do not meet the BBSRC residence criteria for PhD funding must provide evidence of full funding as part of their application.

Informal enquiries are welcome. Please contact Daniel Barker, email db60@st-andrews.ac.uk or tel. +44 (0)1334 463598.

Best regards,

Daniel

– Daniel Barker http://bio.st-andrews.ac.uk/-staff/db60.htm db60@st-andrews.ac.uk db60@st-andrews.ac.uk

UVermont ArthropodEvolution

Please help me in circulating this graduate assistantship with potential students. This position will start this fall at the University of Vermont. The application deadline is March 1.

Graduate Teaching Assistantship in Agroecology and Sustainable Pest Management (MS or PhD) ?C The University of Vermont, Department of Plant and Soil Sciences seeks a graduate assistant. Research themes include: 1) understanding the evolutionary origins of insect pests in agriculture, 2) how ecological and anthropogenic factors influence pest outbreaks in agroecosystems, and 3) using ecological information to improve sustainable pest management. Please click here for a full description of the position.

http://www.uvm.edu/%7Epss/?Page=pssdeptweb/-gradopps.htm&SM=graduate_menu.htm One of the my research interests are in the evolution of arthropods in agriculture. I am interested in the histories in insect pests, their population structure, and how they evolved to become pests. My research involve population genetics, ecology, and insect-plant interactions. Many of the most famous cases of rapid speciation have involved agricultural systems.

Closing date: March 1

Contact Information

Yolanda H. Chen, Assistant Professor Department of Plant & Soil Science

University of Vermont Email: *Yolanda.Chen@uvm.edu; ychen@irrialumni.org* Fax: 802-656-4656

Yolanda Chen <yfanslow@gmail.com>

WageningenU AvianEvolution

Dear all,

there are a few possibilities of master projects within the framework of ornithology, ecology and genetics which I would like to share with you. If anybody is interested in more information please check my webpage (http://www.reg.wur.nl/UK/Staff/Kraus/). Master projects will be carried out at the Resource Ecology Group (Prof. H.H.T. Prins) at Wageningen University (The Netherlands). This can also be changed according to other requirements, e.g., as studies carried out elsewhere than Wageningen. Here only the headings:

- Developing a SNP set in the mallard, Keywords: genomics; SNPs; in silico (starting Apr. - Jul. 2008) - The genetic link of mallards between North America and Europe, Keywords: molecular ecology; bird migration; SNPs; connectivity of gene pools; population genetics (starting Jun. - Aug. 2008) - The influence of migration strategy on body condition in mallards, Keywords: physiology; body condition; heterozygosity; stable isotopes (starting Oct. - Nov. 2008)

Starting dates, titels and also any content can be discussed freely. The information given is just to give you an impression the coarse ideas and opportunities

Looking forward to hearing from you, Robert

Robert H. Kraus PhD student Wageningen University Resource Ecology Group Droevendaalsesteeg 3a 'Lumen' Building, Number 100 6708 PB Wageningen The Netherlands

Phone +31 317 483530 Fax +31 317 419000 Email robert.kraus@wur.nl http://www.reg.wur.nl/-UK/Staff/Kraus/ robert.kraus@wur.nl

WageningenU WildBoarPopGenetics

PhD researcher 'Wild Boar Population Genetics' (Gelderland), 38 hours per week Wageningen University and Researchcentre

Job description

The aim of this project is to analyze the effects of the population structure of the European Wild Boar on the prevalence and transmission of parasites, as well as the selective effects on immune related genes. The Wild Boar is increasing its range, reaching levels previously unrecorded. This has already contributed to spread of many contagious diseases. This can negatively affect the fitness and trophy quality of game species, public health, livestock health, and the conservation of endangered species.

Wild Boar populations throughout Europe will be sampled that differ with respect to population size and density, connectivity and migration with other populations, and parasite prevalence. One will try to relate various classes of immune related genes to individual fitness, estimated by morphometric and reproductive characteristics and the presence of parasites. Parasite exposure will be estimated amongst others by antibody prevalence. Additionally, comparisons will be made with neutral genetic markers.

Requirements

University Graduate

You have a university Master's degree with specialization in animal ecology, genetics or population genetics.

Organization

Wageningen University and Researchcentre Resource Ecology Group

De Resource Ecology Group verricht onderzoek en onderwijs op het gebied van populatie-ecologie van grote herbivoren, met speciale aandacht voor de interactie tussen herbivoren en de vegetatie.

De voornaamste onderzoeksterreinen zijn savannes, graslanden in tropische en gematigde gebieden.

Het meeste onderzoek wordt uitgevoerd door de postdocs en PhD-studenten, ondersteund door de staf. Resultaten hebben betrekking op de natuurbescherming en beheer.

Conditions of employment

Estimated maximum salary per month: eur 1500 - 2000

Employment basis: Temporary for specified period

Duration of the contract: 1 year

Maximum hours per week: 38

Additional conditions of employment:

It concerns a vacancy for four years; appointment will initially take place for a period of one year to evaluate suitability; if suitability is determined to be adequate, the employment contract will be extended for the remaining duration of the PhD programme. Maximum salary amount is 1933 Euro's a month (gross), scale promovendi, based on a fulltime employment.

Additional Information

Additional information about the vacancy can be obtained from:

Dr W.F. van Hooft

Telephone number: 0317-484320

E-mail address: pim.vanhooft@wur.nl

Or additional information can be obtained through one of the following links.

* About the department

Application

You can apply for this job before 01-03-2008 by sending your application to:

Wageningen UR, afd HRM, departement Omgevingswetenschappen

C. Linders

Postbus 47

6700 AA wageningen

E-mail address: vacatures.dow@wur.nl

You can apply for this job before 1-03-2008 by sending your application, mentioning the referencenumber, preferably to: vacatures.dow@wur.nl or by post to Wageningen UR, dept. HRM Environmental Sciences, towards Clim Linders, P.O. box 47, 6700 AA Wageningen.

When applying for this job always mention the vacancy number DOW-08-REG-06-J.

The short URL code for this job opening is: 00363-2415.

You can use this as a direct link to the job by adding the code to the URL www.academictransfer.org/

Dr. Pim van Hooft

Lecturer

Wageningen University

Resource Ecology Group

Droevendaalsesteeg 3a 6708 PB Wageningen The Netherlands

E-mail: pim.vanhooft@wur.nl <mailto:pim.vanhooft@wur.nl>

Tel: +31-317-484320

Fax: +31-317-484845

Building 'Lumen', building number 100 (central wing, first floor), room 1.320

Internal post: Bode number 95

Pim.vanHooft@wur.nl Pim.vanHooft@wur.nl

Jobs

CornellU BioinformaticsProgrammer

Bioinformatics Programmer/Analyst Position at Cornell University

The Department of Biological Statistics and Computational Biology at Cornell University seeks a highly motivated individual to develop software tools, databases, and web resources to support the research group of Dr. Adam Siepel. Responsibilities of the position include but are not limited to: (1) Developing, maintaining, and supporting a software package called PHAST (PHylogenetic Analysis with Space/Time models) for phylogenetic analysis and comparative genomics; (2) Assisting in genome-wide comparative genomic analyses, by developing scripts and utilities, running analyses on large compute clusters, and integrating, organizing, and analyzing program output; (3) Maintaining and improving a local mirror of the UCSC Genome Browser; and (4) Developing and maintaining the general software and database infrastructure of the lab.

Minimum qualifications include: Bachelor's degree in computer science, engineering, or a related field, and 2-3 years of experience in software development. Experience with C/C++. Basic knowledge of algorithms, data structures, and object-oriented programming. Experience in a Unix/Linux environment, including proficiency in shell scripting, and scripting in a language such as Perl or Python. Experience with relational databases (mysql or similar). Basic knowledge of web programming (HTML). Strong interpersonal skills and ability to work as part of a diverse team. Strong oral and written communication skills. Ability to manage multiple projects in a dynamic environment with changing priorities. Ability to work independently and solve problems as they arise. Interest in molecular biology, genetics, and evolution, and willingness to learn concepts and terminology from these fields as needed. Some experience in bioinformatics, statistics, or machine learning is desirable but not required.

The Siepel Lab does interdisciplinary research at the interface of computer science, statistics, and genomics, including both development of novel computational methods and analysis of the latest genome-wide data sets. Recent research has focused on the discovery of novel human genes, the identification of functionally important noncoding elements in mammalian genomes, and the detection of genomic sequences that are potentially responsible for key differences between humans and other primates. This work depends critically on the organization and management of very large data sets, on the development and maintenance of reliable software tools, and on the efficient implementation of algorithms for genome-wide analyses. The group is dynamic and interactive, and most projects require close teamwork among students, postdocs, and staff. The candidate will have opportunities to contribute to scientific publications, and to expand his or her knowledge of evolutionary genomics, computational statistics, machine learning, and other relevant scientific areas.

Term: This is a 2-year position with possible extension.

Salary: A competitive salary commensurate with experience and skills will be offerred, and a full benefits plan is available.

For the complete job ad, with instructions for applying, see https://cornellu.taleo.net/servlets/CareerSection?art_ip_action=FlowDispatcher&ctx=1&flowTypeNo=13&pageSeq=2&art_servlet_language=en&reqNo=123569&csNo=10164 For more information about the Siepel Lab, see http://compgen.bscb.cornell.edu/~acs/ Adam Siepel <acs4@cornell.edu>

CostaRica EvolTropicalStudies

Brian,

An evolutionary biologist would be perfect for the job. I wrote that someone with a Ph.D. in evolutionary biology it is qualified for the job. Please let me know if I have to make it more specific

Thanks vivian

Resident Professor for the Undergraduate Semester Abroad Program

Organization for Tropical Studies

The Organization for Tropical Studies (OTS) is seeking applicants for the position of Resident Professor with the OTS-Duke University Undergraduate Semester Abroad Program in Costa Rica. This is a field-based program designed to provide undergraduate students with outstanding training in tropical ecology, field research, environmental science and policy, and Spanish language and culture. Successful applicants will work closely with the Education Director, program coordinator and other Resident Professors in curriculum design and implementation, and will be responsible for team teaching 3 field-based courses in tropical ecology, environmental science and policy, and field research. The field research course includes the supervision of student independent projects, and emphasizes hypothesis testing. The position is based in Costa Rica, and requires a commitment to 8-9 weeks in the field and several weeks in the office during each semester.

This is a full-time appointment beginning August 15, 2008. At least a one-year commitment is required.

Qualifications:

Ph.D. in biology, evolutionary biology, ecology, or a related field.

Professional research experience in the tropics.

A strong interest in team teaching and interdisciplinary collaboration.

Experience in field-based education and hands-on experiential teaching a plus.

Excellent communication skills.

Bilingual (Spanish/English).

Ability to work a flexible schedule and to spend 9+ weeks, twice a year, living with students and other faculty at field stations.

Anticipated Start Date:

August 15, 2008

Application deadline:

April 1st, 2008

To apply:

Submit cover letter, curriculum vitae with list of 3 references, statement of teaching philosophy and statement of research interests to the Undergraduate Program Coordinator, Vivian Mendez. Electronic applications are preferred and may be submitted online via the OTS website (www.ots.ac.cr < http://www.ots.ac.cr/ >). Web-based submissions require that all application materials be in one word or pdf file. Email submissions may be made to vmendez@ots.ac.cr.

OTS is an equal opportunity and affirmative action employer.

Vivian Mendez <vmendez@ots.ac.cr>

GenevaU EvolutionaryAnthropology

The Faculty of Sciences of the University of Geneva (Switzerland) has an opening for a position as

Full or Associate professor (professeur ordinaire ou adjoint) in Evolutionary Anthropology

Full-time appointment. Teaching will be in French. The successful candidate is expected to conduct a research group. Anthropological research in biometry, epidemiology or demography of present and / or past human populations will be considered with particular attention ; social anthropology is excluded. The position is also opened for Assistant Professors (Tenure Track).

DEGREE REQUIREMENT : Ph.D or equivalent.

STARTING DATE : August 1st, 2008, or as agreed

Applicants with relevant experience in research and teaching should send their application before April 11, 2008 to : Dean of The Faculty of Sciences, Quai E.-Ansermet 30, CH-1211 Geneve 4, Switzerland, where further information concerning the job description and working conditions may be obtained.

Applications from women are particularly welcome.

For more information, please contact the Department of anthropology and ecology at +41 22 379 69 67. – Prof. Alicia Sanchez-Mazas Laboratory of Anthropology, Genetics and Peopling history (AGP) Department of Anthropology and Ecology University of Geneva 12, rue Gustave-Revilliod Case postale, 1211 Geneve 4, Switzerland Tel. +41 (0)22 379 69 84 Fax +41 (0)22 379 31 94 http://agp.unige.ch/en/ Alicia.Sanchez-Mazas@anthro.unige.ch

---

ImperialCollegeLondon ShortResearchProject WildlifeEpidemiology

ImperialCollegeLondon.ShortResearchProject.WildlifeEpidemiology

Summer Research Assistant Based at Imperial College London and the University of Aberdeen, United Kingdom

Temporal and Spatial Dynamics of a Vector-borne Wildlife Disease System

Fixed term: 4 months Start date: 1 May 2008 (slightly flexible) Salary: £1851 per month

We are seeking a graduate or higher level researcher with good quantitative skills to join a 4 month project starting May 2008 to investigate the epidemiology of Louping Ill (LI), a tick-borne wildlife disease affecting northern areas of the United Kingdom. The LI system involves a variety of hosts, including red grouse, mountain hares, sheep and red deer, and is of economic importance to sheep and grouse moor management. This project aims to develop models of the temporal and spatial dynamics of LI transmission between tick vectors and the hosts of the disease, exploring the impact of seasonality and host density on LI epidemiology. The project would be suitable as the placement project for an appropriate Masters course.

The successful applicant will have an interest in ecology and epidemiology along with programming skills (for example in C++, Mathematica or Matlab) and ability to analyse differential equations. The applicant will be based primarily at the Centre for Population Biology, Silwood Park Campus, Imperial College London, and will have opportunities to visit the University of Aberdeen.

Applications (including CV and cover letter) or enquiries should be sent to Dr Penelope Hancock (p.hancock@imperial.ac.uk) or Dr Steve Palmer (s.palmer@abdn.ac.uk).

Websites:

http://www3.imperial.ac.uk/cpb http://www.aces.ac.uk/projects/ http://www3.imperial.ac.uk/people/p.hancock http://www.abdn.ac.uk/biologicalsci/staff/details.php?id=3Ds.palmer&fit

Closing date: 20th March 2008

p.hancock@imperial.ac.uk p.hancock@imperial.ac.uk

InstZooLondon Tech MHCMolEvol

INSTITUTE OF ZOOLOGY ZOOLOGICAL SOCIETY OF LONDON

RESEARCH TECHNICIAN POST MOLECULAR ECOLOGY Starting salary £18.978 to £20,827 (including London Weighting) Dependent on relevant experience

Applications are invited for a post as research technician on a NERC-funded project to investigate the evolution of major histocompatibility genes in divergent morphs of Arctic charr in relation to parasite load. Experience in molecular biology techniques, particularly DNA cloning, sequencing and microsatellite genotyping, is essential. Also, previous experience in morphometric techniques and/or parasite identification will be advantageous.

The post is for 20 months and is available from 1st April 2008.

For informal enquiries contact: Dr W.C. Jordan (bill.jordan@ioz.ac.uk Tel: 020 7449 6631).

Applications, with a current CV and names and full contact details of three referees, should be sent to Human Resources, Zoological Society of London, Regent's Park, London NW1 4RY, UK (email HR@zsl.org), from whom further details are available.

CLOSING DATE: 11th March 2008

Read about the Institute of Zoology on http://www.zoo.cam.ac.uk/ioz/ and ZSL's work on http://www.zsl.org REGISTERED CHARITY NO. 208728

w.jordan@ucl.ac.uk w.jordan@ucl.ac.uk

LosAngeles NHM CuratorialAssist

The Natural History Museum of Los Angeles County is inviting applications for the position of Curatorial Assistant in our Marine Biodiversity Processing Center. We seek an individual with expertise in crustaceans, mollusks, echinoderms, or other marine invertebrate groups. Our research collections are used in a broad variety of systematic and evolutionary studies. This position will complement existing staff and reflect the institution's commitment to the Center. The successful individual will assist with curation, sorting, databasing, and physical integration of collections into the museums marine invertebrate collections. Applicant should have a B.S. degree in Biology, at least one year of experience with one of the taxonomic groups noted above and knowledge of contemporary museum collection and specimen conservation techniques. Good oral and written communication skills are essential and experience with collection databasing is desirable. Learn more about the Museum by visiting http://www.nhm.org. For an overview of the Center visit http://collections.nhm.org . This position is full-time and available immediately. Salary: $36,500/year plus full benefits.

Please send your curriculum vitae, name and contact information for three referees, and a cover letter that describes your curatorial experience to:

Regina Wetzer, PhD. Director, Marine Biodiversity Processing Center Natural History Museum of Los Angeles County 900 Exposition Blvd., Los Angeles, CA 90007 rwetzer@nhm.org

Regina Wetzer <rwetzer@atiniui.nhm.org>

Marseille EvolutionaryBiology

An assistant professor position in Evolutionary Biology (concepts and bioinformatic) will be open this year the Laboratoire Evolution biologique et Modï¿½lisation lab . For more information contact Pierre Pontarotti

UMR 6632 Universite de Aix Marseille/CNRS . Laboratoire Evolution biologique et Modelisation , case 19 3 place Victor Hugo 13331 Marseille Cedex 03 France http://sites.univ-provence.fr/evol/ Pierre.Pontarotti@univ-provence.fr

MichiganStateU GeneticalGenomics

Genetical Genomics postdoctoral position in the Department of Animal Science, Michigan State University

Applications are invited for a one-year postdoctoral position in genetical genomics. The successful applicant can reside either at the University of Wisconsin under the supervision of Dr. Guilherme Rosa, Department of Dairy Science or at Michigan State University under the supervision of Dr. Robert Tempelman in the Department of Animal Science. The successful applicant will participate in a USDA funded research project involving 960 F2 pigs generated from a Duroc x Pietrain resource population established at Michigan State University. The research project has a rich and comprehensive database containing growth, carcass merit, meat quality and sensory phenotypes as well as genetic marker data on F0, F1 and F2 pigs. In addition, gene expression microarray data comparing within-litter phenotypic extremes for loin muscle area and backfat based on a selective phenotyping experimental design is available. Excellent training in statistical genetics is required, particularly with respect to quantitative trait loci (QTL) analysis. Experience with multiple trait QTL analysis and linkage disequilibrium mapping is highly desired. The ultimate objectives of the project will be to estimate QTL effects for gene expression jointly with observed phenotypes in an effort to discover new candidate genes for growth, carcass merit and meat quality, as well as to infer upon potential regulatory pathways. The successful candidate is then expected to assist in the development of statistical methodologies that integrate genetical genomics information into schemes used for improving livestock populations as well as publish their findings in a timely fashion. Applications will be accepted until the position is filled. This position can be filled immediately. Interested candidates are encouraged to email their curriculum vitae and names of two references jointly to Dr. Robert Tempelman (tempelma@msu.edu) and Dr. Guilherme Rosa (grosa@wisc.edu).

tempelma@msu.edu tempelma@msu.edu

NESCent BioinformaticsProgrammer

The National Evolutionary Synthesis Center (NESCent) (http:// nescent.org) seeks a highly motivated Bioinformatics Programmer responsible for design, implementation, and maintenance of databases and surrounding software used by both evolutionary biology researchers and educators, and by NESCent administration. The position is within the Center's informatics team.

NESCent's Informatics program (http://informatics.nescent.org) offers a vibrant environment with ample opportunities to interact and work closely with a wide array of researchers in evolutionary biology and related disciplines. Aside from supporting the IT needs of the Center administration, the group provides visiting and resident scientists with cutting-edge electronic collaboration infrastructure and software engineering capabilities ranging from modern multi-tiered applications with highly interactive user interfaces to sound data models with integrated semantics. In addition, the Center's Informatics program pursues an ambitious agenda of cyberinfrastructure initiatives to promote interoperability, data and service integration, and open development among the evolutionary biology community. Above all, we are enthusiastic about our work, the stimulating atmosphere at the Center, and the potential of informatics to enable more and better science.

Job Description:

The incumbent will work within the Center's informatics team with other software developers and system support staff, and collaborate with scientists visiting or resident at the Center as well as other Center staff. The responsibilities of the job range from designing data models, to architecting and implementing server-side middleware, service-oriented APIs, and managing data flow. The incumbent will gather requirements from scientists, Center staff, and collaborating developers and translate these into functional and technical specifications; analyze, design, develop, maintain, document, and test new and existing database schemas, object models, APIs, and software; use and contribute to existing and emerging standards; create technical documentation, present work at scientific meetings, and contribute to scientific publications. The incumbent will also collaborate with the Assistant Director of Informatics and Center Leadership to advise of priorities, problems and proposed solutions; to assist in setting priorities and goals for scientific database support, to structure development with respect to specific timelines and milestones, and to make decisions required to create and deploy database applications.

Required Qualifications:

* Bachelor's degree (M.S. or Ph.D. preferred) in biology, computer science, or related field. Four or more years of significant experience in designing and implementing database and database- interfacing technology, or an equivalent combination of relevant educa-

tion and experience. * Experienced in the use of major relational database management systems (preferably PostgreSQL). * Knowledge of relational data modeling, and proven experience with translating domain models into normalized relational schemas. * Thorough command of SQL, including DDL, and understanding of advanced elements of SQL (e.g., sub-queries, views, integrity enforcement) * Knowledge of and experience with object-relational mapping technologies, preferably in Java (e.g., CMP, JDO, Hibernate). Demonstrated ability to architect, design, and implement object models and middleware on top of databases (preferably in Java). * Proven team orientation, and outstanding interpersonal and communication skills.

Preferred Qualifications:

The ideal candidate has a rigorous background in software engineering best practices, and has demonstrated the ability to independently and collaboratively manage the entire life cycle of projects involving multiple scientific stakeholders. In addition, the ideal candidate has demonstrated deep knowledge as well as current awareness in emerging trends in one or more of the following areas: * Advanced database technologies such as SQL server-side programming (e.g., database triggers, PL/SQL, PL/pgSQL) and data warehousing (OLAP, Data Marts). * Elements of the semantic web (such as DL, RDF, OWL, ontologies, reasoning, software agents) and service-oriented software architecture (SOA) (such as Web Services, SOAP, REST, RMI). * Evolutionary Biology or a related field.

The demonstrated ability to contribute to scholarly publications is highly desirable.

Benefits:

NESCent offers comprehensive benefits (health, dental, vision, leave, 403b, etc) and a competitive salary commensurate with qualifications and experience.

How to Apply:

Please send cover letter, resume, and the contact information for

— / —

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 SummerTraining Bioinformatics

Summer Training Opportunity for Graduate Students or Postdocs in Data Curation and Informatics

The Phenoscape project (http://phenoscape.org) is a pioneering effort in the use of ontologies to relate traditional character descriptions from fish evolutionary studies to zebrafish genetics and mutant phenotypes.

We have summer funding for graduate students and postdocs interested in gaining expertise in informatics and the application of ontologies to evolutionary, anatomical, developmental, and genetic data. Opportunities are available to work with our personnel in data curation using ontologies (at the Academy of Natural Sciences, Philadelphia, or at the University of South Dakota) or in database and application programming (at the National Evolutionary Synthesis Center, http://nescent.org).

Stipends of $5,000 will be given to participating students to cover travel, room and board for 12 weeks (a shorter term of 10 weeks is possible). To apply, please provide the information below via email (in Word or PDF format) to Dr. Paula Mabee (pmabee@usd.edu) before March 15, 2008. Funding decisions will be made by April 1.

Required information: 1. Cover sheet with your name, current status (grad or postdoc), institutional affiliation and research supervisor, dates of proposed exchange, and a summary (150 word maximum) describing the relevance of the internship opportunity to your research.

2. A brief description (1 page maximum) of your current research, its goals, and an indication of where you are in your research time line. Please provide some details of the type of training that you already have experience with (e.g., morphology, paleontology, molecular/developmental biology, informatics, computer science).

3. A curriculum vitae no longer than 2 pages listing educational background (including relevant coursework), work experience, publications, and presentations.

4. A letter of recommendation from your advisor, and the names and contact information of two other references.

Reporting Requirement: Recipients will be expected to submit a 1-page report describing the accomplishments and value of the training within one month after the end of the internship.

Further inquiries about the position may be directed to Dr. Mabee by email, or by phone at (605) 677-6171.

NESCent, the Academy of Natural Sciences, and the University of South Dakota are equal opportunity employers. Applications from women and underrepresented minorities are specifically encouraged. PhenoScape is committed to releasing all software code as open source.

– Hilmar Lapp -:- NESCent -:- informatics.nescent.org :

hlapp@nescent.org

NorthCarolinaStateU HeadDeptGenetics

Job: NCSU Dept Head Genetics

The Department of Genetics at North Carolina State University seeks applications for the position of Head of the Department of Genetics . This is an outstanding opportunity for an established scientist who has a broad appreciation for the role of a basic science department within a land grant university. The successful candidate will 1) provide dynamic and innovative leadership in graduate and undergraduate education,

2) foster a positive environment conducive to high quality basic research, 3) conduct an active, externally funded research program, and 4) be a strong and effective voice for the department within the University and across the broader scientific community.

The Department of Genetics is one of five basic science departments within the College of Agriculture and Life Sciences at NCSU. The Department is approaching its fiftieth year and has long been recognized internationally for its faculty strengths in quantitative, population, evolutionary, molecular and developmental genetics. Traditionally strong in research and graduate education, we have held graduate training grants in plant genetics and quantitative genetics, and have trained a large number of graduates who have gone on to highly successful careers in academia, industry and government. Currently the Department is strengthening its commitment to undergraduate education, including developing new curricula and establishing an undergraduate major in Genetics.

The Department is comprised of a core of 20 full-time faculty members, several of whom have international reputations in evolutionary and molecular genetics. The Department is among the best-funded departments in the College and over the past 5 years, our faculty has received millions of dollars in research funds from NIH, NSF, USDA, and private foundations. Moreover, the Department provides a key integrative role at NCSU and we have an additional 19 associate and adjunct members. Associate faculty members have their tenure home in other departments, including Forestry , Food Science , Plant Biology , Plant Pathology , Entomology , Molecular and Structural Biochemistry , Zoology , Crop Science and Animal Science , but may teach courses and train graduate students within Genetics. This arrangement provides for a highly diverse and dynamic teaching and research faculty.

The Genetics Department is housed in a newly-remodeled building with ample space for research and teaching. We have a well-developed genomics and bioinformatics infrastructure and are next door to a large vertebrate animal research facility and a phytotron for environmentally controlled experiments. In addition, there are ample greenhouse and experimental farm facilities.

North Carolina State University, together with the University of North Carolina at Chapel Hill and Duke University, form a strong base for the world-famous Research Triangle Park. Our relationships with RTP provide numerous opportunities for research and training interactions, as well as a viable source of employment for our graduates.

The position announcement can be viewed in its entirety on the Department of Genetics Web site: http://www.cals.ncsu.edu/genetics/ . Applicants should submit a letter of interest, curriculum vitae, statement of their philosophy/vision as a Department Head to include research and teaching functions, and 3 - 5 representative publications electronically to http://ncsu.edu/jobs , position number 01-64-0714.

Nominations and questions concerning this position should be sent to Damian Shea, Chair Genetics Head Search Committee, Department of Zoology, Campus Box 7617, NC State University, Raleigh, NC 27695-7617 or via email to d_shea@ncsu.edu .

Review of applications will begin 15 February 2008 and continue until the position is filled.

fred_gould@ncsu.edu fred_gould@ncsu.edu

RoyalHolloway 5 EvolutionaryBiology

Royal Holloway is seeking to fill five permanent positions in Biology in various areas. For those with an evolution interest the senior lecturer/reader position in biological sciences (equivalent to associate professor) is probably most relevant. We are seeking to employ in someone in the area of organismal biology/plant biology area, and in are particularly in interested in the areas highlighted.

Feel free to contact me if you need further information on this position

Vincent Jansen (vincent.jansen@rhul.ac.uk)

ROYAL HOLLOWAY SCHOOL OF BIOLOGICAL SCIENCES

The School of Biological Sciences (< http://www.rhul.ac.uk/biological-sciences >) constitutes 3 highly-integrated and dynamic research centres: Biomedical Sciences, Plant Molecular Sciences; and Ecology, Evolution & Behaviour. In addition, staff are associated with Faculty-based inter-departmental research centres in Computational Biology, Neuroscience and Nanobiotechnology. The School holds grade 5 research assessment (2001 RAE) status, and a maximum grade 24 teaching quality assessment (QAA) rating. Research and teaching activities are underpinned by technologies spanning functional genomics, metabolomics, molecular genetics, microbiology, gene therapeutics, computational & systems biology, advanced cell biology, model organism analysis, population studies, ecology, evolutionary biology, mathematical biology and advanced microscopy facilities.

Applications are invited for five academic posts in the School.

Lecturers (2) in Biomedical Sciences (Ref KB/4926)

Applications in the fields of neurosciences, cell signalling, molecular microbiology/parasitology, infection and immunity or epidemiology are especially welcome.

Lecturer in Chemical Biology (Ref KB/4927)

Candidates should have a strong background in chemistry to contribute to bioscience chemistry teaching and research experience especially in the fields of medicinal chemistry, nutraceuticals, natural product chemistry or cell signalling.

Professor/Reader in Neuroscience (Ref KB/381)

Applicants should have expertise in molecular and cellular neuroscience or neurophysiology.

Senior Lecturer/Reader in Biological Sciences (Ref KB/4928)

Applicants with particular interest in the areas of behaviour/behaviour ecology, modelling or ecological genomics are especially welcome.

Informal enquiries are welcome to the Head of School, Professor Peter Bramley (tel. +44 (0)1784 443555; email: p.bramley@rhul.ac.uk)

Salaries in the range of: Lecturer £36,927 - £43,073 p.a., Senior Lecturer £44,925 - £51,017 p.a. Professorial salaries are negotiable starting at £53,229 p.a. All salaries are inclusive of London Allowance.

All posts are tenable from 1 September 2008 unless otherwise stated in the further details.

The closing date for all posts is 27 February 2008. Further details and a copy of the application form are available at www.rhul.ac.uk/Personnel/JobVacancies.htm < http://www.rhul.ac.uk/Personnel/JobVacancies.htm >

We positively welcome applications from all sections of the community.

Vincent Jansen

School of Biological Sciences Royal Holloway, University of London Egham, Surrey TW20 0EX, U.K.

Tel : (..) 44 1784 443179 Fax : (..) 44 1784 470756 Email: vincent.jansen@rhul.ac.uk Web : http://www.rhul.ac.uk/Biological-Sciences/AcademicStaff/Jansen/ Vincent.Jansen@rhul.ac.uk Vincent.Jansen@rhul.ac.uk

UBath PopBioLectureship correction

POPULATION BIOLOGY LECTURESHIP, UNIVERSITY OF BATH

Ref: 08H025A

Title: Lecturer in Population Biology - 08H025A

Department: Biology and Biochemistry

Description: Applications are invited from outstanding and highly motivated individuals for a Lectureship in population biology. The subject area is defined broadly and can include, but is not limited to, experimental evolution/ecology, comparative and ecological genomics, behavioural ecology, evolutionary ecology and conservation biology. You should have demonstrated excellence in original research and achievement in a relevant area, and the potential to develop and sustain a productive research programme at Bath. You will be expected to contribute to undergraduate and postgraduate teaching in the department. The appointment will be held in the Department of Biology and Biochemistry which is RAE grade 5 and very well equipped for molecular life science research. Further information about the Department is available at http://www.bath.ac.uk/bio-sci/ Informal enquiries are welcome and should be directed to the Head of Department, Dr Richard Hooley on bssrah@bath.ac.uk

Salary: In the range 33,779 - 40,335

Contact: Please email: jobs@bath.ac.uk or call 01225 386924 quoting ref number 08H025A

Closing Date: 28th February 2008

Further Particulars: http://www.bath.ac.uk/jobs/-job_desc.cgi?08H025A Professor Tamas Szekely Professor of Biodiversity Dept of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK 01225 383676 (phone), 01225 386779 (fax), T.Szekely@bath.ac.uk (email) http://www.bath.ac.uk/bio-sci/biodiversity-lab/index.htm SEX, SIZE AND GENDER ROLES: evolutionary studies of sexual size dimorphism http:/-/www.oup.com/uk/catalogue/?ci=9780199208784 bssts@bath.ac.uk

UGeorgia InsectParasiteEvolution

The Department of Entomology at the University of Georgia is developing a core research area in the study of parasite- and microbial-insect interactions and evolution. As part of this initiative, the Department seeks to fill two positions at the level of Assistant or Associate Professor. Areas of interest include pathogenic or symbiotic associations, as well as studies on vector species in animal or plant systems. Candidates using innovative approaches in the molecular sciences, evolutionary genetics, or ecology will be carefully considered. Expertise in Entomology and elsewhere on campus offers unique collaborative potential in genetics, genomics, parasitology, microbiology, ecology, and evolution.

Applicants must have a Ph.D. degree (or equivalent) and suitable experience. Successful candidates will be expected to establish a strong extramurally funded research program and contribute to instruction in the Department. To apply, submit a cover letter, curriculum vitae, and a description of research and teaching interests by email to: entomolo@uga.edu (open search in the subject line). Applicants should arrange to have 3 letters of reference sent to: Open Search Committee, c/o Dr. M. R. Strand (Chair), Department of Entomology, University of Georgia, 413 Biological Sciences, Athens, GA 30602-2603. Complete applications received by March 31, 2008 are assured of full consideration.

Ken Ross

– Kenneth G. Ross Department of Entomology University of Georgia Athens, GA 30602-2603 USA (706) 542-7699 kenross@uga.edu

UHelsinki Programmer

The Mathematical Biology Group at the Department of Biological and Environmental Sciences, University of Helsinki, Finland (leader Dr. Otso Ovaskainen) is seeking an outstanding, highly motivated Scientific Programmer. The position is available for 2 years, with the possibility of a 3-year extension.

The candidate is required to have a MS degree (PhD degree being counted as an advantage) in computer science, computational biology, bioinformatics, statistics, engineering, math, or a related field. The main selection criterion is the applicant's ability and experience in scientific computing with both functional languages (Mathematica) and object-oriented languages such as C# (Microsoft Visual Studio), Object Pascal (CodeGear Delphi), or C++ (CodeGear C++ Builder). In particular, expertise with advanced matrix operations (e.g. sparse matrix algebra), MCMC computations (e.g. adaptive Bayesian methods), and spatial statistics is appreciated.

The successful candidate will be responsible for developing and maintaining algorithms used in research projects at the interface between mathematics and ecology and evolutionary biology. The main emphasis is on developing efficient algorithms for computationally heavy problems, but the work involves also development and documentation of user-friendly interfaces.

The Mathematical Biology group is part of the Metapopulation Research Group (leader prof. Ilkka Hanski), which is a Centre of Excellence in Research supported by the Academy of Finland. We offer an international research environment with excellent possibilities to cooperate with experts in mathematics, statistics, population biology, and evolutionary ecology. Salary and social benefits according to the University of Helsinki Salary system, depending on the experience and performance of the employee (2,300 - 3,500 ? / month).

Applications including a short CV (max 3 pages) and the e-mail addresses of two researchers willing to write a letter of reference should be sent to otso.ovaskainen@helsinki.fi with cc to tuuli.ojala@helsinki.fi; write “scientific programmer” on the subject line. For more details on our research projects and on the application procedure, see http://www.helsinki.fi/science/metapop/-MBG/positions/index.htm Deadline for applications 14th March 2008, starting date 1st May 2008 (negotiable).

Otso Ovaskainen Academy Research Fellow Department of Biological and Environmental Sciences P.O. BOX 65 (Viikinkaari 1) 00014 University of Helsinki FINLAND

otso.ovaskainen@helsinki.fi otso.ovaskainen@helsinki.fi

ULibredeBruxelles PlantInteractions

Free University of Brussels (ULB)

Academic position in Organism Biology

Specialisation: Interactions of plants and other organisms

The Université Libre de Bruxelles invites applications for a full-time academic position in Organism Biology, to begin 1st October 2008.

Applicants must have a PhD in Biology or Agronomy (or equivalent)

Research

The candidate must demonstrate his/her capacity to conduct high quality research in the field of interactions of plants with other organisms. He/she will establish a vigorous, independent research program. The candidate is expected to favour a whole-organism, plant-centered, approach.

Teaching

The candidate will join the teaching staff in plant biology in the “Académie Universitaire Wallonie-Bruxelles”. He/she will participate in graduate instruction and training in botany (including lectures, practicals, field work). He/she will supervise Master and PhD theses.

For further details, please get in touch with Prof. Yves ROISIN, Département de Biologie des Organismes, Tel +32 2 650 4512, yroisin@ulb.ac.be.

Applicants should provide:

.A complete curriculum vitae including teaching experience and publication list, presented as required in the following webpage: http://www.ulb.ac.be/tools/-CV-type.rtf .A teaching project

.A research project (max. 3500 signs)

.A commented list of his/her most significant publications.

Applications should be sent in duplicate to: The Rector, Université Libre de Bruxelles, Avenue FD Roosevelt, 50, B-1050 Brussels, Belgium.

An electronic copy of the application should be submitted to Prof. Yves ROISIN, yroisin@ulb.ac.be

Deadline for applications: 15 March 2008

Please refer to the official version of this document (in French) for further details: http://wwwdev.ulb.ac.be/-greffe/files/2011.pdf

Yves Roisin <yroisin@ulb.ac.be>

UNottingham FrozenArkProject

The Frozen Ark Project is an international consortium that aims to save the DNA of endangered animals before they go extinct. It is not a substitute for saving the animals themselves, but a necessary 'back-up' to store the information they contain. Details about the project can be found at http://www.frozenark.org It is expected that the post will be advertised shortly. However, its funding is conditional on finding a candidate of sufficient merit. To avoid a 'catch 22' situation, we need to solicit informal expressions of interest.

We seek an exceptional person who is not only a distinguished scholar and teacher but is also able to run an international organisation, to recruit new members, and to raise additional financial support. The post will be based at the University of Nottingham, associated with the evolutionary research group within the School of Biology. It will require extensive national and international travel to liaise with current and prospective consortium members, and to organise international meetings. Very good personal and organisational skills will be necessities.

Salary will be in the range for a full professorship in The UK. Excellent laboratory and office space will be available, along with technical and secretarial help.

If you are interested in the post, and can meet the criteria, please write, telephone or email informally and confidentially to Bryan Clarke (not to evoldir!).

Professor B.C. Clarke FRS Institute of Genetics Queens Medical Centre Clifton Boulevard Nottingham NG7 2UH England

Tel: +44 (0) 1949 81243

Email: bryan.clarke@nottingham.ac.uk

Uppsala AnimalEvolutionaryGenetics

The Swedish University of Agricultural Sciences announces a position as

PROFESSOR IN MOLECULAR ANIMAL EVOLUTIONARY GENETICS

at the Department of Animal Breeding and Genetics, Faculty of Veterinary Medicine and Animal Science

(This text can also be found at: http://dokument.slu.se/ansti/taf/ledans_rd.taf?function=3DsluwebbaktE) Deadline March 25.

Ref nr 110/08 Subject description: Molecular genetics, especially exploration of the genome in domestic animals and the effects of genes on the variation in production and diseases of domestic animals and in other traits of importance for animal welfare and the interaction with man.

Duties: Overall responsibility for research and teaching at bachelor and master levels within the subject. Main duties include research, education at doctorate level and teaching within the department's comprehensive teaching task at bachelor and master levels, as well as the associated administration. International collaboration is expected.

An applicant who meets the criteria for appointment as professor has shown both academic and pedagogic skills. Equal importance shall be attached to the evaluation of pedagogic skills as to the evaluation of academic qualifications.

Criteria for assessment include the degree of scientific and pedagogic skills required for the appointment. Moreover, the degree of administrative and other skills that are important with regard to the appointment's scientific content and duties will be considered. The degree of skill in developing and leading activities and staff at the university, as well as the ability to collaborate with the outside community and to convey information about research and development work will also be considered.

In the appointment, importance shall be attached to scientific and pedagogic skills of which importance shall particularly be attached to scientific skills. Importance shall be attached to both current research and capacity to independently initiate and lead innovative and pioneering research, ability and interest to attract external funding as well as the applicant's well documented scientific competence on a high international level within the subject area. A good ability to collaborate with researcher on the national and international level is also important. When considering pedagogic proficiency, importance shall be attached to experience in planning, carrying out and evaluating teaching, as well as supervision and examining.

The scientific and pedagogic works that the applicant wants to cite must be given in the application and one copy of each must be submitted to the Rector. A maximum of ten scientific and ten pedagogic works, including popular science and research information, can be submitted. A complete publication list must be submitted, where cited works are indicated. When the three expert evaluators have been selected according to communication from the administrator one copy of each cited work must be sent to each one of the experts.

SLU (the Swedish University of Agricultural Sciences) develops our understanding and sustainable use of biological natural resources. This is achieved through research, teaching, environmental monitoring and assessment and information extension.

About 5000 bachelor, master and doctorate students are enrolled at SLU. 3000 people are employed at the University. The turnover is about 2,2 billion SEK. Main campuses are located at Ultuna, Alnarp, Skara, and Umeï¿½.

The Faculty of Veterinary Medicine and Animal Science is one of four faculties at SLU with 450 employees and 1000 bachelor, master and doctorate students. The Faculty office and most of the departments are located in Uppsala, but important research and teaching activities are also carried out in Skara.

The faculty is the only faculty in Sweden with a specific responsibility for teaching and research in veterinary medicine and animal science. The research and education aim to promote the health and well-being of animals as well as humans and to develop a biologically and economically sustainable animal management.

The faculty's research area comprises animal management, animal health, animal welfare, veterinary public health and the influence of animals for the health and well-being of humans. Within all these areas research and education are conducted at bachelor, master and doctorate levels.

The Department of Animal Breeding and Genetics is responsible for education at bachelor, master and doctorate levels, research and research information on molecular genetics and bioinfomatics, quantitative genetics with biometry, genetic evaluations and strategies for sustainable breeding programmes for different domestic animal species. Extensive collaboration takes place with the animal breeding industry both nationally and internationally as well as with institutions responsible for R&D in

— / —

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

Uppsala EvolutionaryGenetics

ASSISTANT PROFESSOR IN EVOLUTIONARY GENETICS AND GENOMICS

at the Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University, Sweden

The Department conducts evolutionary genetic research with increasing genomic emphasis, see http://www.egs.uu.se/evbiol/. The position concerns research that uses genomic data or tools to address evolutionary questions.

To qualify for appointment as Assistant Professor, the candidate needs to have a PhD. Priority is given to applicants who have completed their PhD within 5 active years of the application deadline. When judging scientific expertise particular attention will be paid to expertise in large-scale analysis of genomic data, for example, DNA sequences, polymorphisms or gene expression.

The Evolutionary Biology Centre (http://www.ebc.uu.se) is situated in recently-built localities in central Uppsala. The working atmosphere is international with a regular recruitment of post-docs from abroad. The Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 400 scientists and graduate students, and with research programs in ecology, systematics, genetics, genomics, functional genomics, and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated close to Stockholm.

The full announcements including instructions on how to apply is available at http://www.personalavd.uu.se/ledigaplatser/269forass_eng.html Closing date is March 6, 2008. For further information please contact Hans Ellegren (Hans.Ellegren@ebc.uu.se).

Professor Hans Ellegren Dept of Evolutionary Biology Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

Email: Hans.Ellegren@ebc.uu.se Phone: +46-18-4716460 Fax: +46-18-4716310

Lab home page: http://www.egs.uu.se/evbiol/index.html My home page: http://www.egs.uu.se/evbiol/Persons/Hans.html Hans.Ellegren@ebc.uu.se Hans.Ellegren@ebc.uu.se

URichmond Two one-year positions EvolutionaryBiology

Two One-Year Visiting Positions in Ecology and/or Evolution: University of Richmond:

The Biology Department at the University of Richmond seeks to fill two visiting positions beginning August 1, 2008. We are looking for broadly trained biologists with expertise in the ecological and/or evolutionary sciences. We seek individuals with a strong commitment to high quality undergraduate education. Teaching expectations include participation in the introductory courses of Evolution and/or Ecology, and upper-level electives in area of expertise. Field biologists are especially encouraged to apply. Candidates should hold a Ph.D. degree or be ABD with an anticipated completion by Fall 2008. Candidates are encouraged to provide evidence of teaching excellence. The application deadline is March 15, 2008, but qualified applicants will be considered until the positions are filled. The University of Richmond is committed to developing a diverse faculty and student body, and to modeling an inclusive campus community which values the expression of differences in ways that promote excellence in teaching, learning, personal development, and institutional success.

Details on the position and the application procedures can be found at: http://as.richmond.edu/teaching/searches/biology.html If anyone has specific questions about these positions, please email Malcolm Hill (mhill2@richmond.edu).

Please send completed applications to: Chair, E&E Search Committee Biology Department University of Richmond Richmond, VA 23173 (804) 289-8871

mhill2@richmond.edu

USouthCarolina Tech 454Bioinformatics

Immediate opening for skilled master's level student for Research Technician II position at the University of South Carolina ($32K/year with benefits). Position is part of the rapidly growing Environmental Genomics Core facility (http://www.sph.sc.edu/engencore/index.htm) with emphasis on Roche/454 FLX pyrosequencing. Knowledge of Perl and Linux a plus. Please send email of 3 references and CV to engencore@gwm.sc.edu with "454 technician position" in subject line.

– Environmental Genomics Core Facility Director 921 Assembly Street, Room 413 University of South Carolina Columbia SC 29208 (t) 803-777-4338 (l) 831-777-3999 (e) engencore@gwm.sc.edu (w) http://www.sph.sc.edu/engencore/

Joe Jones <engencore@gwm.sc.edu>

USydney ChairGeneticsComputationalBiol

Chair in Animal Genetics and Computational Biology Faculty of Veterinary Science Reference No.: S08/057

With the retirement of Professor Frank Nicholas after a long and distinguished career in Animal and Veterinary Genetics, applications are invited from suitably qualified people for the Chair in Animal Genetics and Computational Biology in the Faculty of Veterinary Science at the University of Sydney. This chair has been created with a vision for the future in animal systems-biology and to provide leadership in research and education in animal quantitative genetics and computational biology, and its application to relevant industries.

The successful candidate will be a distinguished and active researcher and educator with strong leadership qualities and a commitment to multidisciplinary approaches and have a strong track record in quantitative genetics and/or computational biology, with a focus on the livestock industries.

A proven record of gaining high levels of external support and research funding together with an ability to attract and supervise a strong team of postgraduate research students and postdoctoral fellows, provide leadership in postgraduate coursework through the Animal Breeding Management degree program, develop a postgraduate course in animal computational biology, and contribute to and improve undergraduate educational experiences in the BVSc and BAnVetBioSc degrees will be essential.

The Professor of Animal Genetics and Computational Biology is expected to be an effective communicator, with the capacity to involve and gain support of all relevant sectors of the livestock industries, to engage in research with impacts for the whole of the livestock sector, through national and international collaborations, whilst enhancing Faculty research, particularly through postgraduate research and coursework opportunities. Strong internal collaborations with the Faculty's Advanced Technologies in Animal Genetics and Reproduction (Reprogen) group and the University's Centre for Mathematical Biology and Sydney Bioinformatics are expected.

The position is full-time continuing, subject to the completion of a satisfactory probation and/or confirmation period for new appointees. Membership of a University-approved superannuation scheme is a condition of appointment for new appointees.

Further specific information about the position can be obtained from the Director of Reprogen, Professor Herman W. Raadsma (e-mail:raadsma@camden.usyd.edu.au, phone +61 2 9351 1603), Professor Christopher Moran (e-mail: Chris.Moran@vetsci.usyd.edu.au phone +61 2 9351 3553, or the Dean, Professor Leo Jeffcott, e-mail: dean@vetsci.usyd.edu.au .

For general enquiries including those about the application process and to apply, contact Kevin Mitchell, Senior Recruitment Manager on +61-2-9036-7294 or at srsacademic@usyd.edu.au <mailto:srsacademic@usyd.edu.au> to receive a full information pack.

Remuneration package: $160,975 p.a. (which includes a base salary Professor Level E $136,515 p.a., leave loading and up to 17% employer's contribution to superannuation)

Closing: 21st March 2008

The University is a non-smoking workplace and is committed to the policies and principles of equal employment opportunity and cultural diversity. The University reserves the right not to proceed with any appointment for financial or other reasons.

————)__(Imke Tammen Dr.med.vet., M.Ed. (Higher Education) ______-(**)- Senior Lecturer in Animal Biotechnology / oo /| _____|| Postgraduate Coordinator - Camden * || || Reprogen: Centre for Advanced Technologie in Animal Genetics and Reproduction

The University of Sydney 425 Werombi Road PMB3, Camden NSW 2570, Australia http://www.vetsci.usyd.edu.au/reprogen/ < http://www.vetsci.usyd.edu.au/reprogen/ >

FAX: +61-2-46550618 Phone: +61-2-46550604 (Camden) +61-2-93518620 (Sydney) email: itammen@camden.usyd.edu.au

Imke Tammen <i.tammen@usyd.edu.au>

Vienna Bioinformatics

Tenure track group leader position in bioinformatics

Details about the position and the host institution can be found at: http://i122server.vu-wien.ac.at/pop/opportunities.html We are searching for dynamic and enthusiastic scientist with an excellent track record and preferably with a proven ability to attract extramural funding. Candidates should have a strong interest to interact with research groups on the campus as well in the Vienna Research Area. Interest in evolutionary biology and population genetics would be a bonus.

Vienna offers an excellent environment for the future post holder, as strong groups in bioinformatics (Arndt von Haeseler, David Kreil) and evolutionary & population genetics (Reinhard Bürger, Joachim Hermisson, Christian Schlötterer) provide opportunities for future collaborations.

Apart from a great scientific environment, Vienna also offers an extraordinary quality of living. Affordable housing, excellent public transport, great restaurants, two operas, 2 music centers, many theaters and museums in combination with a pleasant climate make Vienna one of the most attractive cities in Europe.

Further questions and applications should be sent to Christian Schlötterer (christian.schloetterer@vu-wien.ac.at, +43-1-250775603)

The search will continue until the position is filled. For full consideration applications need to be received before 14.3.2008

Christian Schlötterer Institut für Tierzucht und Genetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-250775603 fax: +43-1-250775693 http://i122server.vu-wien.ac.at/pop/pop_gen.html christian.schloetterer@vu-wien.ac.at christian.schloetterer@vu-wien.ac.at

WoodsHole ResAssist MarineEvolution

Full-Time Research Assistant [RA II or III] Biology Department Woods Hole Oceanographic Institution

Application Deadline: March 30, 2008

Ref#: 08-02-03

The Biology Department at WHOI seeks a highly motivated individual to join the Tim Shank lab as a full-time Research Assistant II or III. The successful applicant will contribute to projects that focus on the ecology and evolution of fauna from chemosynthetic, seamount, and other marine ecosystems.

Responsibilities include but are not limited to the: 1) generation of integrative ecological and genetic data (via DNA and RNA extractions, standard and quantitative PCR, and high throughput DNA sequencing); 2) performance of genetic analyses for population genetic and phylogenetic studies; 3) management of laboratory activities; and 4) active participation in sea-going research expeditions.

Education: B.A., B.S. or M.S. in biology, ecology, or a related field and prior experience in an active research lab are desired. Excellent written, verbal, and interpersonal skills, attention to detail, and a strong work ethic are essential.

Applicants should have an interest in ecology, evolution, oceanography, molecular biology, and conservation, while possessing a genuine drive to perform basic research. This position requires an independent, organized, and motivated individual with laboratory experience. Salary and placement level will be commensurate with experience and education.

Potential applicants are encouraged to visit the Shank lab website at http://www.whoi.edu/science/B/people/tshank/, and the Biology Department website at http://www.whoi.edu/science/B/dept/. Application for this position (ref #08-02-03) should be conducted using WHOI's on-line Career Center at http://jobs.whoi.edu/ . Timothy M. Shank Biology Department, MS 33 Woods Hole Oceanographic Institution Woods Hole, MA 02543-1049 phone: 508-289-3392 fax: 508-457-2134 http://www.whoi.edu/science/B/people/tshank/ http://oceanexplorer.noaa.gov/edu/oceanage/05shank/welcome.html tshank@whoi.edu tshank@whoi.edu

YorkU MolecularEvolution LabTech

York University's Molecular Evolution Lab (YUMEL) has a fulltime lab technician position starting as soon as March 24, 2008. Lab research will involve working on an exciting project examining patterns of extrapair paternity and genetic screening of blood parasites in purple martins (Progne subis), a migratory songbird.

Skill set will include (but not be limited to) DNA extractions, running agarose gels, DNA quantification, conventional and rt-Q PCR, and fragment analysis using an automated DNA sequencer. Relevant molecular lab experience is required. The successful candidate must also have excellent interpersonal communication skills, be very responsible, hard working, willing to pay close attention to detail and accuracy, have strong computer skills, be very organized, have high regard for working safely with chemicals and equipment, and enjoy working in a collegial environment. The successful candidate will work closely with the YUMEL manager and lead researcher, but also must be comfortable working independently.

Salary will be approximately $2,000/mo, commensurate with lab experience. This is an excellent opportunity for a recent BSc or molecular biotechnology graduate with molecular evolution lab experience to obtain fulltime employment in a dynamic and supportive university research environment, while also gaining valuable lab research experience and exposure to cutting edge techniques.

Please submit (via email) as three separate attachments: (1) a cover letter summarizing your suitability for this position; (2) a one-page research statement thoroughly detailing your relevant research interests and experience; and (3) a current resume/curriculum vita. Please also include e-mail and telephone contact information for three (3) appropriate references at the end of your resume/curriculum vita. Review of applications begins March 10, 2008.

Email applications to:

Dr. Scott A. Tarof, Ph.D. 203H Lumbers Building Dept. of Biology York University Toronto, ON M3J 1P3 (starof@yorku.ca)

starof@yorku.ca starof@yorku.ca

Other

ABI Veriti reviews

Hello all.

My lab has received an aggressive offer from ABI to sell us their Veriti 96-well thermocyclers. These are fairly new machines (about a year old), and we wondering if anyone out can comment on their experience with them. Any quirks? Any issues? Any good things?

Any reviews positive or negative would be greatly appreciated.

Thank you.

Anders.

ag2057@columbia.edu ag2057@columbia.edu

CallforEuropean PopGenetics Research Consortia ConGen

The ESF Programme on "Integrating Population Genetics and Conservation Biology: merging theoretical, experimental and applied approaches" (ConGen) is launching a Call for European Research Consortia. More information is available in the attached document and on the following website:

http://www.esf.org/congen ************ Call for ConGen European Research Consortia

The ESF Research Networking Programme on "Integrating Population Genetics and Conservation Biology: merging theoretical, experimental and applied approaches" (ConGen) aims at providing a venue for concerted action in the field of conservation genetics combining and integrating theoretical, experimental and applied approaches. The Programme, which runs until November 2009, pursues these objectives by training young scientists through travel, exchange grants and courses, and by organising workshops.

To ensure long-standing collaborative research in the field of conservation genetics beyond November 2009, the Steering Committee (SC) has decided to promote and stimulate the establishment of European Research Consortia that successfully can apply for research funding from different granting organisations like the EU. To this end, the SC has decided to provide funding to organise an initiating discussion meeting between prospective collaborating researchers. ConGen is offering a maximum of 7500 EUR for such a 2-3-day meeting. We expect collaboration between researchers from at least four different European countries. The Call is open for all researchers working within or having affiliations to institutions eligible for support by, or which are part of, agencies that are Member of the ESF. However, some preferences may be given to consortia which include a significant number of, or are chaired by, researchers from ConGen contributing countries (http://www.congen.biz or http://www.esf.org/congen).

Application procedure

Applications should include:

(i) a clear description of the long-term aims of the consortium and the research questions addressed (1 A4 page), (ii) prospects about the possibility of getting further funding in a general way (iii) name and affiliation of all participants of the consortium including a short CV providing expertise and five recent relevant publications of each participants (iv) the name of the researcher leading the consortium (Chair) responsible for the application (v) and a calculation of the costs of the meeting.

Deadline

The next ConGen SC meeting is scheduled for the first week of March 2008. We, therefore, would like to receive pre-applications by 1 March 2008, so that the SC already can get an impression of the propective at its meeting. Please send your pre-application by email to the Chair and Co-Chair of the Programme, namely Kuke Bijlsma (r.bijlsma[at]rug.nl) and Volker Loeschcke (volker.loeschcke[at]biology.au.dk).

The deadline for submitting full applications online will be 1 April 2008.

****

Celine Seewald Life, Earth and Environmental Sciences unit (LESC) European Science Foundation 1 quai Lezay Marnesia BP 90015 67080 Strasbourg Cedex France T. +33 3 88 76 71 58 F. +33 3 88 37 05 32 cseewald@esf.org

Celine Seewald <cseewald@esf.org>

DNA extraction formol answers

With this I am posting the responses (mainly the references I was given) I received for my question:

“I need to extract DNA from fish specimens that have been in formol for 3 years to less than six months. If anyone has had success extracting DNA in such circumstances, I would extremely appreciate if you could share the protocol used”

Cheers, Ella

1. Jingjing Li, Xianghua Liao, and Hong Yang. 2000. Molecular Characterization of a Parasitic Tapeworm (Ligula) Based on DNA Sequences from Formalin-Fixed Specimens. Biochemical Genetics, Vol. 38, Nos. 9/10,, 309-322

2. Selma O. Klanten, Lynne van Herwerden and J. Howard Choat. 2003. ACQUIRING REEF FISH DNA SEQUENCES FROM FORMALIN-FIXED MUSEUM SPECIMENS. BULLETIN OF MARINE SCIENCE, 73(3): 771-776, 2003

3. Rosembaum et al. 1997. Mol. Ecol 6: 677-681,

4. Andrew M. Shedlock, MargoG. Haygood1, Theodore W. Pietsch and Paul Bentzen. 1997. Enhanced DNA Extraction and PCR Amplification of Mitochondrial Genes from Formalin- Fixed Museum Specimens. BioTechniques 22:394-400

5. Coombs et al. 1999. Nucleic Acid Research 27(16): e12-

6. Dear Ella, I extracted DNA from some paratypes that had been in formalin for a few weeks before being transferred to alcohol. I dissected out tissue - muscle, liver, spleen and then put the tissues through a series of 1/10 TE/alcohol soaks. I started with either 40% or 50% EtOH / 60% or 50% 1/10 TE and worked the EtOH up to 90% EtOH /10% 1/10 TE. I left the tissues in each for 24 hours. I think I may have done the first one twice. The DNA was degraded but I was able to get enough to amplify 400-500 bp pieces.

Best, Peter Wimberger Professor, Biology University of Puget Sound Tacoma, WA

Ella Vázquez Domínguez Instituto de Ecología, UNAM Tel. (5255) 5622 9015 Ap. postal 70-275 Fax. (5255) 5616 1976 Ciudad Universitaria evazquez@ecologia.unam.mx México DF 04510

http://www.ecologia.unam.mx/academicos/vazquez/ella_contacto.htm evazquez@miranda.ecologia.unam.mx

evazquez@miranda.ecologia.unam.mx

Grouper DNA extraction

Dear Evoldir I am working on a species of grouper, Plectropomus areolatus. I am trying to extract the DNA and it does not work. I think that the problem occurs during the first steps since the fin tissue is never lysed: the fin remains intact after 4-5 hours incubation at 56C with the lysis buffer with added proteinase K. I have tested several extraction methods/kit: - Extraction in CTAB - Extraction with Qiagen Kit “DNeasy blood and tissue kit”. - Kit Puregen with cell lysis solution, proteinase K, protein precipitation, isopropanol - Extraction with Chelex. Did anybody encounter this problem? Does anyone have suggestions? Many thanks in advance. Please reply elisabeth.rochel@univ-perp.fr Cheers Elisabeth

Please note my new email address!!! cecile.fauvelot@univ-perp.fr

Dr. Cecile FAUVELOT Charge de Recherche Institut de Recherche pour le Developpement (I.R.D.) UR 128 - Coreus (Communautes Recifales et Usages) Centre de Biologie et d’Ecologie Tropicale et Mediterranenne Universite de Perpignan, 52 Av. Paul Alduy - 66860 Perpignan cedex, France Tel : (33) (0)4 68 66 20 55, Fax : (33) (0)4 68 50 36 86

Web page: http://www.ird.nc/COREUS Personal web page: http://www.ecology.unibo.it/page/cecile.htm

Haplotype network building

Hi all.

I am attempting to build a network of mtDNA haplotypes for a segment of the control region for the flatfish Paralichthys lethostigma. Because this region is hypervariable, attempts to recover a network without a high degree of reticulation and median vectors have so far been unsuccessful. I have tried star-contraction, changing the value of epsilon, weighting transversions as high as 3:1 over transitions, to no avail. Just about the only thing that works is to invoke the frequency $>$ 1 filter, which eliminates singleton haplotypes (those that occur only in a single individual) from the network. This results in a very clean network with only two reticulations that can be resolved systematically.

My question is this. Has anyone come across literature or done their own investigations as to how the frequency $>$ 1 criterion affects the accuracy of network topology? Specifically, I want to use my resolved MP network for nested clade analysis or a coalescent approach, but I haven't worked out whether or not these methods remain meaningful if a great deal of haplotypes have been eliminated from the dataset in non-random fashion.

Thanks in advance for any ideas on this.

Joel Anderson Natural Resource Specialist Perry R. Bass Marine Fisheries Research Station Coastal Fisheries Division, Texas Parks and Wildlife ph: (361) 972-5483 fax: (361) 972-6352

Joel.Anderson@tpwd.state.tx.us

Heparin and DNApreservation

Dear all,

I am planning to draw blood from small lizards using glass micro hematocrit capillary tubes (i.e. minicaps) and to preserve it on FTA cards (or analogues) for latter genotyping using microsatellite DNA loci. Minicaps are available with and without heparin. Although heparin is recommended for easier collection of blood, I do not know the implications of heparin on DNA preservation and latter amplification.

I wonder whether anyone may aid me in deciding on the most suitable minicaps (i.e. with or without heparin) for my purposes.

Best regards, Pedro Moreira

Pedro Lopes Moreira Centro de Biologia Ambiental Faculdade de Ciï¿½ncias da Universidade de Lisboa Campo Grande C2 1749-016 Lisboa, Portugal

pedrolmoreira@yahoo.com

HighMolWeight DNA

Dear Evoldir members We are interested in extracting high molecular weight DNA from fresh tissues (not cell cultures), and would like to know if anyone has any experience or expertise in this area? In particular we are keen to minimise shearing to the DNA, so aim to avoid conventional kits that tend to shear things down to under 100kb. So if anyone has any suggestions, we would love to hear from you Thanks in advance for your help Tom Gilbert

mtpgilbert@gmail.com

Dr Tom Gilbert Associate Professor/Lektor Department of Biology University of Copenhagen Universitetsparken 15 DK2100 Copenhagen Denmark

mtpgilbert@gmail.com

Moss samples needed

Dear all,

I'm a first year PhD student working on the genetic diversity of genus Dicranum Hedw. (Musci, Bryophyta). I going to do a phylogeny of this genus but as I have problems to get good DNA from herbarium samples, I need fresh material. That is to say 10 to 15 gametophytes (plants) from different populations from the most countries. I'm interrested by all the species even the most commons. Besides I need some informations about the sampling place (coordinates...). You'll find a sheet to fill with this e-mail or I can send it to you if you can't read it.

Thanks in advance,

Amelie PICHONET

PhD Student, Teaching Assistant National Museum of Natural History Departement of Systematique and Evolution, Bryology Team Case 39, 57 rue Cuvier 75005 Paris - France Tel : 00 33 1 40 79 31 88 Fax : 00 33 1 40 79 35 94 Email : pichonet@mnhn.fr

pichonet@mnhn.fr

Nb estimation using linkage answers

Here is my original question:

Dear EvolDir folks,

I have a sample from a single cohort of juvenile frogs and am wondering if I can apply the linkage disequilibrium method (as implemented in the NeEstimator program) to this sample to get an estimate of the effective number of the parents (*N*b) that produced the juvenile cohort. Can anyone verify or refute this? I have microsatellite genotype data for the juveniles as well as the adults, so I will have an *N*b estimate from the temporal method as well. I am hoping to use the LD method to get an additional estimate of *N*b.

Any of your comments on this issue will be greatly appreciated!

Thank you,

Ivan

And here are the answers I received:

Yes, you certainly can get an estimate of parental Nb from your samples of juvenile frogs (you can also get another estimate from your sample of adults). You can get such an estimate from NeEstimator, but you might want to consider as an alternative a program (LDNe) we wrote and have described in a paper in press at Mol. Ecol. Notes. LDNe has a couple of advantages over other methods based on linkage disequilibrium: * it implements the bias correction described in Waples 2006 (Con. Genetics 7:167-184.) * It provides separate estimates based on different user-specified criteria for excluding rare alleles. this facilitates evaluation of potential biases from use of microsat data. it is easy to use and reads standard input files (FSTAT, GenePop). you can access the program, user's manual, and related files at http://fish.washington.edu/xfer/-LDNE/ you might also consider using OneSamp (recently described in an online early paper by Tallmon et al. in Mol. Ecol. Notes). this program uses approximate Bayesian computation methods to derive an estimate of effective size based on a single sample.

for your temporal estimate, if you have sampled the adults non-lethally you have Plan I samples and you should make sure you use an estimator that accounts for the correlation in allele frequencies between parents and offspring. this requires an estimate of N, the total number of adults your initial sample was (presumably randomly) sampled from.

best wishes, and let me know if you have any questions.

Robin Waples

Regarding your question posted on EvolDir:

First of all I suspect you already have the references on this method? Here are some - there may be more:

Bartely D, Bagley M, Gall G, Bentley B (1992). Use of linkage disequilibrium data to estimate effective size of hatchery and natural fish populations. Conservation Biology, 6, 365-375.

England PR., Cornuet J-M, Berthier P, Tallmon DA, Luikart G (2006). Estimating effective population size from linkage disequilibrium: severe bias in small samples. Conservation Genetics, 7, 303-308.

Hill WG (1981). Estimation of effective population size from data on linkage disequilibrium. Genetical Research, Cambridge, 38, 209-216.

Waples RS (1991). Genetic methods for estimating the effective size of cetacean populations. Report of the International Whaling Commission (special issue 13), 279-300.

Waples RS (2005). Genetic estimates of contemporary effective population size: To what time periods do the estimates apply? Molecular Ecology, 14, 3335-3352.

Weir BS, Hill WG (1980). Effect of mating structure on variation in linkage disequilibrium. Genetics, 95, 477-488.

I've used Ne estimator to estimate the number of breeders from a single cohort of amphibian progeny as you outline. With my dataset (40 tadpoles per population and 9 microsatellite markers), I definitely received estimates within a plausible range, when applying this method. Not knowing the actual number of breeders in the various populations, I had no way of testing the reliability however. I can only say that in general the results appeared in the range we expected, and that large populations yielded a larger Ne-estimate than small populations.

Nonetheless, I think you should be very careful to use any of the Ne methods isolated, and the results should always be interpreted with caution. To employ several methods in combination and use a large number of polymorphic markers would of course be preferable.

I would be very keen to see the answers you get, so please post them, if you receive anything useful. Also, I would appreciate to learn your opinion and experiences with the method once/if you chose to apply it to your data.

Cheers,

Morten

Morten E. Allentoft

M.Sc., Ph.D. candidate

School of Biological Sciences

University of Canterbury

Private Bag 4800

Christchurch New Zealand

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

Plant fixed heterozygote micros

Dear Evoldir members,

I am working with microsatellite in diploid plant species. We have tested six microsatellite primers described for congener species. However, two of them showed fixed heterozygotic genotype. Somebody knows what can produce fix heterozygote in a microsatellite locus?

Thank in advance,

Miguel Angel

Dr. Miguel Angel Gonzalez Perez Departamento de Biologia Campus Universitario de Tafira Universidad de Las Palmas de Gran Canaria 35017 Las Palmas Islas Canarias Spain

Phone: +34.928.45.45.43 Fax: +34.928.45.29.22 e-mai: HYPERLINK "mailto:mgonzalez@becarios.ulpgc.es" mgonzalez@becarios.ulpgc.es

mgonzalez@becarios.ulpgc.es

Pollinia DNA extraction

I am working with the common milkweed plant (asclepias syriaca) and I need to extract DNA from the pollinia. I was wondering if anyone knows of any protocols specific to pollinia (asclepias or orchids) DNA extraction or just for extracting DNA from very small amounts of plant material? Thank you.

Aaron Howard Georgetown University Department of Biology 37th and O Street NW Reiss 406 Washington DC 20057

doublearon83@gmail.com

Program to rename sequences

Hello Everybody,

Does anyone knows whether there is a program which is able to automatically rename the sequences in a (fasta or other format) file ?

In other words a program which is able to assign a new identification number to each sequences written in the file ?

Why ? because many bioinformatic programs truncate sequences when names are too long and lead sometimes to redundant names and then to a corrupted file which often kill the computing process and generate an error ...

Thanks a lot in advance for the solutions !

Xavier

– Xavier Bailly Station Biologique de Roscoff Place George Teissier BP 74 29682 Roscoff Cedex France

tel: (00 33) 2 98 29 23 23 fax: (00 33) 2 98 29 23 24

email: bailly@sb-roscoff.fr http://www.sb-roscoff.fr/ bailly@sb-roscoff.fr bailly@sb-roscoff.fr

Sampling Australian Skates Rajidae

Dear Evoldir members, I am a PhD student in Environmental Sciences at the University of Bologna (Italy) and I work within the group of Dr. Fausto Tinti (http:/-/www.dipartimentobiologia.it/research/rutinti.asp < http://www.dipartimentobiologia.it/research/rutinti.asp >). Since 2000 the Tinti's group has been focusing research activities on the micro- and macro-evolutionary patterns and mechanisms in marine fish of the North-eastern Atlantic and Mediterranean. Relevant achievements have been obtained with the reconstruction of spatial and temporal evolutionary patterns and processes of cartilaginous fish (Rajidae) and the development of on-line data bank for the monitoring and conservation of Mediterranean skates and rays (http://www.med-skate.unibo.it < http://www.med-skate.unibo.it/ >).

Some publications are: - Valsecchi, E., Pasolini, P., Bertozzi, M., Garoia, F., Ungaro, N., Vacchi, M., Sabelli, B., Tinti, F. 2005. Rapid Miocene-Pliocene dispersal and evolution of Mediterranean rajid fauna as inferred by mitochondrial gene varation. J. Evol Biol., 18:436-446 - Tinti, F., Ungaro, N., Pasolini, P., De Panfilis, M., Garoia, F.,Guarniero, I., Sabelli, B., Marano, G., Piccinetti, C. 2003.Development of molecular and morphological markers toimprove species-specific monitoring and systematic of North-East Atlantic and Mediterranean skates (Rajiformes). J. Exp.Mar. Biol. Ecol. 288: 149-165.]

At present we are investigating the bio-geographical phylogeny of Rajidae on a broader range, with both an interdisciplinary bio-geographical and molecular approach. The main goal is to test the hypothesis of a Tertiary Gondwanic dispersal and evolution of Rajidae, along northward evolutionary pathways. For this purpose we would need to extend the analysis to austral hemisphere faunas. Presently, we have already collected samples from several location in South-western Atlantic (Brazil and Argentina) and South-eastern Atlantic (South Africa). Since in a period between March-May 2008 I will be in Australia, Sydney; I would like to make the most of my staying, trying to collect some tissue samples from Rajidae species occurring in that area.

Thus, I'm wondering if anyone of you think there might be any opportunity for me to join some sampling campaign where I can collect those fishes or to have access to voucher specimen collection already available. The sampling of individuals consists of the collection of a digital picture and of a small part of fin or muscle tissue which will be stored in ethanol 80% into microtubes.

In the case you are so kind to help me, I will be financially fully supported by the University of Bologna. I also have some friends already working at University of New South Wales that can host me and help me in organizing any required travel.

I only need support for the search of samples.

I hope that this will be the beginning of a fruitful collaboration between our research groups. If you should need further details, don't hesitate to contact me. Also, any advice is welcome.

Looking forward your kind reply I thank you for your time and attention.

Best regards Alessia Cariani Dott.ssa Alessia Cariani Molecular Genetics for Environmental & Fishery Resources Laboratory -GenMAP- Interdept. Center for Research in Environmental Sciences -CIRSA- University of Bologna via Sant'Alberto, 163 I-48100 Ravenna, Italy Tel.+39 0544 937408 Fax +39 0544 937411 E-mail: alessia.cariani@unibo.it

Alessia Cariani <alessia.cariani@unibo.it>

Software DAMBE 5 0 5

Dear All,

I have uploaded a new version of DAMBE (version 5.0.5, at http://dambe.bio.uottawa.ca/dambe.asp) with many improvements. Here is a partial list relevant to evolutionary biologists:

1. Much improved ML method.

The maximum likelihood method is now much faster (it was fast to start with because the function was mostly based on the fastDNAML program), and generate better trees than many other comparable programs. You may use highly diverged sequences to test its performance against other phylogenetic software. Or you may just use the included vertCOI.fas file to try it out (Click 'File|Open standard sequence file' and select vertCOI.fas).

In addition to speed, I have also added a tree editor for you to input prior knowledge about the phylogenetic relationship among OTUs. Typically we know the phylogenetic relationships among a subset of OTUs, and we really just need to resolve the phylogenetic relationship of the rest of the ingroup. When you click 'Phylogenetic|Maximum likelihood|DNAML', you can change the runmode to 'Start with a partial tree' in the ML dialog box. This will start a tree editor with a star tree. If you use the included vertCOI.fas file, then you will have eight leaves all branching off the same root. Just drag the nodes to each other to create a new tree, or drag OTUs (whose phylogenetic relationships are unknown a priori) to the garbage bin. The result should be an unrooted but fully resolved partial tree. Now click 'File|Export and exit' and then click the 'Run' button to do a maximum likelihood reconstruction. Supplying a subtree decreases the time spent in creating the initial ML tree which will then be rearranged (depending on how you set the options). It is important that the subtree is a very good one because otherwise rearranging the initial ML tree will be time-consuming, thus defeating the purpose of creating the initial subtree.

(This "initial subtree" option has in fact been available in DAMBE since its publication, but users often monkey-wrench a wrong tree, either with OTU names in the tree different from those in the sequences or with wrong tree format. The result is always the same: DAMBE crushes. Introducing a tree-drawing function hopefully will eliminate this problem.)

2. Evaluating statistical support of alternative topologies:

If you choose to keep more than one tree in the ML dialog box, then the relative support of the alternative trees will be evaluated by three tests, the paired-sample t-test, the SH test and the RELL test. While these tests are all based on site-specific log-likelihood (lnL), the paired-sampled t-test will always generate the same result, but the other two tests are from bootstrapping results and will consequently differ slightly between runs. C/C++ programmers can get the implementation of such tests in several open-source programs (e.g., PAML), VB programmers may ask me for an implementation in VB.

If you have several different trees and wish to evaluate their relative statistical support, you may choose the user tree as the runmode option. If you use the vertCOI.fas file, then you may choose the vertCOITree4.nhm file which contains four different trees.

3. Selecting best-fitting nucleotide substitution models.

For model selection among nucleotide-based substitution models, three commonly used criteria were implemented, the hierarchical likelihood ratio test, AIC, and BIC. To try the function, read in a sequence file, e.g., vertCOI.fas, and click 'Phylogenetics|Select best nuc. sub. model'. You will be asked to either create a new tree or import a user tree from a tree file. In either case, the previously mentioned tree editor will be shown: choosing 'New tree' option will start with a star tree in the tree editor, and choosing 'User tree from tree file' will display the tree in the tree editor just to make sure that the tree is displayed properly. You should ensure that the tree from tree file has OTU names identical to those sequence names. If you use the vertCOI.fas file, I recommend that you choose the "User tree from tree file' option and open the vertCOIUnrooted.dnd which contains an unrooted tree. Remember to click 'File|Export and exit' in the tree-drawing window. Click the 'Run' button and DAMBE will evaluate substitution models from JC69 to GTR based on likelihood ratio test, AIC and BIC. I personally consider BIC a conceptually wrong criterion for evaluating substitution models. We normally should use a simple model with limited data (e.g., when sequences are short), but can afford to use a parameter-rich model with long sequences. The BIC criterion tends to tell us to do the opposite, i.e., it favors parameter-rich model when sequences are very short, but is against parameter-rich models when sequences are very long. What a silly criterion it is! The model evaluation is in fact done with a minor modification of the

— / —

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

Software TreeRot BugFix

Thanks to reports from users, we've been able to fix a few minor and one major problem in TreeRot version 3. If you use the program for determining decay indices (Bremer support) and/or partitioned support, please trash your current version of the program and download it again.

Thanks, Mike

http://people.bu.edu/msoren/TreeRot.html Michael Sorenson Associate Professor Department of Biology Boston University 5 Cummington St. Boston, MA 02215

(617) 353-6983 FAX: (617) 353-6340

msoren@bu.edu msoren@bu.edu

Sorbus micros

Dear Evoldir members,

Nowadays, we are working in conservation genetics and population genetic in Sorbus aria, native specie from the Canary Islands. Is there somebody that has characterized and isolated microsatellite loci in Sorbus sp?

Thank in advance,

Miguel Angel

Dr. Miguel Angel Gonzï¿½lez Pï¿½rez Departamento de Biologï¿½a Campus Universitario de Tafira Universidad de Las Palmas de Gran Canaria 35017 Las Palmas Islas Canarias Spain

Phone: +34.928.45.45.43 Fax: +34.928.45.29.22 e-mai: HYPERLINK “mailto:mgonzalez@becarios.ulpgc.es” mgonzalez@becarios.ulpgc.es

mgonzalez@becarios.ulpgc.es

Thomson spams authors

Dear Colleagues,

A few years ago I began to receive many email and paper mail advertisements at my work addresses from companies selling scientific products. Most of these messages were of no interest to me, and their numbers have increased to the point of becoming a nuisance.

It turns out that Thomson Scientific (the Web of Science and Science Citation Index people) may be behind this flood of spam and junk mail that many of us receive. Thomson offers a product called “Scientific Direct” that harvests author contact information from the papers that we publish and sells it to marketers.

Here is a description from their website (http://scientific.thomson.com/products/scientificdirect/):

“The Process is Simple First, you consult with one of our list selection experts to create highly focused profiles. These profiles are then run against the multidisciplinary Thomson Scientific database. The resulting names are sent to you in the form of postal addresses or e-mail addresses, chosen carefully from the more than 500,000 international authors who have published papers in the top scientific, peer-reviewed journals.”

I was disappointed to read this. I have never provided my contact information in a scientific paper with the goal of it being used to send me spam or thousands of pages of worthless and wasteful paper catalogues.

If you wish to contact Thomson about this practice, I suggest beginning here:

http://scientific.thomson.com/press/mediacontacts/ or here: customsales@thomson.com Please let me know if you get a reply.

Thanks,

Steve

Steve Jordan Department of Biology Bucknell University Lewisburg, PA 17837 Office: 310 Bio. Bldg. +1 570-577-1254 Lab: 331 Bio. Bldg. +1 570-524-3816 Fax: +1 570-577-3537 http://www.facstaff.bucknell.edu/sdjordan/jordan.html

steve.jordan@bucknell.edu

Trout LDH purpose

Dear colleagues,

I am looking for colleagues who have used the method of McMeel/Ferguson (see ref. bellow) on trout LDH-C1. I would like to discuss on the results with people who have analysed both allozymes AND gene amplification; because of surprising discrepancies.

Patrick Berrebi

McMeel O. M., Hoey E. M. and Ferguson A. (2001) Partial nucleotide sequences, and routine typing by polymerase chain reaction-restriction fragment length polymorphism, of the brown trout (Salmo trutta) lactate dehydrogenase, LDH-C1*90 and *100 alleles. Molecular Ecology 10, 29-34.

Patrick BERREBI - Directeur de recherche CNRS UMR 5554 “Institut des Sciences de l’Evolution” Equipe Genetique et Environnement / Metapopulations, Conservation et Co-Eolution Universite Montpellier II, CC 065. Place E. Bataillon 34095 Montpellier Cedex 5 (France) berrebi@univ-montp2.fr France 04 6714 3732 - International 33 4 6714 3732 Fax France 04 6714 3622 - International 33 4 6714 3622 Web: http://www.isem.cnrs.fr/-spip.php?article526 berrebi@univ-montp2.fr

---

UGlasgow VolunteerFieldAssist GreatTitEvolution

Research assistants needed for field work on great tits and blue tits in spring/summer 2008

We are currently looking to recruit volunteers for a research project investigating breeding ecology in blue tits and great tits. Fieldwork assistant posts are available April-June 2008. Posts are available for varying periods starting on different dates.

Field activities include nestbox monitoring, measuring eggs and nestlings, clutch size manipulation, invertebrate sampling, nestbox camera setup and video analysis.

You will be working as part of a team with Dr Kathryn Arnold (www.gla.ac.uk:443//ibls/staff/-staff.php?who=PGe˜Pn) and Dr. Terje Lislevand at the University of Glasgow, UK.

Requirements: An interest in animal ecology and animal behaviour. Candidates should preferably have a background in biological sciences. Experience with handling birds is preferred but not essential.

Posts are available for at least 3 weeks. Applicants must be reasonably fit and able to climb ladders (for fieldwork).

Basic living costs and travel within the UK will be covered. Accommodation during fieldwork is provided at field station of Glasgow University, SCENE, Rowardennan, within Loch Lomond National Park (http://-/www.gla.ac.uk/departments/scene/).

E-mail applications are accepted and encouraged. Please send a CV with a covering letter and details of two referees (academic or field biology related - with e-mail address) to:

Lindsay Henderson Division of Environmental and Evolutionary Biology, Graham Kerr Building, University of Glasgow, G12 8QQ Scotland, UK (E-mail: l.henderson.1@research.gla.ac.uk)

Please remember to indicate dates you are available.

Closing date: Friday 14th March.

Dr. Terje Lislevand http://www.gla.ac.uk/-departments/eeb/researchinterests/pdra/-terjelislevand/ tl37r@udcf.gla.ac.uk

---

UGroningen VolFieldAssist EvolAvianLifeHistory

Volunteer field assistant needed for work on Skylarks and Woodlarks in the Netherlands

Volunteers are needed between April and mid of July 2008 for a research project investigating â Seasonal dynamics in the evolution and ecology of avian life histories: an integrative field study of disease risk, energetics & immunology, in members of the Lark family Alaudidaeâ.

Our goal is to better our understanding of how different lark species all over the world cope with seasonal and environmental variation. Improved knowledge of avian physiology is important to understanding more clearly how life histories evolve since the range of life history traits that species can adopt are likely constrained by their physiology. Thus, by understanding the physiological mechanisms behind adaptation to seasonal and environmental variation, we will be able to better explain how such variation might lead to different life histories in different habitats. The project is carried out by the Animal Ecology Group of the University of Groningen / The Netherlands.

With this advertisement we are looking for volunteer field assistants helping with the field work on Skylarks and Woodlarks in the Netherlands.

Volunteers will participate in the field work of an international research team. The main task of the volunteer will be searching for nests, observing colour-ringed birds and catching Larks. Participation in investigations using modern eco-immunological and physiological methods is also possible.

Field work area is a dune and heather area in the Drents-Friese Wold National Park in the northern Netherlands. The study area contains about 50 pairs of Woodlarks and about 100 pairs of Skylarks as well as many other interesting species.

Applicants must have good experience with ornithological field work and bird observations. Time and length of stay can be agreed on personal preferences. We provide housing and food, but volunteers must pay their own travel costs (a small contribution to these costs might be possible, depending on the outcome of a grant application). The working language of the group is English. Applicants must be prepared for cold and rainy conditions requiring warm outdoor gear, including hats and gloves.

To apply: Please send a CV, a covering letter addressing any relevant experience, two references with e-mail addresses and the time you would be available to the address below.

If you have any questions please feel free to contact me Arne Hegemann

Please forward this message to people who might be interested.

Arne Hegemann, Animal Ecology Group, Centre for Ecological and Evolutionary Studies, University of Groningen, P.O. Box 14, 9750 AA Haren, The Netherlands, tel +31 (0)50 363-3409, email a.hegemann@rug.nl

Â

Arne Hegemann Animal Ecology Group Centre for Ecological and Evolutionary Studies University of Groningen P.O. Box 14 9750 AA Haren The Netherlands

tel +31 (0)50 363-3409 email a.hegemann@rug.nl

Arne Hegemann <a.hegemann@rug.nl>

PostDocs

BangorU 2 FishPopGenetics

Position 1. EU-funded Post Doc in Molecular Ecology, Bangor University

School of Biological Sciences, Bangor University POSTDOCTORAL RESEARCH OFFICER IN MOLECULAR ECOLOGY (08-7/107) Salary: 21,478 - 23,883, R&A Grade 1A The structure of fish populations and traceability of fish and fish products: FishPopTrace

Applications are invited for a full time 3 year EU-funded Postdoctoral Research Officer in Molecular Ecology to work in the Molecular Ecology and Fisheries Genetics Laboratory (MEFGL) (http://biology.bangor.ac.uk/research/mefgl/) at Bangor to investigate population genetic structure and traceability of commercial marine fishes in European waters. The appointee will be primarily responsible for the development of a forensically-validated marker system (single nucleotide polymorphisms, SNPs) to identify stocks of commercial marine fishes, especially, cod, Gadus morhua, as a basis for description of population genetic structure and for traceability. The appointee will also assist the Bangor team in coordinating the 15-partner consortium (FishPopTrace), comprising fish biologists, geneticists, forensic biologists and representatives of the fishing and commercial sectors.

The successful candidate should have experience in the application of molecular tools, in particular SNPs and/or microsatellites, and familiarity with analysis of molecular genetic data. The candidate will have a Ph.D. in molecular ecology, with research interests in population genetic structure, fisheries genetics, forensics, or related topics. Furthermore, good communication, presentation skills and a strong commitment to timely publication of results will be essential.

The Molecular Ecology and Evolution Group at Bangor is organized into 2 main areas: The Molecular Ecology and Fisheries Genetics Laboratory (MEFGL), and the Evolution of Reptiles Unit. Both laboratories share common molecular facilities, group meetings and office space. The MEFGL team currently comprises 30 scientists engaged in projects focusing on the population and species biodiversity of primarily aquatic animals, providing a dynamic interactive environment. It is housed in the new, £8 million Environment Centre Wales, comprising a suite of fully integrated molecular laboratories including a 96 lane ABI automated sequencer/genotyper and a Beckman-Coulter capillary sequencer, an ABI 7900HT Fast Real-Time PCR system, wide range of thermal cyclers and associated support, and a new dedicated ancient DNA facility. Bioinformatic facilities are enhanced by a dedicated Biowulf cluster and server, with a new bioinformatics suite located adjacent to the molecular laboratories.

Applications and Informal Enquiries Application forms and further particulars should be obtained by contacting Human Resources, Bangor University, Bangor, Gwynedd LL57 2DG; tel: (01248) 382926/388132; e-mail: personnel@bangor.ac.uk, quoting 08-7/107. Position summaries are also available via the group website:

http://biology.bangor.ac.uk/research/mefgl/mefgl_opportunities.htm . The closing date for applications is February 22nd 2008. Informal enquiries can be made by contacting Professor Gary Carvalho (g.r.carvalho@bangor.ac.uk; +44(0)1248382100)), or Dr Martin Taylor (m.taylor@bangor.ac.uk; +44-1248382344.

– Si Creer Post Doctoral Research Fellow Molecular Ecology and Fisheries Genetics Group School of Biological Sciences University Wales, Bangor Bangor Gwynedd LL57 2UW UK

e-mail: s.creer@bangor.ac.uk Tel: +1248 382302 Fax: +1248 371644 Home Page: http://biology.bangor.ac.uk/ ˜ bssa0d/ "S.Creer" <bssa0d@bangor.ac.uk>

Position 2. NERC funded Post Doc in Molecular Ecology, Bangor University

POSTDOCTORAL RESEARCH OFFICER IN MOLECULAR ECOLOGY (ref: 08-7/111) Starting salary: 21,478 R&A Grade 1A

Population structure of cod around the UK: scale, mechanisms and dynamics

Applications are invited for a 19 month Postdoctoral Research Officer in Molecular Ecology to work in the Molecular Ecology and Fisheries Genetics Laboratory (MEFGL) (http://biology.bangor.ac.uk/research/mefgl/) at Bangor to investigate population genetic structure and the development of spatially-resolved population models for cod (Gadus morhua) in UK and NW European coastal waters. The appointee will be primarily responsible for the development and screening of cod populations using single nucleotide polymorphisms, (SNPs) to assess levels of structuring. Data will be integrated with partner results from microsatellites, tagging studies, and otolith microchemistry to generate spatially resolved population dynamics models

— / —

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

---

CambridgeU SystemsBiology

University of Cambridge, UK

Research Associate in Systems Biology

Department of Physiology, Development and Neuroscience

Vacancy Reference No: PM03000 Salary: £25,134-£32,796

Limit of tenure applies*

We seek a post-doctoral Research Associate to join an interdisciplinary BBSRC funded project to study the dynamics of gene regulatory networks in the fly. The major aims are to elucidate the temporal characteristics of the transcriptional response to Notch signalling, and to develop predictive models from these data that will inform our understanding of the regulatory circuits. This post will focus on the development of stochastic models of network connectivity, and the statistical tools for inference in such models, using time courses of expression and ChIP-chip data. The post will be based in the Cambridge Systems Biology Centre, home to a number of research groups working in systems biology (see http:// www.sysbiol.cam.ac.uk/index.php).

The successful applicant will have a PhD or equivalent in computational biology or a relevant quantitative field such as statistics, applied mathematics, engineering or physics. Experience in computational statistics and strong programming skills in languages such as R, Matlab or C++ is required. Experience in statistical analysis and/or stochastic modelling in molecular biology will be an advantage.

Questions may be addressed to Dr Sarah Bray (sjb32@mole.bio.cam.ac.uk) or Prof Simon Tavare (st321@cam.ac.uk). Applications, to include a current CV and contact details of three referees in pdf format only, plus form PD18 (parts I & III, downloadable from www.pdn.cam.ac.uk/jobs), should be sent to reception@pdn.cam.ac.uk.

Consideration of applicants will begin 14 March 2008.

* Limit of tenure: up to three years

Closing date: 14 March 2008.

The University values diversity and is committed to equality of opportunity.

The University has a responsibility to ensure that all employees are eligible to live and work in the UK.

s.tavare@damtp.cam.ac.uk s.tavare@damtp.cam.ac.uk

Cardiff ParasiteInvasion

Marie Curie Research Fellow/Senior Research Fellow in Molecular Ecology

Cardiff School of Biosciences, U.K.

This post is fixed-term for 24 months, or until 30 April 2010 if appointed as a Marie Curie Fellow or Fixed-term for 18 months, or until 30 April 2010 if appointed as a Marie Curie Senior Fellow.

Closing date: 3 March 2008.

In a global economy, the transfer of parasites to novel hosts can pose a major threat to both farmed and wild animal stocks. The effects of parasite invasion can have significant impacts on rural economies and biodiversity, but are difficult to evaluate in the short-term, since adaptation to new hosts occurs over an evolutionary time-scale. This project will study neutral genetic variation and adaptive evolution of morphology and virulence of gyrodactylid parasites associated with historical translocations of the guppy (Poecilia reticulata).

This group of fish-parasites may comprise ca. 20,000 species, the majority of which are still unknown to science. Gyrodactylids are renowned for their colonization abilities and pathogenicity, and one species alone, Gyrodactylus salaris has cost the Norwegian Salmon Industry >500 million in 25 years. Gyrodactylids demonstrate biological plasticity including host-shifts, an evolutionary characteristic important for parasite invasion.

We will utilise a multi-disciplinary approach integrating morphometrics, molecular ecology and experimental parasitology to identify and describe novel species, to study their invasion potential, and to establish DNA barcoding for this group.

You must have a strong background in evolutionary biology, genetics, ecology and/or epidemiology. You will join a team of parasitologists (Cardiff and Oslo) and evolutionary biologists (Cardiff and Hull) engaged in a four-year Transfer of Knowledge (ToK) Marie Curie Programme (GYROSCOPE). You will be based in Cardiff for 18 to 24 months, dependent on the position, but there will be the possibility of short periods of fieldwork overseas.

You should have a PhD submitted in an appropriate discipline (awaiting PhD viva) and expertise in parasitology/microscopy or molecular biology are essential. (Marie Curie Fellow). For Marie Curie Senior Fellow, a PhD and experience of microsatellite, AFLP and/or SNP analysis are essential.

In order to comply with EU ToK appointment requirements, applicants must be able meet the eligibility criteria. For example, British nationals would not normally be eligible to apply for this post. Further information regarding eligibility can be found at: http://ec.europa.eu/research/fp6/mariecurie-actions/action/level_en.html And http://www.ukro.bbsrc.ac.uk/mariecurie/fp6/application_info/handbooks/05_handbooks/0508_mc_handbook_tok.pdf For further information, contact Dr. Jo Cable (e-mail: cablej@cardiff.ac.uk), Prof. Mike Bruford (BrufordMW@cardiff.ac.uk) and/ or Dr. Cock van Oosterhout (C.van-oosterhout@hull.ac.uk). For general information on the Schools of Biological Sciences at Cardiff University and the University of Hull visit our websites at http://www.cardiff.ac.uk/biosi/research/biodiversity/index.html and http://www.hull.ac.uk/biosci/staff/academic/MolecularEcologyandEvolution/CockvanOosterhout.html respectively.

Salary: EU-funded positions, salary dependent on EU experienced researcher qualifications approximately *28,000 per annum (Marie Curie Fellow) or approximately *41,928 per annum. (Marie Curie Senior Fellow).

To work for an employer that values and promotes equality of opportunity, visit www.cardiff.ac.uk/jobs telephone + 44 (0) 29 2087 4017 or email vacancies@cardiff.ac.uk for an application form quoting vacancy number 2008/0128.

Joanne Cable <cablej@Cardiff.ac.uk>

DalhousieU ComparativeGenomics

POSTDOCTORAL OR RESEARCH ASSISTANT POSITIONSX

Bioinformatics, comparative genomics, endosymbiosis and genome evolution

Department of Biochemistry and Molecular Biology, Dalhousie University Halifax, Nova Scotia CANADA We seek highly skilled and self-motivated researchers at the postdoctoral and/or research assistant level to explore the impact of secondary endosymbiosis on eukaryotic genome evolution and cell biology. Specifically, the research will revolve around the bioinformatic analysis and interpretation of nuclear genome sequences from two unicellular algae (http://www.jgi.doe.gov/sequencing/why/CSP2007/guillardia.html).

The Archibald and Gray Laboratories are part of a collegial and internationally recognized community of comparative genomics and molecular evolution researchers at Dalhousie University. The successful applicants will have the opportunity to work collaboratively with these researchers and with those at other institutions. Demonstrated skills in bioinformatics, comparative genomics and genome evolution are essential, as are strong written and oral communication abilities.

The positions are available starting May 1, 2008 (actual start date negotiable) and will run for an initial 1-year period, with the possibility of extension to 3 years given satisfactory performance. All qualified and interested persons are encouraged to apply. Applicants should email (1) a brief cover letter outlining their qualifications and research interests, (2) a Curriculum Vitae and (3) contact information for three references to:

John Archibald and Michael Gray jmarchib@dal.ca

http://myweb.dal.ca/jmarchib/,
http://www.biochem.dal.ca/faculty/facultypages/gray/

CLOSING DATE: April 15, 2008.

John Archibald <jmarchib@dal.ca>

FrenchGuyane TreePhylogeography

We seek a broadly-trained and enthusiastic researcher to investigate the phylogeographic history of tree communities in French Guyane.

The postdoctoral position is funded by CNRS for 2 yr and will be based at the University of Toulouse (UMR 5174 CNRS) where the applicant will work with Jerome Chave. The targeted starting date is September, 1st or October 1st 2008.

Candidates must be experienced in DNA sequencing and phylogenetic/ phylogeographical analyses, preferably with additional experience in comparative phylogenetics and/or approaches using phylogenies to test models of species assembly. They must have the capacity and willingness to conduct field work at remote sites. Experience in taxonomy of neotropical plants will be favoured.

More details on the project can be found on the CNRS website https://www2.cnrs.fr/DRH/post-docs08/?pid=1&action=view&id=591&lang=en as well as general conditions for applications to CNRS post-doctoral positions http://www2.cnrs.fr/en/349.htm Closing date for applications is 30 March 2008. To apply, candidates should fill the CNRS application form https://www2.cnrs.fr/DRH/post-docs08/medias/tpl/-

pdf/publique/doss-candidat_pdocs.pdf and email it with a full CV to Jerome Chave (chave@cict.fr) and Brigitte Crouau-Roy (bcrouau@cict.fr)

“\”C. Thebaud\“” <thebaud@cict.fr>

HarvardU ExpEvolution MetabolicSystems

Postdoctoral position in experimental evolution of metabolic systems

Applications are being entertained for an NIH-funded postdoc position in the lab of Christopher Marx in the Department of Organismic and Evolutionary Biology at Harvard University (www.oeb.harvard.edu/faculty/marx/). This project is conducted in close collaboration with the lab of co-PI, Daniel Segre at Boston University (prelude.bu.edu). An abstract describing the project’s aims and goals is listed below.

Outstanding candidates from a variety of relevant backgrounds will be considered, but particular attention will be paid to those who have experience in biochemistry, microbial physiology, metabolism, or analytical chemistry. Applications will be reviewed upon receipt, and the position is available as soon as possible. Salary will be determined based upon candidate qualifications. Please send a CV and a statement of research interests in relation to the project to Christopher Marx (cmarx@oeb.harvard.edu).

Systems-level physiological basis of selection and epistasis in adaptation.

Is it possible to predict both the potential for selection and epistatic interactions across a biological network? Here we propose to quantitatively address the physiological basis of adaptation through the integration of experimental and computational approaches. Our model system is one in which the central, essential and highly interconnected metabolic pathway of Methylobacterium has been disabled and replaced with a foreign, unrelated pathway. The unique advantage of this engineered system is that this replacement specifically results in a 3-fold reduction in fitness, growth rate and metabolic flux, as well as 2.5-fold lower yield and a 30-fold redistribution of flux within the central metabolic hub. Because this alteration directly causes sub-optimal performance, we hypothesize that this will focus selection upon this subsystem during experimental evolution such that adaptation will largely proceed through mutations in the substituted pathway and/or those that it physiologically interacts with. Furthermore, we suggest that increasingly extended and verified mathematical models of this metabolic subsystem and its connections to the metabolic network will allow us to make testable predictions of the fitness effects of altering the activity of individual system components, as well as epistatic interactions between enzymes. Our preliminary results support both our model’s predictions and the assertion that adaptation will strike this central metabolic hub. Our specific aims are to 1.) explore the potential for selection with metabolic models and directly test predictions by modulating expression levels of enzymes, 2.) evolve replicate populations of the ancestral strain and examine phenotypic and genetic changes throughout the course of adaptation and 3.) test the role of epistasis in the adaptive trajectories observed or synthesized. The result of this project will be a novel model system and conceptual framework to apply a comprehensive, systems biology approach to understanding the physiological basis of selection and epistasis in adaptation. It also represents the opportunity to address adaptation occurring after introduction of new genetic material via horizontal gene transfer. We anticipate that placing selection and epistasis into a quantitative framework will have public health impacts ranging from the adaptation of pathogens, the modeling of metabolic diseases, to prognostic predictions of the ’adaptive’ fate of a population of cancer cells with mutated oncogenes and tumor supressors.

Christopher J. Marx Assistant Professor of Biology Department of Organismic and Evolutionary Biology Harvard University Biological Laboratories, Room 3083 16 Divinity Avenue Cambridge, MA 02138 617.496.8103 617.495.8848 (fax) www.oeb.harvard.edu/faculty/marx/ Christopher Marx <cmarx@oeb.harvard.edu>

KansasStateU Genomics

POSTDOCTORAL RESEARCH FELLOWSHIP IN ECOLOGICAL GENOMICS at Kansas State University

To view the following announcement on a webpage, please visit

http://www.k-state.edu/ecogen/Recruit-Postdoc-EcogenVS.htm .

A postdoctoral research fellowship is available through the Ecological Genomics Institute (www.k-state.edu/-

ecogen) at Kansas State University (K-State). Our interdisciplinary Institute seeks to understand responses of organisms to their natural environment by combining functional genomic and ecological/evolutionary approaches. The postdoctoral fellow will have access to excellent university resources including the Konza Prairie Biological Station, a core Long-Term Ecological Research (LTER) site (www.climate.konza.ksu.edu), the K-State Gene Expression Facility (www.k-state.edu/gene-exp), and infrastructure of the Division of Biology and Departments of Entomology, Agronomy and Plant Pathology. For additional information about the Ecological Genomics Institute please visit the Ecogen website!

Candidates must have excellent oral and written communication skills, demonstrate evidence of past research achievement, and have completed requirements for a Ph.D. by the start date. This full-time position provides a competitive salary and benefits. The anticipated start date is summer 2008.

Full applications must include:

1. A cover letter detailing your qualifications and proposed start date.

2. A research proposal (three page maximum, not including references). *Proposals utilizing genetic and/or genomic approaches to examine ecologically relevant traits or interactions will receive highest priority.

3. A current curriculum vitae.

4. Two letters of recommendation from referees who are familiar with the applicant's research. Major advisor or members of supervisory committee preferred.

Completed applications can be e-mailed to Doris Merrill at dmerrill@k-state.edu.

Applications can also be sent by regular mail to:

Ecological Genomics

Kansas State University

Division of Biology, Ackert Hall

Manhattan KS 66506-4901

Review of applications will begin March 15, 2008.

This position is sponsored by a Kansas State University Targeted Excellence Award in Ecological Genomics.

K-State is an Equal Opportunity Employer, and actively seeks diversity among its employees.

Doris Merrill, Program Coordinator

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

PLAN NOW TO ATTEND THE 6th ANNUAL ECOLOGICAL GENOMICS SYMPOSIUM: Genes in Ecology, Ecology in Genes

November 14 - 16, 2008, in Kansas City.

Visit http://www.k-state.edu/ecogen/symp2008-Brief.html for more details.

dmerrill@ksu.edu dmerrill@ksu.edu

Montpellier 1year EvolutionOfSenescence

Applications are invited for a one-year CNRS funded postdoctoral position on the general theme: Evolution of senescence and sexual conflicts: investigations through experiments and natural populations.

The candidate will study the interplay between the evolution of senescence and sexual selection, using long-term observational data from birds and experimental data from manipulations on a freshwater hermaphroditic snail. The post-doc will be based at the Centre dâEcologie Fonctionnelle et Evolutive (CNRS, UMR 5175) in Montpellier, where the applicant will work with Anne Charmantier, Patrice David, and Philippe Jarne. The post can start on September 1st or October 1st 2008 and will run for one year. Gross salary will be 2500â¬*permonth.*

More details on the project and candidate profile < https://www2.cnrs.fr/DRH/post-docs08/?pid=-1&action=view&id=587&lang=en > can be found on the CNRS website, as well as general conditions < http://www2.cnrs.fr/en/349.htm > for applications to CNRS postdocs.

Closing date for applications is 30 March 2008; candidates should download the application file < https://www2.cnrs.fr/DRH/post-docs08/-medias/tpl/pdf/publique/doss-candidat_pdocs.pdf > from the CNRS website and send it to Anne Charmantier (anne.charmantier@cefe.cnrs.fr <mailto:anne.charmantier@cefe.cnrs.fr>).

Best wishes, Anne Charmantier

If the hyperlinks do not work, copy and paste the links below: - project and candidate profile: https://www2.cnrs.fr/DRH/post-docs08/?pid=-1&action=view&id=587&lang=en - application file: https://www2.cnrs.fr/DRH/post-docs08/medias/tpl/-pdf/publique/doss-candidat_pdocs.pdf Nous recrutons un postdoctorant pour un contrat CNRS de 1 an sur le sujet : Evolution de la sÃ©nescence et conflits sexuels : approches expÃ©rimentale et en population naturelle.

Le candidat Ã©tudiera lâinteraction entre lâÃ©volution de la sÃ©nescence et la sÃ©lection sexuelle, sur la base dâanalyses de donnÃ©es Ã long terme dans une population dâoiseau, ainsi que dâune expÃ©rience menÃ©e sur un escargot dâeau douce. Cette Ã©tude sera basÃ©e au Centre dâEcologie Fonctionnelle et Evolutive (CNRS, UMR 5175) de Montpellier ; le postdoctorant y travaillera avec Anne Charmantier, Patrice David et Philippe Jarne. La prise de fonction se fera le 1er Septembre ou 1er Octobre 2008, pour une durÃ©e de 1 an. Le salaire brut est de 2500 â¬*parmois*.

Vous trouverez sur le site du CNRS les dÃ©tails sur le projet et le profil du candidat < https://www2.cnrs.fr/DRH/post-docs08/?pid=1&action=view&id=587 > ainsi que sur les conditions et procÃ©dure de candidature < https://www2.cnrs.fr/DRH/post-docs08/ > pour les postdocs CNRS.

Les candidats ont jusquâau 30 mars 2008 pour adresser un dossier de candidature < https://www2.cnrs.fr/DRH/post-docs08/medias/tpl/pdf/publique/doss-candidat_pdocs.pdf > Ã Anne Charmantier (anne.charmantier@cefe.cnrs.fr).

Dr Anne Charmantier CEFE-CNRS, UMR 5175 1919, route de Mende F34293 Montpellier Cedex 5 France

Tel : +33 4 67 61 32 05 Fax : +33 4 67 41 21 38 Email : anne.charmantier@cefe.cnrs.fr <mailto:arnaud.gregoire@cefe.cnrs.fr>

Anne.CHARMANTIER@cefe.cnrs.fr

Montpellier DiseaseModeling

Dear Colleagues,

Applications are invited for a one-year CNRS funded postdoctoral position on the general theme: Inference of epidemiological processes by maximum likelihood analysis of genetic data; application to Malaria.

The candidate will implement and evaluate the performance of coalescent algorithms for likelihood inference under models of recent population expansions and apply them to malaria biology. The post-doc will be based at the Institut des Sciences de l'Evolution (CNRS, UMR 5554) in Montpellier, where the applicant will work with François Rousset and collaborators in Montpellier, (François Renaud, CNRS/IRD) and Paris (Raphaël Leblois, Museum National d'Histoire Naturelle, CNRS UMR 5202). The post can start on September 1st or October 1st 2008 and will run for one year. Gross salary will be 2500? per month.

More details on < https://www2.cnrs.fr/DRH/post-docs08/?pid=1&action=view&id=532&lang=en >the project and candidate profile can be found on the CNRS website, as well as < http://www2.cnrs.fr/en/349.htm >general conditions for applications to CNRS postdocs.

Closing date for applications is 30 March 2008; candidates should download the < https://www2.cnrs.fr/DRH/post-docs08/medias/tpl/pdf/publique/doss-candidat_pdocs.pdf >application file from the CNRS website and send it to Francois Rousset (<mailto:francois.rousset@univ-montp2.fr).

Best wishes,

F. Rousset

If the hyperlinks do not work, copy and paste the links below:

- project and candidate profile: < https://www2.cnrs.fr/DRH/post-docs08/?pid=1&action=view&id=532&lang=en >https://www2.cnrs.fr/DRH/post-docs08/?pid=1&action=view&id=532&lang=en

- application file: < https://www2.cnrs.fr/DRH/post-docs08/medias/tpl/pdf/publique/doss-candidat_pdocs.pdf >https://www2.cnrs.fr/DRH/post-docs08/medias/tpl/pdf/publique/doss-candidat_pdocs.pdf

frousset@univ-montp2.fr

Montpellier Forest Genetic Diversity

Postdoc

Projet post-doctoral 2007 Reference P-EFPA-4 Axe de recherche INRA : Environnement et espace rural Departement de recherche : Ecologie des forests, prairies et milieux aquatiques (EFPA) Champ thematique du departement : Adaptation des organismes et des populations e leurs milieux Nom de l'unite de recherche : UMR Biodiversite, genes et communautes (BIOGECO) Responsable de l'unite :

A Kremer Responsable scientifique : C Plomion (Christophe.Plomion@pierroton.inra.fr) (INRA), JM Bouvet (CIRAD) Titre : Etude de la diversite nucleotidique de genes candidats impliques dans la composition chimique du bois chez l'eucalyptus et le pin / Pattern of nucleotide diversity in candidate genes for wood chemical properties in eucalyptus and pine

Discipline(s) scientifique(s) : Genetique des populations, genetique moleculaire, Genomique / Population genetics, Molecular genetics, Genomics This project is driven by our desire to understand the genetic basis of wood formation, a unique feature of trees, and by our ambition to exploit this knowledge to accelerate and improve tree breeding for wood and end-use properties. There is a great need to accelerate breeding in forest trees because of their long generation times and the projected demand for increased production of good quality fibres. However, ecological concerns and market acceptability require knowledge-based, non-GMO tree improvement. In this context, our goal will be to identify genes and nucleotide polymorphisms that govern naturally occurring phenotypic variation of wood and end-use properties in breeding populations of Pinus pinaster and Eucalyptus urophylla, two species belonging to the main forest tree genera used in industrial plantations.

Rational/Backgroung : During the past 40 years, optimisation of sylvicultural practices combined with the introduction of improved varieties have contributed to increase the productivity of our forest in temperate and tropical regions. Gains in productivity have often been followed by a reduction in harvest age which has led to a greater proportion of lower quality juvenile wood being harvested. In order to maintain the utility of plantation grown wood, there is now a critical need to focus breeding efforts on the improvement of wood quality. INRA and CIRAD have developed multidisciplinary researches in order to study whether these traits are variable and heritable and whether simple and early selection criteria can be defined. In addition, QTL analysis and the tool kits of genomics have been used in concert in order to identify the genes putatively involved in wood properties.

Objectives : The main objective of this project is to study the landscape of nucleotide variation of candidate genes for wood chemical composition, as a prerequesite toward the application of gene assisted selection. First, the level and structuration of the diversity will be described in the genetic pool from which the breeding populations were derived. Second and keeping in mind the potential adaptive value of wood, we will test whether the pattern of nucleotide diversity is compatible or not with the effect of natural selection.

Methodology, Partner, and Schedule: Re-sequencing and cloning will be used to describe nucleotide diversity in a discovery panel of 20-40 genotypes. In Eucalyptus, emphasis will be made on cellulose biosynthesis related genes. The study will be carried out in Montpellier for one year, within the forest genetics unit of CIRAD (http://www.cirad.fr/ur/genetique_forestiere). In pine, 2000 amplicons are being re-sequenced in USA (NSF project coordinated by D Neale), and will be used in association study for several wood properties including chemical composition. Genes for which SNPs will be significantly associated with trait variation will be selected for full length resequencing. The study will be carried out in Bordeaux for one year, within the BIOGECO research unit (http://www.pierroton.inra.fr/biogeco/). Nucleotide and haplotype diversity, extent of linkage disequilibrium, departure from the neutral model of evolution will be the main outputs of this study. In perspectives, relevant polymorphisms will be selected for association mapping in both species.

–

Jean-Marc Bouvet CIRAD, Biologcal System Department Head of Research Unit 39: "Genetic Diversity and Breeding of Forest Tree Species" Campus international de Baillarguet TA A-39/C 34398 Montpellier Cedex 5 FRANCE Tel: 33 (0)4 6759 3728 Fax: 33 (0)4 6759 3732 Web site : http://www.cirad.fr/ur/genetique_forestiere Personal web site : http://agents.cirad.fr/index.php/jean-marc.bouvet@cirad.fr jean-marc.bouvet@cirad.fr

Oslo 4 CenterEcolEvolSynthesis

4 Post-doctoral Research Fellow/ alt. Researcher

4 POST-DOCTORAL RESEARCH FELLOW/alt. RESEARCHER POSITIONS

available at the Center for Ecological and Evolutionary Synthesis (CEES), Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo.

The positions are available for a period of three years and are funded by the Norwegian Research Council.

The CEES is a centre for integrative biological research that has recently been awarded the status of a national centre of excellence by the Norwegian Research Council. The centre is an important part of the Department of Biology, and researchers at CEES collaborate with many of the faculty staff that are not directly connected to the centre. The purpose of the CEES is to combine competence from various fields of biology, molecular biology, bioinformatics and statistics in order to approach major, but still unresolved, scientific challenges. An overall goal is to achieve an increased understanding of how living organisms respond and adapt to environmental changes. The centre has funding to engage in cutting-edge research, it features a modern and well-equipped molecular lab facilitated for high-throughput sequencing, as well as a broad spectrum of field facilities. We are focusing both on development of new theoretical/ statistical methods/models and on diverse ecological and evolutionary questions in empirical systems ranging from microorganisms and plants to aquatic and terrestrial vertebrates. On-going research includes subjects such as gene flow and the early stages of diversification, selection and evolvability, evolutionary effects of human-altered ecological systems (e.g., harvesting and climate change) and genetic aspects of reproductive isolation. Read more about our research and possible research projects at http://www.cees.uio.no/about/vacancies/sff2008.html . The post-docs/researchers we seek will play an important part in the integrative work of the CEES and we particularly look for individuals with strong interests and abilities for inter-disciplinary scientific work. Two of the positions will be allocated for theoretical biology and statistics, while the remaining two positions are open for candidates with any relevant background.

The CEES provides an international and inspiring research environment. The centre is chaired by Nils Chr. Stenseth and currently employs 17 faculty members, 34 postdocs/researchers, 27 PhD students, 25 Master students, and 33 official collaborators.

Applicants must hold a degree equivalent to a Norwegian doctoral degree in biology, statistics or other relevant fields. The main purpose of post-doctoral/ researcher fellowships is to qualify researchers for work in top academic positions within their disciplines. Applicants should submit a letter of application describing their scientific experience and interests with emphasis on how they expect to contribute to the CEES,

a project description, at least 2 references/letters of recommendation, curriculum vitae including a list of published work, four sets of copies of certificates, and copies of at most five publications. When evaluating the application, emphasis will be given to the project description and the applicant's academic and personal prerequisites to carry out the project. Applicants may be called for an interview.

Please consult our web page (http://www.cees.uio.no/about/vacancies/sff2008.html) and do not hesitate to contact any members or the centre leader Nils Chr. Stenseth (n.c.stenseth@bio.uio.no) for more information.

Applicants who have already been employed as post doc may be employed as researcher (1109). Please also refer to the regulations pertaining to the conditions of employment for postdoctoral/researcher positions: http://www.uio.no/admhb/reglhb/personal/tilsettingvitenskapelig/guidelinespostdoctor.xml Applications should be sent to the Faculty of Mathematics and Natural Sciences, (marked with the REF:NR.), Attn.: Senior Executive Officer Bente Schjoldager, P.O.Box 1032, 0315 OSLO, NORWAY.

The University of Oslo wishes to attain a more equal gender distribution for academic positions. Therefore, women are in particular encouraged to apply.

The University of Oslo has an agreement for all employees aiming to secure rights to research results a.o.

—–

For further information please contact: Professor Nils Christian Stenseth, phone: +47 22854584, e-mail: n.c.stenseth@bio.uio.no.

For more information on the positions and the centre, please see: http://www.cees.uio.no/about/vacancies/sff2008.html Post-doctoral research fellowship, SKO 1352

— / —

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

Porto Portugal Genomics

Job/Fellowship Reference: C2007-CIIMAR/Genomic and Proteomic/06 b

Genomics and Proteomics Research Assistant

Job summary: The CIIMAR opens a position for postdoctoral fellow to develop studies in genomics and proteomics of eukaryotes and prokaryotes, to estimate the responses of model organisms to the presence of toxins and xenobiotics in the environment and potential use as biomarkers. The PhD to be hired, whether Portuguese of foreign national, must have at least 3 years of relevant post-doc experience and a significant scientific production in molecular toxicology.

Job description: The Centre of Marine and Environmental Research of the University of Porto (CIIMAR) opens a position for a scientist to work in genomics and proteomics applied to ecotoxicology, focusing in the identification of the effects and mechanisms of toxicity of toxins and xenobiotics. This will be used to analyze specific toxicant pathways and mechanisms of action and to asses the risk of exposure to contaminants. The CIIMAR is one of the leading centres in this research field in Portugal. The CIIMAR is part of the CIMAR ? Associate Laboratory. The CIMAR ? LA is dedicated to research and to dissemination and transfer of technology in Aquatic Sciences. Its main objective is to carry out basic and applied research on the processes occurring in aquatic ecosystems including the study of impacts of human activities on these ecosystems. The CIIMAR members are organized in different laboratories. More information about CIIMAR and CIMAR ? LA can be found at http://www.cimar.org or http://www.eracareers.pt/-opportunities/index.aspx?task=global&jobId=8661 The PhD to be engaged, for an initial 5 year period. Preferentially, the candidate should have experience in real-time PCR, cDNA arrays, hybridization and analysis. Also background on in situ hybridization and immunohistochemestry will be an advantage. Experience in extraction/purification techniques using chromatographic separation will be considered. The candidate must have solid knowledge on research techniques used for protein expression studies, namely extraction, purification and quantification of proteins, 2 ? DE and analysis of results from MALDI-TOF and LC-MS-MS. The successful candidate will collaborate in the supervision of PhD students and post-docs. The job implies the submission and coordination of national and international projects, within the scope of the research lines of the two laboratories. The candidate will be assigned to the staff of the Laboratory of Environmental Toxicology (http://www.ciimar.up.pt/-letox) and Laboratory of Ecotoxicology Augusto Nobre (http://www.ciimar.up.pt/lean), joining research studies between those two laboratories. Payment will be made in accordance with the position of Assistant Researcher (salary before taxes ca. 42.000?). The selection panel will be constituted by: Maria Armanda Reis Henriques (President of the Jury, CIIMAR, University of Porto, Portugal); Vítor Vasconcelos (CIIMAR, University of Porto, Portugal); Pedro Moradas Ferreira (IBMC, University of Porto, Portugal); and Cláudia Wiegand (IGB, Berlin, Germany). Candidates should apply by sending a cover letter, curriculum vitae and copies of academic certificates. All documents must be sent by email, in PDF format and with clear indication of the Job Reference and the title for this particular position. Use the email: eafonso@ciimar.up.pt

Vacant posts: 1 Type of contract: Contrato a termo certo Job country: Portugal Job city: Porto Job company/institute: CIIMAR

Application deadline: 21 Abril 2008 (The Application's deadline must be confirmed on the Job Description)

2. Dados de contactos da organização 2. Organization contact data Organization/institute: CIIMAR - Centro Interdisciplinar de Investigação Marinha e Ambiental Address: Rua dos Bragas, n.o 289 Porto - 4050 - 123 Portugal Email: eafonso@ciimar.up.pt Website: http://www.cimar.org 3. Habilitações académicas 3. Required education Level Degree: PhD

Degree field: Biological sciences

4. Línguas exigidas 4. Required languages Language: English Priority: High Reading: Excelent Writing: Excelent Comprehension: Excelent Conversation: Excelent

vmvascon@fc.up.pt

QueenMaryU ViralVirulenceEvolution

We are looking for an experienced Postdoc to investigate the evolution of virulence in the chickenpox virus (varicella-zoster).

The project builds on previous work in our group (Quinlivan et al 2007, PNAS 104,208) which investigated live vaccine strains than have caused rashes. You would use reverse genetics to reconstruct live viruses carrying the relevant mutations. These viruses will be analysed in epithelial models to determine whether the rash mutations in the vaccine strain confer a replication advantage in skin.

You should have a PhD and preferably at least 3 years post doctoral research experience. A background in virology, genetics or cell biology is preferred. Experience with any or all of the following: sequencing technologies, cell culture, recombinant DNA technology, and confocal microscopy would be helpful. Further details of the project are available from Prof Judy Breuer, Centre for Infectious Disease (Tel +44 20 7882 2308, email j.breuer@qmul.ac.uk) or Prof Richard Nichols (Biological & Chemical Sciences, Queen Mary Univ. London

R.A.Nichols@qmul.ac.uk)

Formal details of the post and application procedure are here: http://webspace.qmul.ac.uk/ranichols/advert.pdf r.a.nichols@qmul.ac.uk r.a.nichols@qmul.ac.uk

StateUNewYorkAlbany EvolImmuneFunction

Post-Doctoral Associate: Pathogen/host interaction, Ecological Immunology

I am currently recruiting a post-doctoral associate to join my lab in the Department of Biological Sciences at the State University of New York at Albany. Highly motivated individuals interested in the evolutionary ecology of immune function and pathogen/host interactions are encouraged to apply. Experimental and genetic/genomic approaches are used in my lab to understand factors contributing to the evolutionary maintenance of disease susceptibility in Drosophila populations. Current projects include examining the causes and consequences of 'costs' of immunity, the evolution of cooperative virulence mechanisms, characterization and evolution of natural pathogens of Drosophila, and the evolution of sexual conflict, sex- biased gene expression, and implications for immune function. (See: http://www.albany.edu/faculty/kmckean/Site/McKean_Lab_Home.html)

Applicants must hold a Ph.D. from a college or university accredited by the US Department of Education or internationally recognized accrediting organization. The successful candidate will possess a working familiarity with population genetics, evolutionary ecology and basic molecular biology (PCR, cloning, sequencing, SNP identification, RNA extraction and expression analysis). Experience with Drosophila will be looked upon favorably, but is certainly not necessary. The successful candidate will be encouraged to pursue his/her own ideas and projects.

In addition, the post-doc will have the opportunity to interact with participating faculty, post-docs and students in the new Ecology and Evolution of Disease (EED) initiative at U.Albany. The EED initiative is an interdisciplinary program with faculty from the Department of Biological Sciences and the Department of Anthropology, as well as researchers from the Department of Biomedical Sciences at the Wadsworth School of Public Health. The EED program has sponsored seminar series, various journal clubs and discussion groups, as well as a formative curriculum relevant to this interesting and rapidly growing field of research. Information on this program and other participating faculty can be found here: http://www.albany.edu/biology/EED/index.html .

The initial appointment will be for one year with the possibility of renewal for another year. Salary and benefits are competitive. Interested applicants should send a cover letter detailing their experience and interests, CV and contact information for 3 references to Dr. Kurt McKean (kmckean@albany.edu). Applicants must address in their applications their abilities to work with and instruct a culturally diverse population. Initial review of applications will begin immediately and will continue until the position is filled. The University at Albany is an EO/AA/IRCA/ADA employer.

U. Albany is located in Albany, the capitol of the state of New York. Centrally located between the Catskill and the Adirondack parks, the region provides abundant opportunities for outdoor recreation, and is also close to the metropolitan centers of New York City, Boston and Montreal.

Dr. Kurt A McKean Department of Biological Sciences 329BI SUNY at Albany 1400 Washington Ave. Albany, NY 12222 Phone (office): 518-442-4367 Phone (cell): 518-488-7273 Fax: 518-442-4767 kmckean@albany.edu http://www.albany.edu/faculty/kmckean/Site/McKean_Lab_Home.html kmckean@albany.edu kmckean@albany.edu

UAkron BiomaterialEvolution

Postdoctoral Position in Evolutionary Spider Silk Biomechanics

A postdoctoral position is available to work on the evolution of silk biomechanics and spider webs in collaboration with Dr. Todd Blackledge at the University of Akron. Spider silk is an exceptional biomaterial with high performance properties that make it a model for biomimetic applications in medicine and industry. This interdisciplinary NSF funded project seeks to understand how the mechanical function of spider silk evolves during behavioral transitions in web architecture. Primary responsibilities will include characterizing the material properties of silks spun by diverse species of spiders. In addition, significant opportunities exist to develop independent projects that incorporate ecological, physiological, materials science or engineering approaches to spider silk. More information is available at http://www3.uakron.edu/biology/blackledge/index.htm.

This project is part of the University of Akron's growing emphasis on integrated bioscience research. It takes advantage of Akron's world renowned expertise in materials science and provides postdocs with opportunities for training in diverse fields. The Akron area provides an exceptional lifestyle - a low cost of living with more than a dozen local parks and the scenic Cuyahoga Valley National Park on its doorstep. Other highlights include access to a variety of local sports and cultural events, including the nearby metropolitan city of Cleveland.

Salary will start at $34,000 annually, depending upon experience, plus full benefits, and will include funding for travel expenses for conferences and research. The position is available for up to two years. The starting date is flexible, but summer 2008 is preferred. Candidates should have received their Ph.D. by the start of the appointment. To apply, candidates should submit a cover letter detailing research goals, curriculum vitae, up to 3 representative publications, and the contact information for 3 references. Applications should be submitted to Todd Blackledge, Department of Biology, University of Akron, Akron, OH 44325-3908, USA, via mail or sent via email (Blackledge@uakron.edu). Review of applications will begin late March and continue until filled.

Todd A. Blackledge Assistant Professor Department of Biology University of Akron Akron, OH 44325-3908

Voice: (330) 972-7264 Fax: (330) 972-8445 Email: blackledge@uakron.edu http://www3.uakron.edu/biology/blackledge/index.htm tab27@uakron.edu tab27@uakron.edu

---

UAlaskaFairbanks Evolution of PlantBudDormancy

UNIVERSITY OF ALASKA FAIRBANKS INSTITUTE OF ARCTIC BIOLOGY

POSTDOCTORAL POSITION IN PLANT EVOLUTIONARY GENETICS

A postdoctoral position is available in my lab to examine the genetic basis and evolution of variation in bud dormancy across a latitudinal cline in poplar. I am particularly interested in an individual with skills or interest in population genomics, QTL or association mapping, and/or bioinformatics. The successful applicant will be working on a multi-year project to conduct an association and comparative mapping study in conjunction with labs in Canada, Minnesota and Sweden. Applicants with backgrounds in evolutionary and/or ecological genetics and bench and/or computational/statistical skills and interests are encouraged to apply. The ideal candidate will be organized, pay close attention to detail, and be able to work independently and in groups. The successful applicant also will be expected to work closely with graduate and undergraduate students working on the project.

The start date is July 1, but considerable flexibility can be negotiated. The initial appointment is for 1 year, with an additional 2 years' funding available conditional on satisfactory performance. The annual starting salary for this position is $40,000 and includes benefits. The University of Alaska is an equal opportunity employer and applications from candidates from groups underrepresented in the life sciences are encouraged to apply.

Review of applications will begin on February 19 and continue until the position is filled. Please apply for JOB08-54 Position Number 921391 at < www.uakjobs.com/applicants/Central?quickFinda938 > and include a statement of your interest and qualifications for the position, a CV, a statement of your research interests, and the names and contact information for 3 personal references.

The Olson lab is a part of a vibrant program in ecology and evolutionary biology at the University of Alaska Fairbanks. More information concerning our lab can be found at http://users.iab.uaf.edu/ ~ matt_olson/lab_site.htm ; additional information concerning the Institute of Arctic Biology can be found at http://www.iab.uaf.edu/ . For additional information concerning this position, please contact Matt Olson at matt.olson@uaf.edu.

Matt Olson <matt.olson@uaf.edu>

UAzores SubterraneanBioDiversity

Paulo Alexandre Vieira Borges E-Mail: pborges@uac.pt

POST-DOC POSITION

Post-Doctoral Grant Under the scope of the Project PTDC/AMB/70801/2006 A position will be available for a Post-Doctoral Grant holder under the scope of the project “Understanding Underground Biodiversity: Studies in Azorean Lava Tubes” (reference PTDC/AMB/70801/2006), funded by the Foundation for Science and Technology, Ministry of Science, Technology and Higher Education of Portugal (FCT). The research work will take place in the Centre for Agricultural Research and Technology of the Azores (University of The Azores), under the following conditions: 1. Duration, regime of activity and payment: 1.1 Duration: The grant is due to start on February, 2008 and will last for 12 months. It can be renewed for a maximum of 36 months, depending on the periodic evaluation of the performance of the grant holder. Insufficient performance will lead to termination of the grant. 1.2 Regime of activity: The grant holder will perform the work required under the grant terms in exclusivity, according to the Regulation for Advanced Education of Human Resources of the funding institution (FCT) (http://www.fct.mctes.pt/pt/apoios/-formacao/ambitoprojectos). 1.3 Payment: Payment is in accordance to the values established by the funding institution (FCT): monthly payments of 1495,00 + 79,57 (voluntary social security payment). Payments are carried out by bank transfer to the account of the grant holder.

The grant holder will also have an insurance against work accidents. 2. Object of activity: 2.1 The objectives of the Project, as far as this grant is concerned, are: a. Study the biodiversity of microbial biofilms in lava tubes, identifying the microorganisms they contain by culture-dependent and culture-independent methods. b. Study the antimicrobial potential of microorganisms from caves against antibiotic resistant, pathogenic microbial strains. c. Understand the physical environment within the caves. d. Find biological indicators that serve as surrogates for evaluating the biodiversity of microbial biofilms. e. Provide information to various types of target groups (politicians, technicians, scientists, teachers, visitors, etc.) to spread the obtained knowledge and to promote a balanced exploitation of the caves. 2.2 Within this project, the grant holder will carry out work that requires employing: a) Molecular biology techniques; b) Techniques for the maintenance of microbial cultures; c) Chemical, instrumental analysis techniques, such as chromatographic techniques; d) Field work in the area of speleology. 3. Scientific supervision: Dr. Maria de Lurdes Enes Dapkevicius; Dr. Paulo Borges; Dr. Rosalina Gabriel; Dr. CÃ©lia Silva, Dr. Diana Northup. 4. Qualification and requirements: Candidates must have a PhD in Biological Sciences, Microbiology, Biochemistry, Molecular Biology or similar areas, with good classification. Candidates that have proved previous experience in microbiology, molecular biology techniques, systems for maintaining microbial cultures, instrumental chemistry and good language skills (both in writing and speaking) of Portuguese or English will be preferred. 5. Criteria for the evaluation of the applications: The evaluation of the applications will be based on the merit of the candidate, taking into account its academic education, its curriculum and previous experience in scientific research of relevance for the project. The curriculum evaluation may be completed with and interview, if judged necessary by the jury. 6. Documents for application: 6.1 Applications will be formalized by means of a motivation letter addressed to the president of the jury, to which the following documents must be attached: a) Copy of the document that proves the obtention of the academic degree(s), with a list of all marks obtained in each subject in the course; b) Copy of the legal identification document; c) Detailed Curriculum vitae (maximum 10 pages); d) Support letters (maximum 2). 6.2 If the documents required in a) to c) of the previous item are not presented by the candidate, the application is not valid. Note: The present announcement will be published in http://-www.angra.uac.pt/gba . 7. Applications: Applications will take place within January 14th and January 28th, 2008 (date of the postal stamps). Applications must be sent by post to:

Dr. Maria de Lurdes Enes Dapkevicius Universidade dos Azores Departamento de Cincias Agrrias CITA-A Terra Ch 9701-851 Angra do Herosmo Portugal

Additional informations may be obtained from mariaenes@notes.angra.uac.pt or pborges@uac.pt, as well as by phone +351 295 402 200 (Prof. Dr. Maria de Lurdes Enes Dapkevicius or Prof. Dr. Paulo Borges).

Paulo Alexandre Vieira Borges <pborges@uac.pt>

UCaliforniaIrvine PlantComparativeGenomics

A postdoctoral position in plant evolutionary genetics is available on or after April 1, 2008 in the Department of Ecology & Evolutionary Biology at the University of California, Irvine. The aim of the project is comparative evolutionary analysis of plant genomic sequence data, particularly comparisons of Arabidopsis thaliana to the new genome sequences of Arabidopsis lyrata and Capsella rubella. The successful applicant must have a PhD and demonstrated expertise in molecular evolution and bioinformatics methods. To apply for this position, please send a statement of interest, a CV, and contact information for 3 references to the contact information below:

Applications due by: 02/29/08 The position will remain open until filled.

Contact information:

Dr. Brandon S. Gaut Department of Ecology and Evolutionary Biology 5221 McGaugh Hall University of California, Irvine Irvine, CA 92697-2525 e-mail: bgaut@uci.edu

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

bgaut@uci.edu

UCBerkeley ComparativeBiodiversity

JOB TYPE Post Doctoral Scholar, 2.5 years (beginning March 1, 2008)

JOB AREA University of California, Museum of Vertebrate Zoology (MVZ)

JOB NOTES:

The Museum of Vertebrate Zoology at UC Berkeley is currently engaged in a long-term project to document changes in diversity and distributions of small mammals and birds in California through re- surveys of sites originally examined by Joseph Grinnell and colleagues in the early 20th Century. The intent is to use these data to test the performance of model-based predictions of species responses to changes in climate and land-cover, and thereby improve on predictions of future responses. There is considerable scope for creativity within the broad goals of the project. With support from the National Science Foundation, we seek to recruit two vertebrate ecologists V one at the postdoctoral level and the other a field biologist. Further information can be found at http:// mvz.berkeley.edu/Grinnell/index.html or by contacting the Director of the MVZ, Craig Moritz, at craigm@berkeley.edu.

DUTIES: The Post Doctoral vertebrate ecologist will document changes in diversity and distributions of small mammals and birds in California through resurveys of sites originally examined by Joseph Grinnell and colleagues in the early 20th C. The intent is to use these data to test the performance of model-based predictions of species responses to changes in climate and land-cover, and thereby improve on predictions of future responses. The appointee is expected to lead a field team, analyze data and prepare papers for publication.

QUALIFICATIONS: The ability to lead field survey teams, often in remote locations requiring back-packing and camping, and to commit to extensive periods in the field. Experience with specimen preparation is required as well as strong analytical skills, field experience in small mammal survey, and the ability to communicate its goals and outcomes. Prior experience with spatial modeling or analyses would be an advantage. A PhD and experience in a relevant discipline is required.

Salary range is $34,752 to $41,496 commensurate with skills and experience.

To apply for the postdoctoral position: Please email the MVZ Director, Craig Moritz, craigm@berkeley.edu, with a two to four page statement of interest describing your personal and professional background, experience, interests and goals, your CV, transcripts of graduate coursework, and the names and addresses of three references. You may also apply via mail to the MVZ, Director Craig Moritz, University of California, 3101 VLSB, Berkeley, CA 94720-3160. The application deadline is February 22, 2008.

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

Chris Conroy

Chris Conroy <ondatra@berkeley.edu>

UFribourg EvolutionaryPlantEcology

Postdoctoral Position in Evolutionary Plant Ecology

Rationale: The European knapweed Centaurea maculosa, introduced from Central Europe into North America during the late 19th century, where it covers now an area larger than Switzerland, has become a model for research on the ecological and evolutionary causes and consequences of invasions. We aim to explore the role of rapid evolutionary processes in the invasion success of C. maculosa. This involves the analysis of selection exerted by herbivorous insects (biocontrol agents) on plant life-history traits in different environments and the study of genetic factors (especially polyploidisation) underlying evolutionary change in the exotic range.

We seek a highly motivated person to conduct field and greenhouse experiments, and various lab studies (crossing experiments, molecular markers, flow cytometry, phenotypic traits, etc.). We are part of a large national and international network with which to candidates is expected to interact. New ideas and complementary studies are of course highly invited.

Requirements

- doctoral degree in experimental plant ecology or evolution, or related disciplines; - knowledge of, and experience in one or several of the following areas of research is highly desirable: population ecology, population genetics, plant-herbivore interactions, experimental design and statistics.

Salary and conditions Salary dependent on age and status (gross salary in the first year about CHF 70'000).

Start date: preferentially on 1 April 2008. The position will also include support of research activities of our group. The position is for 1 year, but may be extended depending on funding.

Applications

Applicants should send their CV, including the publication list, a short summary of research experience and interests, and the names of two professional referees to the address below (preferably by e-mail).

For further information, please contact:

Prof. Dr. Heinz Mueller-Schaerer, Département de Biologie, Unité Ecologie et Evolution, Université de Fribourg, Chemin du Musée 10; CH-1700 Fribourg, SWITZERLAND.

tel: + (41) (0) 26-300 88 35 direct, ++ 50 secr., fax: + (41) (0) 26-300 96 98;

e-mail: heinz.mueller@UNIFR.CH; http://www.unifr.ch/biol/ecology/ This is a joint position between H. Müller-Schärer (Uni Fribourg) and Urs Schaffner (CABI Europe-Switzerland, Delémont) within the National Centre of Competence in Research (NCCR) Plant Survival, funded by the Swiss National Science Foundation.

heinz.mueller@unifr.ch heinz.mueller@unifr.ch

UGeorgia EvolutionaryBiology

POSTDOCTORAL POSITION, available immediately.

A postdoctoral position is available to study theoretical and/or experimental aspects of evolution in the lab of Dave Hall at the University of Georgia. Area of interest is open. Current projects in the lab are aimed at understanding chromosome evolution, adaptation and epistasis. We are seeking an enthusiastic and motivated person to work on evolutionary questions using mathematical models and/or experiments with yeast. The Hall lab is located in the Genetics Department, which includes a diverse group of highly interactive faculty (www.genetics.uga.edu). The lab is also a member of the UGA Center for the Study of Evolution, which encompasses almost forty labs from across the university (www.genetics.uga.edu/evolution/evoluga.html). There are thus numerous opportunities for professional development both within the Genetics Department and across campus.

Applicants should have a PhD in evolutionary biology. We offer a competitive salary, with full benefits. Funding is guaranteed through June 2009. The successful applicant will be expected to seek additional funding. Applications should include a curriculum vitae and the names of three references. Applications and inquiries should be sent to Dave Hall at davehall@uga.edu or Life Sciences - Genetics, The University of Georgia, Athens GA 30602-7223. For more information on the Hall lab, visit: http://mendel.genetics.uga.edu/ . davehall@uga.edu davehall@uga.edu

---

UHelsinki Bioinformatics

Post-doctoral Research Associate in Molecular evolutionary biology/Bioinformatics

We seek a post-doctoral researcher with training/experience in bioinformatics and large-scale sequencing to conduct research in two projects based on 454-sequencing and related to population dynamics and molecular evolution. The post doc will work in a large international research group.

One project is concerned with a highly variable gene (Pgi) with strong association with individual performance and fitness in the Glanville fritillary butterfly, which has been the focus of large-scale research since 1991. The research involves sequencing and analysis of large population samples. The second project is concerned with the identification and quantitative measurement of the abundances of fungal species in decomposing tree trunks. This project is related to an ERC-funded project on metacommunity dynamics of polyporous fungi. In both projects the sequencing will be carried out at the nearby high-throughput laboratory of the Institute of Biotechnology, University of Helsinki, using massive parallel sequencing methods.

PhD and prior experience with bioinformatics and molecular biology methods is required. Strong candidates would additionally have interest in molecular evolution and/or population genetics. The position is available for two years with possible extension for up to two more years.

We offer a highly international research environment with excellent possibilities to interact with researchers in ecology and evolutionary biology, molecular biology, mathematics, and statistics. Salary and social benefits according to the University of Helsinki Salary Scale, around 3,100 ? / month (negotiable based on experience).

Applications including a short CV (max 3 pages), list of publications, and the e-mail addresses of two researchers willing to write a letter of reference should be sent to ilkka.hanski@helsinki.fi (cc tuuli.ojala@helsinki.fi; write “mol ecol post doc position” on the subject line). For more details on the research group see http://www.helsinki.fi/science/metapop/. Applications are due by February 29. The position will remain open until filled.

Ilkka Hanski Research professor University of Helsinki http://www.helsinki.fi/science/metapop
otso.ovaskainen@helsinki.fi otso.ovaskainen@helsinki.fi

UHelsinki MathBiology

Postdoc and PhD positions in Mathematical Biology

The Mathematical Biology Group at the Department of Biological and Environmental Sciences, University of Helsinki, Finland (leader Dr. Otso Ovaskainen) is seeking outstanding, highly motivated candidates to join research projects at the interface between mathematics and ecology and evolutionary biology. Successful candidates may have their training either in mathematics or in biology, the main criteria being the potential to perform top-quality research. We anticipate hiring up to 4 postdoctoral researchers or Ph.D. students over the next 3 years. Research projects will be developed in conjunction with the interests of the successful candidates, focused on the following areas:

1. The roles of space and stochasticity in population dynamics
2. Metacommunity dynamics of wood-decaying fungi
3. Animal movement in heterogeneous environments
4. Bayesian approaches in evolutionary quantitative genetics

The PhD student positions are available for 4 years. The postdoc positions are for 1 year, with the possibility of a 2-year extension.

The Mathematical Biology group is part of the Metapopulation Research Group (leader prof. Ilkka Hanski), which is a Centre of Excellence in Research supported by the Academy of Finland. We offer an international research environment with excellent possibilities to cooperate with experts in mathematics, statistics, population biology, and evolutionary ecology. Salary and social benefits according to the University of Helsinki Salary system, around 2,300 /month for PhD students and 3,100 /month for post docs (the latter negotiable).

Applications including a short CV (max 3 pages), list of publications, and the e-mail addresses of two researchers willing to write a letter of reference should be sent to otso.ovaskainen@helsinki.fi with cc to tuuli.ojala@helsinki.fi; write either “postdoc position” or “ PhD student position” on the subject line. For more details on the research projects and on the application procedure, see http://www.helsinki.fi/science/metapop/MBG/positions/index.htm Deadline for applications 14th March 2008, starting date 1st May 2008 (negotiable).

Otso Ovaskainen Academy Research Fellow Department of Biological and Environmental Sciences P.O. BOX 65 (Viikinkaari 1) 00014 University of Helsinki FINLAND

otso.ovaskainen@helsinki.fi otso.ovaskainen@helsinki.fi

ULaval SalmonidFunctionalGenomics

POSTDOCTORATE POSITION IN SALMONID FUNCTIONAL GENOMICS

We are currently looking for a postdoctorate candidate to be involved in our ongoing research program on the elucidation of genetic basis of phenotypic differentiation and adaptive divergence among populations of salmonid fishes. This multidisciplinary project is funded by NSERC (Canada) and part of the research program of the Canadian Research Chair in Genomics and Conservation of Aquatic Resources held by Louis Bernatchez, as well as The Rï¿½seau Aquaculture Quï¿½bec. The project also involves co-investigator Nicolas Derome (functional and microbial genomics) and Celine Audet (comparative physiology).

The specific objective of the proposed research will be to develop a genetic map for the brook charr, Salvelinus fontinalis, that will be built from SNP markers to be identified by 454 sequencing and genotyped using the Sequenom technology, phenotypic QTL, as well as gene expression QTL (eQTL) analysed by means of a 30,000 gene cDNA microarrays.

We are primarily looking for a candidate with strong laboratory skills in genotyping and transcriptomics, a solid theoretical background in quantitative genetics and mapping, as well as expertise in bioinformatics, management and analysis of large data bases. The position is available now and will be offered for 2 years with a possibility of extending to a third year.

To apply, please send a cover letter describing your research interests, a complete CV and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca

To learn more about ...

Quebec city : < http://www.quebec-travelguide.com/ >http://www.quebec-travelguide.com/ http://www.quebec-guidetouristique.com/ Laval University : < http://www.ulaval.ca/ >http://www.ulaval.ca/

The Canadian Research Chair in Genomics and Conservation Genetics < http://www2.bio.ulaval.ca/louisbernatchez/ >http://www2.bio.ulaval.ca/louisbernatchez/

Louis Bernatchez

Titulaire de la Chaire de recherche du Canada en Gï¿½nomique et Conservation des Ressources Aquatiques

Dï¿½partement de biologie Pavillon Charles-Eugï¿½ne Marchand Universitï¿½ Laval, Quebec QC G1K 7P4 Canada

Tï¿½l: 418 656-3402 Fax: 418 656-2043 Couriel: Louis.Bernatchez@bio.ulaval.ca Web: http://www.bio.ulaval.ca/louisbernatchez/

Louis.Bernatchez@bio.ulaval.ca

UMissouriStLouis PlantPhyloSystematics

VACANCY ANNOUNCEMENT

Post-doctoral position description E. Desmond Lee Laboratory of Molecular Systematics University of Missouri-St. Louis

Two post-doctoral positions are available in the Department of Biology, University of Missouri St. Louis, each for one year. 1. Phylogenetic systematics of switchgrass and its relatives. A Ph.D. and experience in plant evolutionary biology or molecular systematics are required. Preference will be given to applicants with experience working with low-copy nuclear genes. 2. Evolutionary developmental genetics of grass inflorescences. A Ph.D. and experience in molecular biology or genetics are required; basic familiarity with plant morphology is also essential. Applications should include a brief cover letter outlining qualifications and interests, curriculum vitae, and names, phone numbers, and email addresses of three references. Send applications via email to Dr. Elizabeth A. Kellogg, tkellogg@umsl.edu. Review of applications will begin on March 1, 2008 and will continue until positions are filled.

The University of Missouri-St. Louis is an affirmative action, equal opportunity employer, committed to excellence through diversity.

Elizabeth A. Kellogg E. Desmond Lee and Family Professor of Botanical Studies Department of Biology University of Missouri-St. Louis St. Louis, MO 63121 Tel: 314-516-6217; FAX: 314-516-6233 http://www.umsl.edu/services/kellogg/ Elizabeth Kellogg <kellogge@umsl.edu>

UPenn DiseaseEcoEvol

Post Doc The Brisson lab at the University of Pennsylvania is seeking a highly motivated post-doc to work at the interface of ecology, evolution, and human health. There are several potential projects involving Borrelia burgdorferi, the causative agent of Lyme disease, and other vector- borne diseases.

We aim to address causes of variation in host and pathogen populations and their consequences to bacterial and host evolution and to public health using a combination of laboratory, field, and computational studies. Specific projects include integrating across scales of biological complexity (i.e. molecular-level, organism-level, and population-level) to identify the molecular and ecological mechanisms maintaining the polymorphisms and to determine the consequences of these mechanisms on the distribution and abundance of B. burgdorferi and on human Lyme disease risk. Additionally, we aim to use our acquired understanding of the life-history strategy and ecological conditions that promote human disease risk to address current public health issues.

The position requires a highly motivated, enthusiastic, and enquiring individual with a background in evolutionary biology, ecology, statistics, or related fields. Molecular and field experience are advantageous. Good quantitative skills are essential.

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

The position is available as early as June 2008; the starting date is flexible and we are willing to wait for an outstanding candidate.

For informal enquiries and formal applications including curriculum vitae, list of publications, a one page statement of research interests and the names of three potential referees (all in a single file if applying by email), can be submitted to:

Dustin Brisson Department of Biology University of Pennsylvania Leidy Laboratories, 326 433 South University Avenue Philadelphia PA 19104-6018

http://www.bio.upenn.edu/faculty/brisson/ http://-brisson.bio.upenn.edu/ dbrisson@sas.upenn.edu

Dustin Brisson <dbrisson@sas.upenn.edu>

UPittsburgh AquaticEvolution

POST-DOCTORAL POSITION

AQUATIC ECOLOGY, EVOLUTION, BEHAVIOR, OR ECOTOXICOLOGY

Second notice: Applications are invited for a post-doctoral position at the University of Pittsburgh in any area of aquatic ecology or evolution under the direction of Dr. Rick Relyea. Current areas of research in the Relyea Lab include inducible defenses (and other forms of phenotypic plasticity), predator-prey communication, animal mating systems, disease ecology, and community ecotoxicology in aquatic communities. Interested applicants should propose potential research ideas that either build upon our existing work or add interesting new dimensions to areas currently being pursued.

The post-doc will reside on the main campus in Pittsburgh from September to March each year and reside at the University's biological field station from April to August (www.pitt.edu/˜biology/pymatuning.htm). For more information about the field station's aquatic facility, go to www.pitt.edu/ ˜ relyea/facilities.html . The starting salary is $34,000 plus excellent health benefits. To ensure a productive field season in 2008, the latest start date is 1 April 2008 (a completed Ph.D. is required prior to the start date).

Applicants should send a cover letter, cv, a research statement (including potential research projects), and letters of reference to Dr. Rick Relyea (relyea@pitt.edu) by 15 February 2008 or until position is filled (all in pdf format).

relyea+@pitt.edu

USDA BeltsvilleMD ComparativePopGenetics

I would appreciate it if you would post the following opportunity for a 2-year posdoctoral position in my USDA laboratory to explore comparative population genetics and genomics of animal parasites.

http://www.afm.ars.usda.gov/divisions/hrd/-hrdhomepage/vacancy/08056.htm ANNOUNCEMENT NO:

RA-08-056H

POSITION:

Research Molecular Geneticist/ Research Microbiologist/ Research Biologist (Bioinformatics)

LOCATION:

Beltsville, Maryland

DESCRIPTION OF DUTIES: The position is located in the Animal Parasitic Diseases Laboratory of the Animal and Natural Resources Institute, Beltsville, Maryland (Metropolitan Washington, DC). The incumbent will identify evolutionarily distinct and conserved characteristics of genomes of animal parasites that compromise livestock and human health using population genetic analyses derived from high throughput 'next generation' genome sequencing. The incumbent will identify and evaluate attributes of zoonotic pathogens (acquired by people from animals) and those occurring in related, less- studied parasites of animals. The incumbent will elucidate how agricultural activities have shaped parasite evolution and dispersal by comparing the extent and distribution of genetic variability among parasites in livestock, wildlife and human beings. Research responsibilities will include obtaining DNA from parasites, preparing and sequencing genomic libraries, and developing and analyzing resulting databases in order to identify conserved and variable markers, establish the extent of synteny among related parasite genomes, and test hypotheses related to the phylogenetic origins of genes implicated as virulence factors in model systems.

QUALIFICATION REQUIREMENTS: Recent Ph.D. in Microbiology, Biology, Genetics, or a closely related field is required. Experience generating, managing, and analyzing genetic and genomic data is desirable.

INFORMATION ON SALARY AND APPLICATION PROCEDURES FOR POSTDOCTORAL POSITIONS is available at: http://www.afm.ars.usda.gov/-divisions/hrd/hrdhomepage/vacancy/pd962.html INFORMATION ON EMPLOYEE BENEFITS is available at: http://www.usajobs.opm.gov/ei61.asp FOR SPECIFIC INFORMATION ON THE DUTIES AND RESPONSIBILITIES OF THIS POSITION OR TO SUBMIT AN APPLICATION, CONTACT:

Dr. Benjamin M. Rosenthal USDA/ARS 10300 Baltimore Avenue Room 104 Beltsville, MD 20705 Phone: (301) 504-5408 Fax: (301) 504-8979

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

USheffield 2 MolecularAdaptation

Two Marie Curie postdoctoral positions are available at the University of Sheffield to work on an EC funded project, MAERO (Molecular Adaptation in Ecologically Relevant Organisms). Both positions are funded until at least the end of 2009 and hopefully for two years. The aim of this project is to analyse high-throughput genome sequence data to distinguish between patterns of selection and demography in wild populations of organisms studied by members of the Molecular Ecology lab at the University of Sheffield (which houses the research groups of Terry Burke, Roger Butlin & Jon Slate).

Fellow 1 will work on Arabidopsis lyrata a close relative of A thaliana. Considerable ecological and genomic data are available from experimental and wild populations from around Europe, collected as part of a larger collaboration investigating the genetic basis of how species adapt to abiotic stress at range margins. The A lyrata genome is currently being sequenced (> 3 million Trace Files are already available).

Fellow 2 will study the molecular evolution of passerine (songbird) genes, possibly with an emphasis on the role of sexual selection driving the evolution of genes associated with plumage variation. Passerine genomics tools are advancing rapidly with the first genome (zebra finch) about to be released and several other classical ecological model species (e.g. great tit, song sparrow, flycatcher) now being analysed with genomics tools.

The fellows will join two other Marie Curie fellows who have recently started on the MAERO project (one studying Soay sheep and the other Littorina winkles). Both positions have very generous salaries, and considerable academic freedom provided they remain within the overall theme of the project. They are ideal positions for somebody working towards academic independence. At least one of the fellows must be a European national, although scientists that have worked in the UK in the last three years are ineligible for the posts. UK nationals working overseas may be eligible. We hope to fill the positions as soon as possible, but they remain open until suitable candidates can be found. A background or expertise in one or more of the following areas would be highly desirable: bioinformatics, molecular evolution, statistical genetics, computer science, evolutionary population genetics. This posts are not predominantly lab-based; rather we are seeking people who enjoy analysing large datasets.

The Department of Animal & Plant Sciences (http://www.shef.ac.uk/aps/) is one of the strongest organismal biology departments in Europe, and Sheffield is a vibrant yet inexpensive city close to the beautiful Peak District National Park. Informal enquiries and requests for further information should be addressed to Jon Slate (j.slate@sheffield.ac.uk).

Dr Jon Slate Dept. Animal & Plant Sciences University of Sheffield Tel: 0114 2220048 Fax: 0114 2220002 Web: http://www.jon-slate.staff.shef.ac.uk/

Jon Slate <j.slate@sheffield.ac.uk>

UTennesseeKnoxville EvolutionaryTheory

Post-doctoral Fellowship in Evolutionary Theory

Applications are sought for a one-year (with possibility to renew for another year) post-doctoral research position in Evolutionary Theory. This position will be held jointly at the labs of Dr. Sergey Gavrilets and Dr. Francisco Úbeda in the Departments of Ecology and Evolutionary Biology and Mathematics at the University of Tennessee, Knoxville. These are active, dynamic and international labs composed currently by 7 graduate students and 2 postdocs from 8 countries in 4 continents.

The research topic is fairly open, although special consideration will be given to applicants developing theory on: kin selection, non-mendelian inheritance (meiotic drive, gene conversion), non-mendelian expression (genomic imprinting), sexual antagonism, and social evolution. The position may begin anytime after Feb the 30^th 2008. Salary will adjust to candidate qualifications. More information about the labs and the department can be found at: http://eeb.bio.utk.edu/ To apply, send a CV and a one-page statement of research interest and research plans to Sergey Gavrilets (gavrila@tiem.utk.edu <mailto:gavrila@tiem.utk.edu>) and Francisco Úbeda (fubeda@utk.edu <mailto:fubeda@utk.edu>) via e-mail. Please include the names of 2-3 potential referees, but applicants need not solicit reference letters at this stage. Review of applications will begin on February 15, 2008, and continue until the position is filled.

Francisco Ubeda <fubeda@utk.edu>

UTexasAustin MolecularEvolution

The lab of Dr. Sara Sawyer at UT Austin is seeking a highly motivated post-doc to work at the interface of molecular evolution and virology. There are several potential projects with available funding. Among other things, our lab studies the process of retroviral integration in hopes that this will help us understand the deadly reservoir of HIV genomes which integrate into the chromosomes of infected people. It is this reservoir that makes HIV essentially incurable once someone has become infected. We have developed model systems in yeast and human cells to test the implications of evolutionary innovation on this process. Please see our website to read about our other research interests. (http://www.people.cornell.edu/pages/mrd6/sara/) Austin is one of America's greatest "un-discovered" cities. Highly cosmopolitan, you will also find warm weather, sunshine, and a culture of wonderful independent music, fantastic food, mountain biking, and water sports. We are aggressively recruiting only the very top candidates to come work in our new lab.

Sara Sawyer Assistant Professor University of Texas at Austin Section of Molecular Genetics and Microbiology Institute for Cellular and Molecular Biology

1 University Station, A4800 Austin, TX 78712 http://www.people.cornell.edu/pages/mrd6/sara/ saras@mail.utexas.edu

Sara Sawyer <saras@mail.utexas.edu>

UToronto EvolutionaryBiology

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 Post-Doctoral Fellowship Program. Positions are for two years, subject to review after one year, and can begin as early as July 1, 2008. The salary is $40,000 Canadian per year, with research expenses covered by the Post-Doctoral 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.

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 for 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: Jan Haugan jhaugan@eeb.utoronto.ca .

For more information about the Department, contact your potential supervisor. Queries regarding the fellowship program should be directed to Demetrios Voudouris dvoudouris@eeb.utoronto.ca . Review of applications will begin on March 21, 2008.

Toronto is a vibrant, multicultural city on the shore of Lake Ontario, with rich cultural options in the arts, music and film, ethnic cuisine, and a high quality of life. The EEB department is home to an interactive, collegial group of ecologists, geneticists, and evolutionary biologists, and currently supports a strong group of Post-Doctoral Fellows with diverse research interests.

–

John Stinchcombe Department of Ecology and Evolutionary Biology University of Toronto, 25 Willcocks St. Toronto, ON Canada M5S 3B2

416-946-5986

http://www.botany.utoronto.ca/ResearchLabs/-StinchcombeLab/ stinchcombe@eeb.utoronto.ca stinchcombe@eeb.utoronto.ca

---

UZurich Post-copulatory sexual selection

A postdoctoral position is available from 1st April, or as arranged, in the Zoological Museum of the University of Zurich, Switzerland. The successful applicant will join an active research group, headed by Prof. Paul Ward, working on post-copulatory sexual selection in the yellow dung fly, Scathophaga stercoraria. The biology of the species is well known and methods for a number of research directions well-developed.

The precise research topic(s) within the broad theme will substantially depend on the interests and background of the applicant. However, preference will be given to candidates with backgrounds in evolutionary biology or insect immunology or physiology.

Applicants must have a completed Ph.D. Postdoctoral experience would be advantageous. A knowledge of, or a willingness to learn, German would also be advantageous. A small amount of teaching, in either English or German, will be required. The position will be offered for two years in the first instance, with the possibility of annual renewal to a maximum of six years.

Please send a curriculum vitae, publication list and a one-page statement of research interests to zmdirektion@zm.uzh.ch. Applications should be sent by the 3rd March 2008.

Applicants for a previous similar position need not reapply

Enquiries to Prof. Paul Ward, Zoological Museum of the University of Zurich, Winterthurerstr. 190, CH-8057 Zurich, Switzerland. Email: pward@zm.uzh.ch.

Prof Paul I Ward Direktor Zoologisches Museum der Universität Zürich Winterthurerstrasse 190 CH 8057 Zürich Switzerland Phone +41 44 635 4760 Fax +41 44 635 4780 email: pward@zm.uzh.ch

Administration: Sabine Marty Mail: zmdirektion@zm.uzh.ch Phone +41 44 635 4761

Paul Ward <pward@zm.uzh.ch>

WesternWashingtonU TundraPhylogeography

Post-doctoral Position: Tundra Phylogeography

A postdoctoral position is available to study how the different environmental histories of arctic and alpine refugia affected genetic divergence in tundra plants. The successful candidate will be responsible for estimating the demographic histories of various species through population genetic and phylogeographic analyses on multiple, anonymous loci and performing comparative analyses of all study species in a coalescent framework. The position includes the possibility of fieldwork in the arctic and alpine tundras of North America and Russia. This is an outstanding opportunity for an early-career scientist to engage in collaborative research and gain advising experience with a diverse group of undergraduate and graduate students. Candidates must have a Ph.D. in evolutionary biology or a related field prior to beginning the position. Strong experience in molecular techniques is required, while experience in phylogeography, botany, and arctic/alpine environments are preferred. This is a one-year position with a possible extension to two years depending on job performance. To apply, please submit a cover letter describing research experience and future goals, as well as other experience relevant to the position; a CV; and three letters of reference. Application materials should be sent to eric.dechaine@wwu.edu or via postal courier to Mary Ann Merrill, AAF Post-doctoral Position, Biology Department MS 9160, Bellingham, WA 98225 USA. Review of application materials will begin on March 15, 2008 and will continue until the position is filled. For additional information about the position, please see http://myweb.facstaff.wwu.edu/˜dechaie. WWU is an equal opportunity/affirmative action employer.

Eric DeChaine, Ph.D. Assistant Professor Department of Biology, BI 237 Western Washington University 516 High St. Bellingham, WA 98225-9160 Tel: 360.650.6575 Fax: 360.650.3148 email: Eric.DeChaine@wwu.edu

Eric DeChaine <Eric.DeChaine@wwu.edu>

WorkshopsCourses

ItalianSociety SchoolforEvolutionaryBiology

La SIBE, Societa Italiana di Biologia Evoluzionistica (www.sibe-iseb.it), in collaborazione con il Parco Nazionale Gran Paradiso (www.pngp.it), organizza la scuola sull'evoluzione per studenti di Master e Dottorato, dal titolo: 'La logica della scoperta evolutiva: strategie sperimentali, metodi statistici e tecniche di inferenza'.

La Scuola, che si terra presso la sede di valle del Servizio Scientifico e Sanitario del PNGP (Cogne, Ao) dal 15 al 18 Maggio 2008, a particolarmente indicata per studenti interessati allo studio dell'evoluzione ed all'inizio della propria carriera di ricerca (Master e primo o secondo anno di Dottorato), ed ospitera un massimo di 15 partecipanti. Previa disponibilita di posti, verranno accolte domande anche da laureandi, da dottorandi all' ultimo anno o da chi ha gia concluso il dottorato. Il numero limitato di studenti garantira un'interazione continua ed efficace tra studenti e docenti. Il corso ha una durata di 3 giorni (15-17 maggio), seguiti da un' escursione finale (18 Maggio).

Come si studia l'evoluzione? Quali sono le strategie sperimentali pia adatte per affrontare le tematiche evolutive? Qual a il contributo che le varie discipline portano alla nostra comprensione dell'evoluzione? Come si integrano teoria ed osservazioni nell'inferenza in campo evolutivo? Come tradurre un risultato di natura statistica in una "legge della natura"? L' obbiettivo della Scuola SIBE 2008 a fornire agli studenti gli strumenti concettuali necessari allo studio dell'evoluzione con l'ausilio di lezioni teoriche ed esempi tratti da diverse discipline biologiche, discussioni con i docenti sulle lezioni svolte ed esercitazioni pratiche. Gli studenti avranno anche l'opportunita di discutere il proprio progetto di ricerca con i docenti e a tale scopo sono incoraggiati a preparare una breve presentazione orale (15 minuti) od un poster.

Il corso sara completato da 3 seminari per la divulgazione dei risultati di ricerca (come presentare un poster, come fare un talk, come scrivere un articolo scientifico) e da almeno un journal club nel quale sara mostrato come dissezionare un articolo scientifico, dal momento che divulgare i propri risultati e presentarli in modo efficace a un aspetto fondamentale del lavoro di ricerca, cosa come imparare a leggere in modo critico un lavoro scientifico.

La scuola si avvale della collaborazione di ricercatori noti a livello internazionale come docenti (indicati sotto), e pertanto le lezioni saranno tenute in inglese:

John Endler (University of Exeter): Ecologia ed evoluzione del comportamento animale http://www.psychology.ex.ac.uk/stafflist.php?id=1160 Lynda Delph (Indiana University): Ecologia evolutiva e riproduzione nelle piante http://www.bio.indiana.edu/~delphlab/ Curt Lively (Indiana State University): Evoluzione e coevoluzione: sesso e diversita genetica nei sistemi ospite-parassita http://www.indiana.edu/~curtweb/ Paolo Sordino (Stazione Zoologica Anton Dohrn di Napoli): EvoDevo

Il costo di iscrizione alla Scuola a di 200 ? ed include: l'alloggio in due foresterie offerte dal Parco Nazionale Gran Paradiso (i partecipanti dovranno munirsi di sacco-a-pelo), l'uso cucina nelle foresterie per la cena con la spesa gia fatta, e pranzo o cena sociale l'ultimo giorno (quest' ultimo da definire). Il pranzo durante i 3 giorni della scuola a carico dei partecipanti ai quali forniremo una lista di ristoratori con prezzi convenzionati.

Per le pre-iscrizioni, inviare una e-mail a Isabella Capellini (Isabella.Capellini@durham.ac.uk) e Ivan Scotti (ivan.scotti@cirad.fr), indicando in breve il vostro livello di preparazione (laureandi, master, PhD e a quale anno di corso, concluso il PhD), il titolo e il tema del vostro progetto di ricerca, i vostri interessi scientifici, e l'indirizzo email del vostro relatore di tesi di dottorato o di laurea. Allegate inoltre il vostro CV. Il tutto deve essere inviato entro il 1 Marzo2008. I risultati della selezione saranno comunicati per email entro il 30 Marzo.

Per ogni ulteriore informazione potete contattare Isabella Capellini o Ivan Scotti.

——— Isabella Capellini, PhD

Evolutionary Anthropology Research Group Department of Anthropology Durham University 43 Old Elvet, Durham DH1 3HN (United Kingdom)

phone: +44 (0)191 3346187

isab972@yahoo.co.uk

Malaysia BorneoBiodiversity Jul1-Aug5

Course announcement: Harvard University/CTFS-AA Field Biology Course: 'The Biodiversity of Borneo' 2008

The Harvard University Summer School, the Arnold Arboretum, and the Center for Tropical Forest Science (CTFS-AA) will offer a field biology course to be held in Sarawak and Sabah (East Malaysia) from 1 July to 5 August 2008. Ten US students will join 10 Southeast Asian students to study terrestrial and marine biodiversity, ecology and conservation, with instructors from Harvard University and other institutions (including Sabah Parks, Sabah Forest Research Center, Sarawak Forestry Corp., Univ. Malaysia Sabah, Yayasan Sabah).

The forests and reefs of northwest and north Borneo have some of the highest levels of alpha-diversity in the world. The forests are home to orang-utans, hornbills, rhinos and as many as 5,000 tree species, and the reefs offer some of the best diving in the world. We will visit world-class parks and reserves (e.g., Lambir, Kinabalu and the Maliau Basin), to gain a thorough understanding of abiotic controls on species composition, and will contrast processes that maintain biodiversity in forests with those operating on coral reefs. Throughout Borneo, intensive logging and marine harvesting have occurred for many years. Our course will explore the complexities of conservation today, including trips to sustainably-managed, carbon-traded, and restored forests. We will also provide opportunities for the students to meet people living in and off the forest, to understand their motivations for forest conversion and conservation, and to consider the human health dimensions of forest change.

A key feature will be the development of skills in research project design, execution and analysis, based around the statistical platform 'R' The students will complete two independent projects, from conception to presentation, and participate in a group project on the coral reef. The students will gain database and web publishing skills by developing a community digital record of the trip.

The course is aimed at advanced undergraduates, recent graduates currently active in biological research, and postgraduate entry-level students. For more information on the course (including instructions for application), see:

http://www.summer.harvard.edu/2008/programs/-abroad/borneo/ Queries and completed application materials should be directed to Cam Webb, c/o <borneo2008@phylodiversity.net>. The deadline for US applicants is 3 March 2008.

cwebb@oeb.harvard.edu cwebb@oeb.harvard.edu

Montreal PopulationGenomics May20-23

Montreal Spring School of Population Genomics and Genetic Epidemiology May 20 - 23, 2008 Montreal, Quebec, Canada

General Information www.montrealspringschool.ca The main objective of the School is to provide training in rapidly developing disciplines that are becoming increasingly important in health sciences. It includes genetic epidemiology and human evolutionary genetics, population genomics and bioinformatics, integrating tools of formal analysis with data retrieval and extensive use of internet resources. The training will be based on real-data examples from the research of the instructors' laboratories. In one module we will also present genealogical resources specific to Quebec and introduce informatics methods for their use in population analysis and epidemiology. The School consists of four days of workshops: genetic epidemiology including biostatistics (2 days), population genomics (1.5 days), and Quebec population resources (0.5 days).

The School, organized by Dr Damian Labuda from CHU Sainte-Justine, will be held at the Universite de Montreal, Pavillon Lionel-Groulx, 3150 Jean-Brillant Street, Room C3001, in Montreal, Quebec, Canada.

Faculty

Alexandre Alcaes Laboratory of Human Genetics of Infectious Diseases Institut National de la Sante et de la Recherche Medicale University Paris Rene Descartes, Necker Medical School Paris, France

Philip Awadalla Assistant Professor Department of Pediatrics, Universite de Montreal CHU Sainte-Justine Research Center Montreal, Canada

Luis B. Barreiro Unit of Human Evolutionary Genetics Institut Pasteur Paris, France

Louis Houde Departments of Informatics and Mathematics Universite du Quebec e Trois-Rivieres Trois-Rivieres, Canada

Alexandre Montpetit Genome Quebec Innovation Centre McGill University Montreal, Canada

Llues Quintana-Murci Unit of Human Evolutionary Genetics Institut Pasteur Paris, France

Marie-Helene Roy-Gagnon CHU Sainte-Justine Research Center Montreal, Canada

Erwin Schurr McGill Centre for the Study of Host Resistance Departments of Human Genetics and Medicine McGill University Montreal, Canada

Marc Tremblay Department of Human Sciences Universite du Quebec e Chicoutimi Chicoutimi, Canada

Helene Vezina Department of Human Sciences Universite du Quebec e Chicoutimi Chicoutimi, Canada

Application Procedures

If you wish to participate in the workshop, please submit (i) the completed application form, including a statement explaining your interest in the School, accompanied by one-page CV and (ii), if a travel award is requested (see below), a short letter explaining your financial needs, accompanied by a letter of support from your academic advisor (if applicable). Please submit these documents by e-mail to Ms. Dominika Kozubska (info@montrealspringschool.ca) no later than Friday, February 24, 2008.

damian.labuda@umontreal.ca

NatlUIreland MolEvol summer

Undergraduate research experience at the Summer School of Molecular Evolutionary Research (the SoMER school) in Ireland.

The Department of Biology of the National University of Ireland, Mynooth is announcing its first summer School of Molecular Evolutionary Research (the SoMER school). Our aim is to provide research training and expertise to enthusiastic undergraduate students with a special interest in molecular evolution, and more generally evolutionary biology.

Every student will be integrated into an active research group at the Department of Biology of the NUI Maynooth, and will be assigned an individual research project. A key focus of the school is that every student should experience every one of the steps involved in evolutionary research. The students will thus participate in field work where they will sample biological specimens, they will extract and sequence DNA from the samples they collected, and they will use bioinformatics/computational techniques to analyse the data they generated.

Other activities will include one day workshops carried out by members of the Department of Biology and invited external speakers (see our website for details).

The SoMER school will run for ten weeks, starting the 9th of June 2008, and will accept 10 students. It is open to undergraduate students from every country and nationality. The only requirement is that you must have a strong interest in evolutionary biology, and an interest in pursing a career in this research area. For every student, funding will be available in the form of a 300 per week salary. Travel expenses will also be covered, up to 300 for EU students, and up to 800 for non-EU students. On-campus, discounted self-catering accommodation will be provided for the SoMER students.

The SoMER school will be based in the Department of Biology of the NUI Maynooth, which is very conveniently located in the Irish countryside, only 34 Km (21 Miles) from Dublin City International Airport, and 28 Km (17 Miles) from Dublin city centre. Maynooth is very well connected to Dublin through regular train and bus services.

Maynooth is a picturesque village, which has hosted universities and colleges since 1795, and currently hosts two independent universities: The National University of Ireland, Maynooth, and a branch of the Pontifical University (St. Patrick's College). Maynooth's culturally rich history is reflected in the architectural beauty of the old campus, and if you are a non-Irish student it is fair to say that Maynooth is probably the ideal place to carry out a research experience, while experiencing life in Ireland.

Visit our website http://bioinf.nuim.ie/ureka/ if you are interested and would like to apply.

Alternatively send us an e-mail: ureka2008@gmail.com

The deadline to apply to the SoMER school is the 14th of March.

Dr. Davide Pisani Laboratory of Evolutionary Biology The National University of Ireland, Maynooth Maynooth, Co. Kildare, Ireland Davide.Pisani@nuim.ie

---

Norway ArabidopsisMolEvol Aug26-29

AMEGO 2008

The Arabidopsis Molecular Evolution Group (AMEGO) is a Nordforsk funded network of Arabidopsis research groups from Denmark, Finland, Norway and Sweden. AMEGO will in the period 2007-2009 arrange international workshops and PhD courses focusing on Arabidopsis evolution and molecular ecology

This years Arabidopsis molecular evolution workshop will be held 26-29 August 2008. The workshop and the PhD course will be held in the Norwegian mountains (Jotunheimen), close to natural sites of Arabidopsis lyrata.

The workshop with talks and posters will be held on Tuesday 26 and Wednesday 27 Aug. Invited speaker on this years workshop is Dr. Markus A. Koch, University of Heidelberg. On Thursday 28 there will be excursions to natural Arabidopsis populations in the Norwegian mountains, while on Friday 29 Aug we will hold the PhD course. The topic of this years PhD course is "Genomics and bioinformatic resources on Arabidopsis lyrata", and will be led by Dr. Mikkel Schierup and Dr. Jesper Bechsgaard, Aarhus University.

For information about the AMEGO 2008 PhD course and workshop, please have a look at our home page www.molecol.net . To go directly to the registration page, please go to http://www.bio.ntnu.no/-amego_2008/pomelding/skjema.php . Best regards, Hans K. Stenoien

–

Hans K. Stenoien, PhD Department of Biology Norwegian University of Science and Technology N-7491 Trondheim, Norway

Phone: +47 7359 6096 Mobile: +47 9189 7592 Fax: +47 7359 6100

stenoien@bio.ntnu.no

Portal Arizona IntlBeeCourse August

The AMNH's bee course will be held in late August. It is suitable for anyone interested in finding out how to identify bees. Information can be found at: http://research.amnh.org/invertzoo/beecourse/ L P <laurencepacker@yahoo.com>

Portugal MEPA08 MolEvol Apr14-18

MEPA08 - Molecular Evolution, Phylogenetics and Adaptation April 14th - April 18th 2008

Highly practical training course. Applications will open 6 weeks before. Extremely popular.

Deadline for applications: March 21st 2008

http://gtpb.igc.gulbenkian.pt Thanks Pedro Fernandes GTPB Organizer

Pedro Fernandes <pfern@igc.gulbenkian.pt>

Seattle StatGenetics SISG Registration open

The registration page for the 2008 Summer Institute in Statistical Genetics is now open at http://-www.biostat.washington.edu Bruce

Bruce Weir <bsweir@u.washington.edu>

TrinityCollegeDublin IntegratingEcolEvol

Undergraduate Research in the School of Natural Sciences, Trinity College Dublin http://www.tcd.ie/-naturalscience/UREKA "Integrating Ecology and Evolution in a Changing World" is a summer, undergraduate research programme based in Dublin, Ireland. Its aim is to provide research training and experience, as well as an introduction to Ireland, to national and international undergraduate students. Students will work within active research groups in Trinity College Dublin, Ireland's premier university.

Full funding is available for ten students to participate in this 10-week programme, from 23rd June - 29th August 2008. International students are also entitled to assistance with travel costs.

All applications must be received by 29th February.

The School of Natural Sciences, comprising the departments of Botany, Geography, Geology and Zoology, and the Centre for the Environment, hosts internationally acclaimed biological, physical and social scientists. It provides a dynamic and exciting research environment, with ~40 academic staff, ~20 post-doctoral fellows, and ~120 graduate students. The summer undergraduate research programme cuts across the ecology and evolution research strands within the School, and offers projects ranging from climate change to behaviour to phylogenetics , and training in both practical laboratory and field skills, as well as generic science communication skills. Students will be embedded within active research groups and receive direct training from PIs, as well as post-doctoral fellows and graduate students. A weekly seminar programme will cover research ethics, the transition to graduate school, current topics in ecology and evolution, and science communication. At the end of the programme students will both write up and present their research project at a one-day symposium.

In addition to the science, an active social programme will introduce students to the delights of Dublin, and the beauty and history of Ireland.

Requirements: - completion (in 2008) of the penultimate year of an undergraduate biological science degree - proficiency in English (written and spoken) - willingness to work hard, and ability to work independently - strong interest in the project of choice - aspiration to pursue research in ecology or evolution

Your application must include a CV, a completed application form, which you will download from the website (http://www.naturalscience.tcd.ie/UREKA), and 2 references (download the form from the website). Details for the application process can be found on the website. All materials must be received by Friday 29 February 2008

Research Projects: Grass phylogenetics; Parasite impacts on host fitness; Shrimp feeding ecology; Plant biodiversity in conservation areas; Sociality in badgers; Spatiotemporal dynamics of plant communities; Genes and development in vertebrates; Phylogeny of Thai plants; Land-use change and soil microbes; Crop greenhouse emissions; Growth and resource availability in bivalves

For more details, please see: http://www.naturalscience.tcd.ie/UREKA or e-mail: fimolony@tcd.ie

mabrown@tcd.ie

UBologna 9thWinterBioinformaticsSchool Feb11-15

9th Bologna Winter School on Bioinformatics

GRAND CHALLENGES IN COMPUTATIONAL BIOLOGY New developments for solving the unsolved problems of Computational Biology

University of Bologna, Giorgio Prodi Hall, Piazza San Giovanni in Monte Bologna (Italy)

Feb 11-15, 2008

In our century grand challenges are at hand in Science. Great expectations have been generated in different fields by the increasing role and impact of computing and computer science in processing terabytes of data. In our era the 'computational thinking' of computer science meets the empirical and theoretical methods of Natural Sciences, from Physics to Biology with an un-precedent effort of accelerating breakthroughs and benefits to society. Ongoing projects aim at understanding the universe and the origin of life for better helping to preserve and protect our planet. Simulation and modeling go global and the novelty is that this is so also in Biology, where Bioinformatics and Computational Biology help in understanding basic mechanisms from molecular biology to systems/organismic biology in order to revolutionizing medicine and healthcare. Data acquired at molecular level from different species and/or individuals need to be analyzed at large and integrated in order to investigate our common origins and how we differentiated from each others, also in relation to environmental factors. Worldwide-integrated platforms for scientific computing, implementing also new mathematical and statistical approaches, and based on new computing paradigms need to be implemented for real time processing of the enormous amount of experimental data, produced at hyperbolic rate by genomics and proteomics efforts. New ideas and/or reorganization of scientific efforts with a better collaboration among researchers in theoretical, computational, experimental areas of investigation are urgently needed.

In the 9th edition of the Bologna Winter School in Bioinformatics, we will then ask the question of what grand challenges Computational Biology and Bioinformatics will explore in the next decade. Different subjects focusing as a test case on the human genome, including genome annotation, biodiversity, alternative splicing and its regulation, epigenetics, information transfer from 1D to 3D genetic code, cellular function and simulation, genomic medicine, SNPs and maladies will be reviewed to highlight present results and future perspectives to cope with the requirement of integrating computation with molecular description to understand basic principles of Biology.

LECTIO MAGISTRALIS

Complexiy at the fundamental level - Antonino Zichichi, CERN, Geneva, CH

TEACHERS - Giovanni Aloisio, University of Lecce, IT - Patrick Aloy, Institute for Research in Biomedicine, Barcelona, ES - Francesco Beltrame, University of Genova, IT - Jaume Bertranpetit, University “Pompeu Fabra”, Barcelona, ES - Alvis Brazma, European Bioinformatics Institute, Hinxton, UK - Joaquin

Dopazo, Centro de Investigacien “Principe Felipe”, Valencia, ES - Arne Elofsson, Stockholm University, SE - Roderic Guigï¿½, University “Pompeu Fabra”, Barcelona, ES - David T. Jones, University College, London, UK - Arthur Lesk, PennState University, USA - Giuseppe Martini, National Research Council, Roma, IT - Christine Orengo, University College, London, UK - Modesto Orozco, Institute for Research in Biomedicine, Barcelona, ES - Graziano Pesole, University of Bari, IT - Bernhard Schelkopf, Max Planck Institute, Tuebingen, DE - Aldo Tagliabue, ALTA srl, Siena, IT - Willie Taylor, National Institute for Medical Research, London, UK - Anna Tramontano, University “La Sapienza”, Roma, IT - Alfonso Valencia, Centro Nacional de Investigaciones Oncolegicas, Madrid, ES

Additional Information: http://www.biocomp.unibo.it/ ˜ school2008/ Contact: school2008@biocomp.unibo.it

For Application send a short C.V. to school2008@biocomp.unibo.it You will be notified by e-mail of acceptance. Deadline for application: January 29, 2008

gigi@biocomp.unibo.it

UNottingham MolecularEvolutionDiversity

UK Summer School in Molecular Evolution and Diversity

The BBSRC (UK) are running a Summer School in Molecular Evolution and Diversity at the University of Nottingham, Nottingham, UK, from Monday, the 14th July until Saturday, the 19th July 2008. The Summer School is designed mainly for postgraduate and postdoctoral researchers in quantitative aspects of Evolutionary Biology, looking at genetic variation both between- and within- species.

The course is mainly, although not exclusively, for early career researchers who wish to gain a greater understanding of the quantitative and theoretical tools that will aid their interpretation of evolutionary data. The course will include plenary talks from experts in population genetics and molecular evolutionary analyses. There will be practical (computer) sessions, intended to help participants in the analysis of sequence and other types of data, and to understand how these analyses can be used to study important biological questions. Those chosen for the project will be asked to present a short talk or a poster about their research project or planned project.

Places on the course are free, and, while we expect 90% of those chosen for the course to be postdoctoral or postgraduate researchers, 10% of places have been reserved for more experienced researchers. All those chosen will be expected to attend the whole meeting. We are unable to pay travel expenses for those attending the course.

Applications will be via the website: http://www.nottingham.ac.uk/biology/apps/summerschool/ On the application form will ask for a poster or talk title and abstract, and also the supervisor's name (if relevant) and department and institution. Places are not restricted to BBSRC-funded researchers. The deadline for applications is Friday, 28th March 2008.

The Summer School will cover the following areas of micro- and macro-evolution: Genetic Diversity Within Populations Genetic Drift and the Coalescent Mutation and Selection Recombination and its Impact of Genetic Variation The Detection of Selection from Population Genetic Data Genetic Diversity Between Populations Phylogeography of Humans and Other Species Measurement of Interpopulation Genetic Variation Genetic Variation Between Species Alignment of DNA sequences Tree-Building Evolution of Development and Environmental Genomics The Evolution of Development Patterns of Selective Constraint in the Genome Microbial Evolution and Systems Biology The Study of Fitness at the Genomic Scale Gene Networks Recombination, Selection and Genetic Variation in Microbial Populations

Plenary Speakers will include: Brian Charlesworth, Deborah Charlesworth, Paul Sharp, Peter Keightley (University of Edinburgh) Susan Ptak (Max Planck Institutefor Evolutionary Anthropology, Leipzig) Martin Lercher (Heinrich Heine University, Dusseldorf) Mark Jobling (University of Leicester) John Brookfield, John Armour (University of Nottingham) Daniela Delneri (University of Manchester) Tim Anderson (Southwest Foundation for Biomedical Research, San Antonio)

If you have any questions please contact John Brookfield at

John.Brookfield@nottingham.ac.uk

Brookfield John <John.Brookfield@nottingham.ac.uk>

UWashington StatisticalGenetics Online

We are please to present the first University of Washington Online Course Offering of the Statistical Genetics STAT/BIOST 550 class:

Statistical Genetics I; Discrete Mendelian traits (http://www.stat.washington.edu/thompson/Stat550/Online_2008/announce.shtml)

with instructor Professor Elizabeth Thompson (http://www.stat.washington.edu/thompson/)

The course will be offered in this new format for the first time in Spring (mid-March to mid-June, 2008). This is a new version of the on-campus class offered at UW since 2000, and offered previously through NCSU Distance Learning (2000, 2001, 2004).

The format will be internet-based with visual and audio presentations and email/discssion board interations.

For more information about the course content please contact Professor Elizabeth Thompson (eathomp@u.washington.edu), Department of Statistics, University of Washington.

For information about tuition and registration please contact Shannon Kuyper (sgarton@EXTN.washington.edu) University of Washington Extension Office.

eathomp@u.washington.edu eathomp@u.washington.edu

Valencia MolEvol May12-16

Thrid Course on Molecular Evolution, Phylogenetics and Phylogenomics

12 - 16 May 2008, Valencia. Spain

Hernan Dopazo and Toni Gabaldon, Co-ordinators

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 course includes a session of phylogenomic analysis and functional annotation including the most recent developments in this area. Among other tools, attendees will become familiar with Phylip, Phyml, PAML, TreePuzzle, MrBayes, Modeltest programs and tools developed in our department such as Phylemon, FatiGO, FatiScan, and ETE. The course is mainly intended for professionals in the field of biology and chemistry who work on areas related to biological sequence analysis.

Course fee is 300 euros, meals included. A limited number of grants will be available.

Local Instructors: Leonardo Arbiza, Jaime Huerta, Marisa Marcet, Toni Gabald??n and Hernan Dopazo.Bioinofrmatics Department.Centro de Investigacion Principe Felipe (CIPF)

Invited Instructors: David Posada, University of Vigo (Spain) and Rafael Zardoya, MNCN-CSIC (Madrid, Spain)

More information:

http://bioinfo.cipf.es/courses/mol_evol_phylo_3ed/ Application Deadline: 14th May 2008 The official language is English.

H –

Hernan J. Dopazo, PhD Comparative Genomics Unit, Bioinformatics Department, Centro de Investigacian Principe Felipe c/ ep Avda. Autopista del Saler 16 (Junto al Oceanografico), 46012, Valencia, Spain. Tfn: (34) 96 328 96 80 ext: 1008 Fax: (34) 96 328 97 01 hdopazo@cipf.es http://hdopazo.bioinfo.cipf.es Hernan Dopazo <dopazoh@gmail.com>

Valencia Phylogenetics May12-16

Thrid Course on Molecular Evolution, Phylogenetics and Phylogenomics

12 - 16 May 2008, Valencia. Spain

Hernán Dopazo and Toni Gabaldón, Co-ordinators

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 course includes a session of phylogenomic analysis and functional annotation including the most recent developments in this area. Among other tools, attendees will become familiar with Phylip, Phyml, PAML, TreePuzzle, MrBayes, Modeltest programs and tools developed in our department such as Phylemon, FatiGO, FatiScan, and ETE. The course is mainly intended for professionals in the field of biology and chemistry who work on areas related to biological sequence analysis.

Course fee is 300 euros, meals included. A limited number of grants will be available.

Local Instructors: Leonardo Arbiza, Jaime Huerta, Marisa Marcet, Toni Gabaldón and Hernán Dopazo.Bioinofrmatics Department.Centro de Investigación Príncipe Felipe (CIPF)

Invited Instructors: David Posada, University of Vigo (Spain) and Rafael Zardoya, MNCN-CSIC (Madrid, Spain)

More information:

http://bioinfo.cipf.es/courses/mol_evol_phylo_3ed/ Application Deadline: 14th May 2008 The official language is English.

H –

Hernan J. Dopazo, PhD Comparative Genomics Unit, Bioinformatics Department, Centro de Investigacian Principe Felipe c/ ep Avda. Autopista del Saler 16 (Junto al Oceanografico), 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>

WoodsHole MolEvol Jul27-Aug15

Workshop on Molecular Evolution, Woods Hole, 2008

http://workshop.molecularevolution.org/mbl/ 27 July - 8 August 2008, and extended topics session 8 August - 15 August 2008

Application Deadline 3 March 2008

Michael P. Cummings, Director

The Workshop on Molecular Evolution has been the finest course in the subject since it was started in 1988. The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. A distinguishing feature of the Workshop is a well-equipped computer laboratory with Apple Macintosh computers and servers for comparative analysis of molecular data. Authors and experts in the use of computer programs and packages such as BEAST, Clustal W and Clustal X, FASTA, GARLI, LAMARC, MAFFT, MrBayes, PAML, PAUP*, PHYLIP, and Seaview provide demonstrations and consultations. This two-week program is designed for established investigators, postdoctoral fellows, and advanced graduate students with prior experience in molecular evolution and comparative genomics. Scientists with a strong interest in molecular evolution, systematics, and population genetics are encouraged to apply. Enrollment is limited to 60 students, and 15 students will be admitted to an extended topics session for the purpose of analyzing their research data sets. Many participants find the extended topics session to be especially useful.

Topics to be covered include:

* Databases and sequence matching: database searching: protein sequence versus protein structure; homology; mathematical, statistical, and theoretical aspects of sequence database searches * Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis; hypothesis testing * Maximum likelihood theory and practice in phylogenetics and population genetics: coalescent theory; maximum likelihood estimation of population genetic parameters * Molecular evolution integrated at organism and higher levels: population biology; biogeography; ecology; systematics and conservation * Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution * Comparative genomics: genome content; genome structure; genome evolution * Molecular evolution integrated at lower levels: biochemistry; cell biology; physiology; relationship of genotype to phenotype

2008 Fees: $2400 (room and board at no additional charge), plus an additional $850 for the extended topics session.

More information is available on the Workshop web site -

http://workshop.molecularevolution.org/mbl/ mike@umiacs.umd.edu mike@umiacs.umd.edu

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.