EvolDir

July 1, 2010

Month in Review

Foreword

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

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

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

—— / ——

Conferences

Basel CichlidEvolution Aug26-29

Dear evoldir user,

We would like to invite you to the Cichlid Science 2010 conference taking place from the 26th to the 29th of August 2010 in Basel, Switzerland. It is going to be an international conference for researchers working on various aspects of cichlid fish biology or which use cichlids as a model system.

This interdisciplinary venture is going to be an ideal opportunity for creating new ideas and collaborations in the lovely scenery of estival Basel. We especially encourage doctoral students and young postdocs to register, since our foremost aim is to give them the opportunity to present and discuss their research.

Registration deadline: 1st July Registration fee: 80 Swiss francs (aprox. 56 EUR, 70 USD) Please register via our conference website: http://www.evolution.unibas.ch/cichlidscience2010/ Unfortunately, we can accept a limited number of participants only!

more information:

http://www.evolution.unibas.ch/cichlidscience2010/

Facebook group: “Cichlid Science 2010”

confirmed speakers include: - J. Todd Streelman (Georgia Institute of Technology, USA) - Hans A. Hofmann (University of Texas at Austin, USA) - Michael Taborsky (University Bern, Switzerland) - Walter Salzburger (University Basel, Switzerland)

If you have any questions, do not hesitate to pose them to:

cichlidscience@unibas.ch

Please spread the word about this conference to your students and collaborators!

Kind regards,

Your organizing committee

Adrian Indermaur, Britta Meyer, Moritz Muschick and Yuri Klaefiger (PhD and Master students of the Salzburger Research Group)

related links:

Our research group http://evolution.unibas.ch/salzburger/ Information about University and arrival http://evolution.unibas.ch/ http://evolution.unibas.ch/contact.htm Information about Basel http://www.basel.com/en/welcome.cfm? Information about Hotels, Youth Hostels and Backpackers http://www.basel.com/en.cfm/uebernachtungen/hotelliste/ http://www.youthhostel.ch/ http:/-

/www.ymcahostelbasel.ch/home_1_e.php http://www.baselbackpack.com/ Information about visa requirements to enter Switzerland from abroad (we assume no liability): http://www.bfm.admin.ch/etc/medialib/data/migration/rechtsgrundlagen/weisungen_und_kreisschreiben/ Weisungen_Visa.Par.0026.File.tmp/anh1-liste1_vorschriften-nach-staat-e.pdf

Moritz Muschick <moritz.muschick@unibas.ch>

Basel CichlidEvolution Aug26-29 reminder

Dear evoldir user,

Please consider the approaching deadline for registration with the Cichlid Science 2010 conference in Basel!

Registration is open until 1st July

Kind regards,

Your organizing committee

Adrian Indermaur, Britta Meyer, Moritz Muschick and Yuri Klaefiger

*****

original invitation:

Dear evoldir user,

We would like to invite you to the Cichlid Science 2010 conference taking place from the 26th to the 29th of August 2010 in Basel, Switzerland. It is going to be an international conference for researchers working on various aspects of cichlid fish biology or which use cichlids as a model system.

This interdisciplinary venture is going to be an ideal opportunity for creating new ideas and collaborations in the lovely scenery of estival Basel. We especially encourage doctoral students and young postdocs to register, since our foremost aim is to give them the opportunity to present and discuss their research.

Registration deadline: 1st July Registration fee: 80 Swiss francs (aprox. 56 EUR, 70 USD) Please register via our conference website: http://www.evolution.unibas.ch/cichlidscience2010/ Unfortunately, we can accept a limited number of participants only!

more information:

http://www.evolution.unibas.ch/cichlidscience2010/

Facebook group: “Cichlid Science 2010”

confirmed speakers include: - J. Todd Streelman (Georgia Institute of Technology, USA) - Hans A. Hofmann (University of Texas at Austin, USA) - Michael Taborsky (University Bern, Switzerland) - Walter Salzburger (University Basel, Switzerland)

If you have any questions, do not hesitate to pose them to:

cichlidscience@unibas.ch

Please spread the word about this conference to your students and collaborators!

Kind regards,

Your organizing committee

Adrian Indermaur, Britta Meyer, Moritz Muschick and Yuri Klaefiger (PhD and Master students of the Salzburger Research Group)

related links:

Our research group http://evolution.unibas.ch/salzburger/ Information about University and arrival http://evolution.unibas.ch/ http://evolution.unibas.ch/contact.htm Information about Basel http://www.basel.com/en/welcome.cfm? Information about Hotels, Youth Hostels and Backpackers http://www.basel.com/en.cfm/uebernachtungen/hotelliste/ http://www.youthhostel.ch/ http://www.ymcahostelbasel.ch/home_1_e.php http://www.baselbackpack.com/ Information about visa requirements to enter Switzerland from abroad (we assume no liability): http://www.bfm.admin.ch/etc/medialib/data/migration/rechtsgrundlagen/weisungen_und_kreisschreiben/ Weisungen_Visa.Par.0026.File.tmp/anh1-liste1_vorschriften-nach-staat-e.pdf

Moritz Muschick <moritz.muschick@unibas.ch>

BathU SexualSelection Sep1-4

Dear friends and colleagues

“New directions in sexual selection research: unifying behavioural and genomic approaches” Bath University September 1st to 4th 2010.

Conference website: http://www.ert-conservation.co.uk/Conference_home.htm (1) Extended call for abstracts:

We have had a large response to the first call for papers. Some people were unable to meet the deadline and have requested an extension. To accommodate this demand, the new submission deadline is Friday 25th June. So far, in addition to our four keynotes, we have selected 26 speakers arranged in the following four sessions:

1: Sexual conflict and male-female coevolution. 2: Post-copulatory sexual selection. (i) Seminal fluid: evolution and function

(ii) Sperm competition and evolution

3: Unifying behavioural and genomic approaches. (i) Ecology, behaviour and genetics of mate choice

(ii) Male and female sex roles

4: Synthesis: next generation sequencing, transcriptomics, proteomics and beyond.

We are seeking about ten new oral papers (no limit on posters). Abstracts should be to be emailed to Mark@ERT-conservation.co.uk Please see the attached pdf for further submission details.

(2) Booking and registration deadline:

The deadline for registration at the conference is Wednesday 21st July. To book your place, go to: http://www.ert-conservation.co.uk/Registration.htm There are 200 delegate places but only 150 accommodation rooms available on the campus. These will be designated on a first-come first-serve basis so please book your place as early as possible.

We would be extremely grateful if you could forward this message to colleagues who you think might be interested in attending the conference, or place the attached pdf on a departmental noticeboard.

We very much hope you will be able to join us in September and look forward to welcoming you to Bath.

With best wishes.

Dr Mark O'Connell, on behalf of the conference science committee.

This conference has been generously sponsored by the Genetics Society.

Ecological Research & Training <mark@ert-conservation.co.uk>

Berlin BioSystematics Feb21-27

Congress announcement:

Dear Collegues,

Congress organizers would be pleased to welcome you in the German capital and look forward to many inspiring contributions towards evolutionary biology:

BioSystematics Berlin 2011 - 21-27 February

7th International Congress of Systematic and Evolutionary Biology (ICSEB VII), 12th Annual Meeting of the Society of Biological Systematics (Gesellschaft für Biologische Systematik, GfBS) 20th International Symposium "Biodiversity and Evolutionary Biology" of the German Botanical Society (DBG).

Call for Symposia is still open.

Registration and abstract submission opens in July.

Proposals corresponding to the five major conference topics are especially encouraged, but all relevant topics will be considered by the organizers. Symposia across more than one group of organisms are welcome and strongly encouraged. Symposium organizers are free to open their session for Contributed papers.

Topics: . Trends in Taxonomy . Evolution and Organisms in Time and Space . The Evolutionary Thought: History, Philosophy and Society . Evolution of Form and Function . Inventorying and Managing Biodiversity

For further submission guidelines see http://-www.biosyst-berlin- 2011.de/. Submissions can be made via Congress Office. Also contact in case of any question: berlin2011@bgbm.org

Birgit Nordt Congress Office "BioSystematics Berlin 2011" Freie Universität Berlin Botanic Garden and Botanical Museum Königin-Luise-Str. 6-8 14195 Berlin Germany Phone: ++49/30/838 50 383 Fax: ++ 49/30/841 729 52 E-mail: berlin2011@bgbm.org Web: www.biosyst-berlin-2011.de BerlinCongress2011 <BerlinCongress2011@bgbm.org>

Brittany SocialEvolution Oct11-15 2

Dear colleagues,

*Registration still open! **There are still 10 places to attend the symposium with a poster presentation or as a participant.*

We organize a conference on "Social systems: demographic and genetic issues" next October (11-15^th) in Paimpont, Brittany, France. We propose the conference to be organized around 2 major themes:

1. /Social organization and demographic structure/ – The influence of philopatry, polygyny, dispersal bias among sexes, natal sex ratio, social reproductive suppression, kin selection and kin discrimination, on demographic structure

2. /Social organization and genetic structure/ –The effects of social organization and group dynamics, the role of group fission, fission-fusion social systems, sex biased dispersal, the influence of dominance rank (lineages or individuals), mate choice on the distribution of relatedness and gene diversity of neutral and functional (for instance MHC) genes. The conference will mix theoretical and empirical approaches, scientific questions with methodological issues.

The conference will be limited to about 75 people. There is no more place for oral communications.

We invite people who wish to present a poster or to attend the conference to send us their abstract and/or to register before June 30.

Organization and registration details including a provisional program can be found on http://socior.univ-rennes1.fr/ Nelly Ménard 1, Nicolas Perrin 2, Eric Petit 1 & Jean-Sébastien Pierre 1

1 Department for the study of Ecology, Biodiversity and Evolution at the University of Rennes 1 and CNRS (National Centre for Scientific Research, France)

– Nelly Ménard, UMR 6553 ECOBIO, Ecosystème, Biodiversité, Evolution; CNRS/Université de Rennes 1; Station Biologique 35380 Paimpont-France;

http://www.sbp.univ-rennes1.fr http://ecobio.univ-rennes1.fr/ tel: 02.99.61.81.72; from abroad: 33.2.99 etc... mail: nelly.menard@univ-rennes1.fr

nelly.menard@univ-rennes1.fr

Coimbra Portugal SoilAdapation Jun12-16

Serpentine soils present extreme edaphic conditions: elevated concentrations of heavy metals (Ni, Cr, Co), low concentrations of essential nutrients, a low Ca/Mg ratio and a low water capacity. Despite these unfavorable conditions, adaptive serpentine tolerance is both geographically and phylogenetically widespread, which renders these soils into systems particularly suited for studying the process of adaptive evolution in nature.

We cordially invite you to attend the 7th International Conference on Serpentine Ecology that will take place in Coimbra, Portugal, from 12-16 June 2011. The conference is organized by the Centre for Functional Ecology (http://ecology.uc.pt) and hosted by the Department of Life Sciences of the University of Coimbra (http://www.uc.pt).

The conference provides an opportunity for the gathering of researchers from around the world, to share and discuss their findings regarding the broad and inter-disciplinary field of serpentine ecology, including the fascinating relationships that exist between extreme geology and life, from organisms to communities and ecosystems. Participants in former conferences included geologists, soil scientists, plant chemists and biochemists, microbiologists, astrobiologists, botanists and geobotanists, zoologists, ecologists, ecophysiologists, restoration ecologists, evolutionary geneticists and conservation biologists.

To highlight the commitment of our scientific community to the conservation of serpentine habitats worldwide, the motto of the VII ICSE will be: "Promoting awareness of serpentine biodiversity".

Conference website: http://icse2011.ultramafic-ecology.org/ To receive updated information register at: http://www.ultramafic-ecology.org/

Draft Program

June 12: Welcome reception June 13, 14: Scientific sessions June 15: Mid-conference field trip to serpentine areas near the city of Bragança, northeast Portugal June 16: Scientific sessions; banquet dinner

June 17-20: Optional post-conference field trip: southern Portugal, Tinto River area (Huelva, Spain), and Sierra Bermeja Range (massive ultramafic territory near the city of Málaga, Spain).

Important dates and deadlines

September 2010 (2nd circular) - Final session topics announced - Website ready (info on accommodation, transportation, proceedings publication, etc.) - Call for abstracts (oral and poster presentations) - Registration opens - Post-conference field trip preliminary registration opens

December 2010 - Deadline for early registration (reduced rates) and abstract submissions (oral and posters) - Deadline for early registration in post-conference field trip

February 2011 - Notification of acceptance of abstracts to authors (oral and posters) - Deadline for late registration and late abstract submissions (posters only) - Deadline for late registration in post-conference field trip

April 2011 (3rd circular) - Notification of acceptance to authors (late abstracts) - Final scientific program - Acceptance of definitive participants in the post-conference field trip

June 2011 - VII ICSE, June 12-16 - Post-conference field trip, June 17-20

Mark this event in your agenda. We look forward to meeting you in Coimbra.

Susana Gonçalves <scgoncal@ci.uc.pt>

CornellU HarrisonCelebration Jul22-23

Genetics and the Origin of Species: The Continuing Synthesis

A symposium in honor of Richard G. Harrison.

July 22-23, 2010, Cornell University, Ithaca, NY.

POSTER ABSTRACT DEADLINE NOW JUNE 22.

For full details, see the website: _http://rickfest.ucdenver.edu/_ Invited speakers:

Charles Aquadro Genes or organisms in conflict: what drives the rapid evolution of reproductive genes?

Theresa Bert Applying evolutionary genetics to fisheries management

Andy Brower "Hybrid speciation" in /Heliconius/ butterflies: is there another explanation?

Richard Broughton Divergence and hybridization in cyprinid fishes

Jonathan Brown The phylogeography of /Eurosta solidaginis /revisited

Tim Collins Finding useful molecular characters for deep phylogenies

Alan de Queiroz Pseudogenes as sensitive indicators of interbreeding between divergent lineages

Erik Dopman Reproductive barriers and the genetic mosaic in pheromone strains of the European corn borer

Rick Grosberg Does life evolve differently in the sea?

David Hawthorne Plant hybrid zones beget herbivore hybrid zones and so on, ad infinitum

Godfrey Hewitt Quaternary biogeography: the roots of hybrid zones

Dan Howard The role of hybrid zones in studies of speciation

Brad Hyman Rampant gene rearrangement and haplotype hypervariation among nematode mitochondrial genomes

Laura Katz Dynamic genomes: inter- and intraspecific genome variation among eukaryotes

Scott Kelley Effects of evolutionary history, host-plant use and secondary chemistry on gut microbial community diversity of Longitarsus flea-beetles

Damhnait McHugh Resolving annelid phylogeny: from genes to genomes as a way forward

Sean Mullen Species' life histories and the origins of barriers to gene exchange

Ben Normark Niche explosion

Merrill Peterson Unraveling the costs of hybridization in a beetle hybrid zone

Rob Roy Ramey On the origin of specious species

David Rand The cytoplasm as a population and mitonuclear coevolution

Charles Ross Pattern and process in cricket mosaic hybrid zones

Kerry Shaw Evidence for the role of sexual selection in speciation

Willie Swanson Adaptive evolution and coevolution of sperm-egg recognition molecules

Chris Willet The nature of interactions that contribute to post-zygotic reproductive isolation in hybrid copepods.

Gerald Wyckoff How do you tell positive selection from negative selection using protein sequences: molecular evolutionary genetics beyond nucleotide comparisons

Benjamin Normark <bnormark@ent.umass.edu>

Galway Ireland ElasmobranchTaxonomy Nov10-13

Dear All,

The Irish Elasmobranch Group (IEG) is delighted to announce that it will be hosting the European Elasmobranch Association (EEA) 14th Annual Scientific Conference in Galway 10th-13th November 2010. This promises to be an exciting conference, and the IEG looks forward to welcoming you to beautiful Galway. This international conference provides an opportunity to showcase elasmobranch research currrently being undertaken in Ireland, Europe and further afield. The EEA welcomes contributions dealing with all aspects of chondrichthyan biology including life-history, population biology, genetic studies and taxonomy. The abstract submission deadline for oral and poster presentations has now been extended until 16th June 2010. Opportunities are still available for oral and poster presentations.

More information on the conference is available on the IEG website (http://www.irishelasmobranchgroup.org) and the abstract submission page can be found here http://www.irishelasmobranchgroup.org/?page_id=-422 . Details of previous EEA meetings including lists of attendants, abstracts and photos can be found on the EEA website http://www.eulasmo.org/-v.asp?level2id=6464&rootid=6464&depth=1 Best wishes, Irish Elasmobranch Group Committee

Sean Michael Fitzpatrick <sfitzpatrick10@qub.ac.uk>

Hilo Hawaii ConservationGenomics Jul26-28 Deadline

July 1 is the online Registration Deadline for the 2010 AGA Symposium, “Conservation Genomics”.

Symposium details and registration at: http://-www.theaga.org/2010 AGA meetings focus on a single topic and last for 2.5 days. This year’s topic is Conservation Genomics, and will include talks by a series of genomicists and conservation biologists, including those who are already shaping this emerging discipline. Our goal is to provide a focused forum for discussion, brainstorming, and development of collaborative efforts that leverage emerging genomic resources for applications in conservation biology.

To encourage broad attendance, we have kept registration low ($150), which includes an opening mixer and evening luau. We have negotiated very reasonable hotel accommodation in Hilo as well as the dormitory space at UH.

Please join us- Hilo is an amazing setting, and we look forward to an engaging, enlightening three days.

Any questions, contact:

Brad Shaffer hbshaffer@ucdavis.edu, President of the AGA, or

Anjanette Baker agajoh@oregonstate.edu, Managing Editor, Journal of Heredity

agajoh@oregonstate.edu

Hilo Hawaii ConservationGenomics Jul26-28 DormRooms 2

Deadline to reserve Dorm Rooms extended to Monday, June 14

UH Hilo has dorm rooms available for any nights from 25-31 June. The housing is “apartment style”, with 2 bedrooms (each has two beds, and sleeps two people), a common area, and a kitchen. The rate is $20/night per person, and a one-time $10 fee for linens.

If you would like to stay in the dorms, please contact Brad Shaffer, hbshaffer@ucdavis.edu by Monday, June 14.

Symposium details and registration at: http://-www.theaga.org/2010 AGA meetings focus on a single topic and last for 2.5 days. This year’s topic is Conservation Genomics, and will include talks by a series of genomicists and conservation biologists, including those who are already shaping this emerging discipline. Our goal is to provide a focused forum for discussion, brainstorming, and development of collaborative efforts that leverage emerging genomic resources for applications in conservation biology.

To encourage broad attendance, we have kept registration low ($150), which includes an opening mixer and evening luau. We have negotiated very reasonable hotel accommodation in Hilo as well as the dormitory space at UH.

Please join us- Hilo is an amazing setting, and we look forward to an engaging, enlightening three days.

Any questions, contact:

Brad Shaffer hbshaffer@ucdavis.edu, President of the AGA, or

Anjanette Baker agajoh@oregonstate.edu, Managing Editor, Journal of Heredity

agajoh@oregonstate.edu

London ASAB SexualSelection Dec2-3

Subject heading: ASAB Winter Conference

Main text:

Interspecific Communication

Signalling and communication, in the context of sexual selection, has been one of the dominant research areas in animal behaviour for the last three decades. The 2010 Winter ASAB conference will instead focus on interspecific communication. This topic is rich in terms of extraordinary natural history and the theory needed to understand what is going on, and has profound implications for evolution and ecology. Sub-themes include: host manipulation by parasites (including brood parasites), plant-pollinator interactions, anti-predator defensive signals, the evolution of mutualism, and alarm-calling.

The plenary speakers at the main conference are:

Redouan Bshary (University of Neuchâtel, Switzerland) Lars Chittka (Queen Mary College, University of London, UK) Rebecca Kilner (University of Cambridge, UK) Leena Lindstrom (University of Jyväskylä, Finland) Rob Magrath (Australian National University, Australia)

The meeting is, as always, also host to ASAB's annual Tinbergen lecture. This year's speaker is Laurent Keller of the University of Lausanne, Switzerland.

We are now seeking contributed talks and posters to complement the exceptional invited speakers. Please send abstracts of potential contributions, using the downloadable form on the ASAB website (http://asab.nottingham.ac.uk/meetings/asab.php), to Adrienne.Whitty@bristol.ac.uk (putting 'ASAB conference' in the subject box).

Deadline for abstract submission: 31st July 2010 Registration: Free. Just turn up! Venue: Zoological Society of London meeting rooms, Regent's Park, London, UK Dates: 2nd - 3rd December, 2010

Andy Radford and Innes Cuthill (organisers), University of Bristol, UK

A Radford <Andy.Radford@bristol.ac.uk>

Marseilles 14thEvolBiology Sep21-24 deadline

Dear All,

We are please to recall you that the deadline of the 14th Evolutionary Biology Meeting at Marseilles 21-24 September 2010 will be on 30th June.

Do not hesitate to go on our website: http://sites.univ-provence.fr/evol-cgr

Best wishes,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

Marseilles 14thEvolutionaryBiology Sep21-24

Dear All,

We are pleased to inform you that the 13th Evolutionary Biology Meeting at Marseilles will take place on 21-24 September 2010, Marseilles, France.

Few spots are still available for oral presentation.

The best presentations will be published in a collective opus edited by Springer.

For more information, do not hesitate to go on: http://sites.univ-provence.fr/evol-cgr Best wishes,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

Melbourne CaveSpeciation July23-30

Dear All,

Being organized is a symposium on Cave Speciation and

Biodiversity Conservation at the XVIII International Botanical Congress at Melbourne 23-30 July 2011.

The aim of this symposium is to exchange knowledge about cave species diversity and their ecology, evolution, and conservation. Therefore this symposium will cover two themes (which is good): systematics, evolution etc. and ecology, conservation etc. Furthermore, it will cover both botany and zoology.

Any botanists or zoologists who are interested in speaking at this symposium are encouraged to contact me immediately.

Thanks and best wishes

Li-Bing Zhang, Ph.D. Assistant Curator Missouri Botanical Garden Box 299, St. Louis, Missouri 63166 Tel: +1-314-577-9454; Fax: +1-314-577-9596 www.mobot.org/MOBOT/Research/curators/zhang.shtml To discover and share knowledge about plants and their environment in order to preserve and enrich life. -mission of the Missouri Botanical Garden

Libing Zhang <gonggashan@gmail.com>

Oregon PhylogeneticsEvolutionInformatics Jun29-30 4

This is a reminder that the Call for Challenge entries for the inaugural conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio) closes in two weeks on June 21, 2010.

The theme of the 2010 iEvoBio conference challenge is “New visualization methods for evolutionary data”. Visualizing evolution is a key part of our discipline and presents opportunities as much as it does obstacles. The iEvoBio Challenge is deliberately wide ranging: entries could range from geophylogenies to visualizing extremely large phylogenetic trees, to mashups showing relationships between lineages and other types of data (e.g. conservation status).

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

The winners of the Challenge will be judged collectively by the iEvoBio participants. There will be cash prizes for the first place ($1,000) and runner up entries.

Challenge entries are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Full talks (closed), 2) Lightning talks, 3) Software Bazaar entries, and 4) Birds-of-a-Feather gatherings. The Calls for Lightning Talks and Software Bazaar entries remain open (see http://ievobio.org/ocs/index.php/ievobio/2010/), and information on the Birds-of-a-Feather session is forthcoming.

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

The iEvoBio 2010 Organizing Committee: Rod Page (University of Glasgow) Cecile Ane (University of Wisconsin at Madison) Rob Guralnick (University of Colorado at Boulder) Hilmar Lapp (NESCent) Cynthia Parr (Encyclopedia of Life) Michael Sanderson (University of Arizona)

hlapp@nescent.org

Oregon PhylogeneticsEvolutionInformatics Jun29-30 BoFs

In anticipation of the inaugural conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio), we solicit all attendees to propose and discuss Birds-of-a-Feather gatherings. See below for details.

Birds-of-a-Feather gatherings (BoFs) are informal, adhoc, focused face-to-face discussion groups that form around a shared interest. BoFs have a leader (usually, but not necessarily, the proposer) who initiates or moderates the discussion, but typically not a preset agenda. The topics of BoFs can range widely, including general cultural or computational infrastructure issues, or narrower questions such as how to make the best use of a particular software tool or how to solve a particular computational challenge.

Anyone willing to lead such a group can propose a BoF.

iEvoBio will provide space that can accommodate up to 8-10 BoFs. Sign-up sheets will be provided on-site on the first day of the conference where attendees can propose a BoF or sign up for one proposed by someone else. BoFs will be about 1 hr in duration and take place in the afternoon of the second day of the conference.

In line with their informal nature, there is no official prior call for or submission of BoFs. However, we encourage those intending to propose one to sound out or rally potential attendees ahead of time. We suggest to employ Twitter (http://twitter.com) for this, using the #ievobioBof tag to mark BoF proposals and comments.

Birds-of-a-Feather gatherings are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Full talks (closed), 2) Lightning talks (waiting list only), 3) Challenge entries, and 4) Software Bazaar entries. The Calls for Challenge entries (http://ievobio.org/challenge.html) and Software Bazaar entries (http://ievobio.org/ocs/index.php/ievobio/2010/) remain open.

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

The iEvoBio 2010 Organizing Committee: Rod Page (University of Glasgow) Cecile Ane (University of Wisconsin at Madison) Rob Guralnick (University of Colorado at Boulder) Hilmar Lapp (NESCent) Cynthia Parr (Encyclopedia of Life) Michael Sanderson (University of Arizona)

hlapp@nescent.org

PacificSympBiocomp Microbiomes DeadlineExtended

Due to the great interest in this subject, we have decided to extend the deadline for submitting manuscripts to the Pacific Symposium on Biocomputing (PSB) special session on "Microbiome Studies" to 18 July.

Please feel free to forward this email to anyone whom you think would be interested. Attached please find an updated poster.

Abstract of special session: Microbes dominate life on earth, measured by biomass, habitat diversity, phylogenetic diversity, or metabolic potential. Nonetheless, microbiome studies are in their infancy. Most natural ecosystems remain uncharacterized. Many human microbiome sites are unexplored, with very few comparisons of healthy versus diseased individuals. Mechanisms for microbial adaption and ecological engineering are poorly understood. Supporting computational tools are just emerging. This session addresses these needs.

For information on PSB: http://psb.stanford.edu/ James A. Foster

"James A. Foster" <foster@uidaho.edu>

UHull PopGroup Jan5-7

The 44th Population Genetics Group (PGG or PopGroup) meeting will be held at the University of Hull, UK, January 5th-7th 2011. This is a yearly international meeting for all types of evolutionary genetics.

The website of the Population Genetics Group can be found at http://www.populationgeneticsgroup.org Registration will open in October, but we have had requests for earlier information this year, so you can now sign up to the mailing list from the website http://www.populationgeneticsgroup.org/contact/ (if you have attended either of the last 2 meetings, Cardiff or Liverpool, you will already be on the mailing list)

Updates can also be got through RSS feeds and twitter announcements http://www.populationgeneticsgroup.org/feed http://twitter.com/popgroup See you in Hull Dave

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

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

UOttawa RECOMB Oct9-11

Due to numerous requests, the deadline for submitting papers to RECOMB CG has been extended two days, to June 9, 2010.

The 2010 RECOMB Comparative Genomics Satellite conference will be held at the University of Ottawa, October 9-11, 2010. The deadline is now June 9 (please contact the organizers for additional information: sankoff@uottawa.ca, Eric.Tannier@inria.fr) and notification June 28. The CFP and submission site as well as early registration can be reached through the website: http://recombcg.uottawa.ca/recombcg2010/- Submitted papers are allowed somewhat greater lengths than some other conferences (12 pages). The proceedings will be published in LNCS and we expect that selected, expanded papers will be published in JCompBio. Our website contains links to previous proceedings, which by now contain a good proportion of the canon of publications in computational comparative genomics.

Invited speakers are:

Brenda Andrews (University of Toronto) Andrew G. Clark (Cornell University) Nicolas Corradi (University of Ottawa) Jan Dvorak (University of California at Davis) Aoife McLysaght (University of Dublin) Nicholas Putnam (Rice University)

We have obtained some financing and expect to be able to contribute significantly to the travel costs of student and postdoc presenters of papers and posters. Hoping to hear from you,

David Sankoff Eric Tannier

Apologies if you receive more than one copy of this (or similar) message.

sankoff@uottawa.ca

Wageningen CoralReefs Dec13-17

The 2010 European meeting of the International Society for Reef Studies (13-17 December in Wageningen, Netherlands) will include a session entitled "Systematics, biogeography and evolution: the evolutionary biology of reef organisms, their distribution and their taxonomy, including systematic relationships to other organisms".

Deadline for submission of abstracts for oral presentations: 1 July 2010

Deadline for submission of abstracts for poster presentations: 1 October 2010

For abstract submission, registration and further information, please visithttp://www.isrs2010.org/home. For inquiries regarding this particular session, please contactjean-francois.flot@fundp.ac.be.

Jean-François Flot, Ph.D. Department of Biology University of Namur Rue de Bruxelles 61 5000 Namur, Belgium

jean-francois.flot@fundp.ac.be

GradStudentPositions

Belgium 2 EvolutionaryComputation

Three open positions for 2 PhD students and 1 postdoc in the area of evolutionary computation / bio-inspired computing Interdisciplinary research project "Bio-inspired computing for coordination and control in large-scale and dynamic systems (BioCo3)"

In this interdisciplinary project (involving computer science, biology, operations research and logistics expertise) we will study decentralized approaches for controlling large-scale, dynamic systems - e.g. for controlling a large number of vehicles that need to accomplish transport tasks for clients (package delivery service). Achieving efficient and effective collective behavior is known to be quite a challenge, esp. if the systems are large in scale and submitted to changing operating conditions. Complex collective behaviour occurs in many socio-biological systems. Social insects, e.g., are able to find the shortest path to food sources without any central control, or can build enormously complex nests with built-in ventilation systems, or divide the work such that the chances of survival are optimal.

Some socio-biological mechanisms for collective behavior have already been studied in the context of computing (e.g. stigmergy and digital pheromones, or in discrete optimization techniques, such as ant colony optimization, artificial immune systems, genetic algorithms). It becomes apparent, however, that (1) large-scale and dynamic systems still hold major challenges, and (2) many socio-biological concepts and techniques have been unexplored.

The project therefore aims to study advanced concepts and mechanisms, known from social biological systems, and their applicability in decentralized control systems. To guide the research, the project will use concrete application scenarios, based on decentralized control in pickup-and-delivery problems (PDPs), and evolutionary algorithms to evolve more efficient control strategies.

Keywords: Multi-agent systems, Discrete optimization, Sociobiology, Social Insects, Biologically-inspired computing, Pickup-and-delivery problems, Ant Colony Optimisation, Evolutionary Algorithms, Genetic Algorithms

The partners in this project are Dept. of computer science, DistriNet labs Prof. Tom Holvoet http://distrinet.cs.kuleuven.be/ Dept. of biology, Laboratory of entomology Prof. Tom Wenseleers http://bio.kuleuven.be/ento/ Dept. of mechanics, Center for industrial management Dr. Paul Valckenaers

http://www.mech.kuleuven.be/en/cib/ Saint-Lieven College, IT department Dr. Greet Vanden Berghe

http://ingenieur.kahosl.be/personeel/greet.vandenberghe/ Requirements For this ambitious project, two PhD positions and one position for a postdoctoral researcher are open. We invite applications from:

either people who have a strong computer science background (master degree for PhD positions, PhD degree for the postdoc position) with a strong affinity and interest in biology,

or people who have a strong a biological background (master degree for PhD positions, PhD degree for the postdoc position) and strong affinity and interest in computer science. The positions are available from October 1, 2010 (negotiable). Further requirements for candidates include

having a scientific, critical attitude being ambitious having good communication and social skills, team player having an independent working style being proficient in English experience as a researcher is welcome but not mandatory for the PhD positions.

For more information and for applying... For more information about the project and the positions, and for applying for a position, please contact the project coordinator:

Prof. Tom Holvoet

DistriNet Labs - Dept. of Computer Science, KULeuven, Belgium

http://people.cs.kuleuven.be/Tom.Holvoet For more information about the KULeuven:

http://www.kuleuven.be/ The deadline for application is

July 15, 2010.

When applying, make sure to include (pdf versions of):

a detailed resume (with publications, if you have any) a motivational letter specifically referring to the open positions copies of marks and degrees/certificates a list of 3 references that we can contact your MSc thesis in English (or a 5-page summary in English).

Please forward this message to interested staff/students... – Prof. Dr. Tom Holvoet DistriNet labs Dept. of Computer Science KULeuven

http://people.cs.kuleuven.be/Tom.Holvoet Celestijnenlaan, 200A B-3001 Leuven Belgium +32 16 32.76.38

Dr. T. Wenseleers Dept. of Biology Zoological Institute K.U.Leuven Naamsestraat 59 B-3000 Leuven Belgium tel. +32 (0)16 32 39 64 mobile +32 (0)472 40 45 96 e-mail tom.wenseleers@bio.kuleuven.be

— / —

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

Berlin PopGenEvolution

PhD opportunity in popgen and evolution of aquatic Diptera at the Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) and the Freie Universitaet Berlin

We have an open PhD student position (funded for 3 years) for someone interested in population genetics and evolution. The student would join a large interdisciplinary study of the effects of light pollution on ecological systems. The student would help to develop and carry out a research project on aquatic Diptera (mosquitoes, midges) involving field and laboratory work. Some knowledge and experience with freshwater ecology, molecular ecology, bioinformatics, or statistics would be beneficial. The working language of the laboratory group (currently 3 post-docs, 1 technician, 2 students) is English, but a willingness to learn or some previous knowledge of german would greatly enhance your time in Berlin. For further information please contact Michael T Monaghan (monaghan@igb-berlin.de).

Please send your application by email directly to me (monaghan@igb-berlin.de) including (1) your CV with details of any field and laboratory experience, (2) one page stating your interests and career goals, (3) the names and contact information for 2 referees. Applications will be accepted until a suitable candidate is found.

Michael Monaghan <monaghan@igb-berlin.de>

DeakinU EvolutionaryGenetics

A PhD position available, Evolutionary genetics of the invasive Northern Pacific Sea Star, Asterias amurensis, in Australia

Supervisors: Dr Craig Sherman (PI), Dr Ben Hayes (Department of Primary Industries) Institution: The Centre for Integrative Ecology, Deakin University, Australia

Aims and background: Invasive species are now recognised as one of the most serious threats to Australias biodiversity. While substantial work has been carried out on the ecology of invasive species, the evolutionary genetics of invasive species has received less attention. However, it is becoming increasingly evident that the establishment and spread of exotic species can be influenced by their adaptive potential and that effective control requires an understanding of the evolvability of invasive species.

The invasive North Pacific Sea Star is a ferocious marine predator and has the potential to have a devastating effect on Australias aquaculture industry and significantly reduce the biodiversity of marine communities. It is estimated that there are more than 90 million in Port Phillip Bay, with the potential for this species to occupy even larger areas from Sydney to Perth. In spite of being listed as one of the ten highest marine risk pests in Australia, virtually nothing is known about its potential for local adaptation and what may constrain its progression along the east and southwest coasts of the continent. This project will provide crucial information on the evolutionary biology of this species and identify key life history traits important for the successful management of this invasive species. More information can be found at: http://www.deakin.edu.au/scitech/les/research/rpa/ecophysiology/opportunities/seastar.php The applicant must hold a first class honours or masters degree (or equivalent) in biology. The candidate should have a strong interest in evolutionary and molecular genetics/genomics, local adaptation, quantitative genetics and experimental molecular work.

How to apply

Expressions of interest with a covering letter, CV, and names and contact details of two referees should be sent to Dr. Sherman (craig.sherman@deakin.edu.au).

Interested candidates should lodge a Research Scholarship application with Deakin University (http://www.deakin.edu.au/research/admin/scholarships/index.php). There are three rounds of applications: The first minor round is open to international and domestic applicants and closes on 30 June 2010. Two major rounds follow, with one restricted to international applications and closing on 30 September 2010 and the other one restricted to Australian and New Zealand citizens and Australian permanent residents and closing on 31 October 2010.

Deakins Research Scholarships are valued at A$ 22,500 per annum and will be topped-up by the CIE to A$ 30,000 per annum for successful applicants. The program will not incur any tuition fees if completed within the appropriate time frame. All candidates are encouraged to contact the director of the CIE, Prof Marcel Klaassen (marcel.klaassen@deakin.edu.au) before application, including a brief CV and a statement of their research interests.

Dr Craig D.H. Sherman Lecturer, School of Life and Environmental Sciences

Faculty of Science & Technology Deakin University, Pigdons Road, Geelong VIC 3217 Phone: 03 5227 1406 International: +61 3 5227 1406 Fax: 03 5227 1040 International: +61 3 5227 1040 E-mail: craig.sherman@deakin.edu.au http://www.deakin.edu.au/scitech/les/about/staff-profiles/display/index.php?username=csherman Craig Sherman <craig.sherman@deakin.edu.au>

KULeuven Belgium 2 SocioMicrobiolEvolution

Two PhD positions are available in the research groups of Prof. J. Michiels and Prof. K. Verstrepen in the framework of an interdisciplinary research project “Socio-evolutionary dynamics of microbes” (KULeuven, Belgium).

Target organisms: Saccharomyces cerevisiae (K. Verstrepen) and Pseudomonas aeruginosa (J. Michiels).

Partner groups: Lab. of Entomology (Prof. T. Wenseleers) and Lab. of Aquatic Ecology (Prof. L. De Meester)

Topics: flocculation and green-beard recognition in yeast and the evolution of antibiotic-tolerance (persistence) in P. aeruginosa.

Key words: experimental evolution, microbial genetics, high-throughput analysis, fluorescence microscopy, flow cytometry, mutant construction, ecological and evolutionary theory (social evolution theory, bet-hedging theory).

As a member of the CMPG, you will be part of a multidisciplinary and international team of researchers using state-of-the-art infrastructure.

Start: autumn 2010 (two 4-year projects)

Required: - Master in life sciences (Bioengineering, Biotechnology,...). - Strong interest for science and outstanding skills to work in a team on an intellectually and technologically challenging project. - Ready to present for an interview.

Application: send your CV and two reference letters to Prof. J. Michiels (jan.michiels@biw.kuleuven.be) or Prof. K. Verstrepen (kevin.verstrepen@biw.vib-kuleuven.be) before June 23, 2010.

General information on the research groups involved: http://www.biw.kuleuven.be/dtp/cmpg/G%26G1/ http://www.biw.kuleuven.be/dtp/cmpg/research.aspx http://bio.kuleuven.be/ento/wenseleers/twenseleers.htm http://bio.kuleuven.be/de/dea/people_detail.php?pass_id=u0008482 Dr. T. Wenseleers Dept. of Biology Zoological Institute K.U.Leuven Naamsestraat 59 B-3000 Leuven Belgium tel. +32 (0)16 32 39 64 mobile +32 (0)472 40 45 96 e-mail tom.wenseleers@bio.kuleuven.be web http://bio.kuleuven.be/ento/wenseleers/twenseleers.htm

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

Munich EvolutionaryProteomics

PhD position in Evolutionary Ecology/Proteomics on the model system Daphnia

A 3-year PhD position is available in the labs of PD Dr. Christian Laforsch and Dr. Georg Arnold (joined project) at the Ludwig-Maximilians-Universität (LMU) in Munich.

We are looking for an enthusiastic and well-motivated person who would like to join our laboratories to study the molecular basis of adaptation to predation stress, focusing on plastic defensive traits in the water flea Daphnia. A holistic proteome approach will be applied to show differences and similarities in protein expression in D. magna faced to vertebrate and invertebrate predators to discover the proteins controlling different defensive strategies. The main objectives of the project are: -to discover candidate proteins, which may play a critical role in building the defensive traits -to compare the expression of candidate proteins in populations with contrasting predator coexistence history -to generate peptide induced antibodies with monoepitopic specificity (iSEPIA) against a set of candidate proteins derived from holistic approaches to enable their functional analysis.

The project is embedded in the European Science Foundation project “Stressflea” - How to live in a mosaic of stressors - an ecological genomics approach on the water flea Daphnia.

Applicants should have a Master’s or diploma degree in biology. Experience in experimental design, handling aquatic organisms, protein biochemistry, statistics and bioinformatics would be advantageous. Applicants should email a cover letter summarizing their research background and interest in the posted position, a CV, an abstract of master/diploma thesis, and contact information for two referees (everything as one PDF document) to both supervisors (laforsch@bio.lmu.de and arnold@lmb.uni-muenchen.de), by July 16. The position is available from 1st September 2010.

laforsch@zi.biologie.uni-muenchen.de

NewcastleU SexPolymorphism

Applications are invited for a 3-year NERC-funded PhD studentship based in the School of Biology, Newcastle University, UK. The studentship will be awarded for one of three topics, one of which is in the area of evolutionary biology:

- The maintenance of sex polymorphism in wild Plantago species: the role of inter-genomic conflict and restorer genes (Lead supervisor: Dr Kirsten Wolff)

For details of the project, eligibility and how to apply: http://www.ncl.ac.uk/biology/postgrad/-research/NERC2010.htm Please note that only UK students are eligible for full funding, and European students are only eligible for part funding. Please check out further details of eligibility.

Please contact me if you are interested and you would like more information. Deadline: Friday 18th June.

Best wishes, Kirsten Wolff

Dr Kirsten Wolff Reader in Evolutionary Genetics Newcastle University, School of Biology Newcastle NE1 7RU, UK Phone: 0191 222 5626 email: kirsten.wolff@ncl.ac.uk www.staff.ncl.ac.uk/kirsten.wolff/ Kirsten Wolff <kirsten.wolff@newcastle.ac.uk>

NewZealand Biogeoinformatics

A PhD position is available in New Zealand on “Biodiveristy science: biogeoinformatics” supervised by Alexei Drummond and Thomas Buckley.

Biodiveristy science: biogeoinformatics

The evolutionary and ecological relationships between the landscape and all its inhabitants represent a story that unfolds over both vast and short time scales. Understanding that story, its natural rhythms and its responses to perturbation, is the prime concern of molecular ecologists and evolutionary biologists the world over. A number of related fields and analysis techniques have developed in this area: historical biogeography, phylogeography, landscape genetics and niche modeling, to name a few.

The foundation of this project is the development of an enabling scientific resource for a new type of biodiversity science: biogeoinformatics. The research aims to enable a transition in the focus of molecular ecology from groups of closely-related species in isolation to spatially explicit genetic samples from species assemblages, communities and ecosystems. When an individual species or closely-related group of species is of primary interest, biogeoinformatics aims to put that species in the context of its wider ecosystem and habitat.

This project involves the design, development, curation and analysis of a national (NZ) repository of geo-located biodiversity data. The software developed will allow the upload, public access and visualization of phylogeographical data. The research data will consist of geo-located, time-stamped genetic and genomic samples from New Zealand fauna and flora. Natural overlays include geological, ecological and species distribution data, niche models et cetera. The main scientific outputs will be (i) a series of combined analyses of all existing NZ phylogeographic data sets to address open questions about NZ biogeography and the origins and history of NZ biota and (ii) the development of a scientific toolkit for biogeoinformatic research. The successful candidate will be a biology-oriented computer science student, or an ecologist/evolutionary biologist with strong computer programming skills. The PhD would be based in the University of Auckland under the supervision of A/Prof Alexei Drummond (University of Auckland, alexei@cs.auckland.ac.nz) and Dr Thomas Buckley (Landcare Research, buckleyt@landcareresearch.co.nz). We anticipate that the successful candidate developing good links with other research groups in NZ that focus on phylogeographical questions.

http://www.allanwilsoncentre.ac.nz/vacancies/-phdstudentships.htm#biodiversity Applicants are advised to contact Alexei Drummond (alexei@cs.auckland.ac.nz) for further enquiries.

Thomas Buckley <BuckleyT@landcareresearch.co.nz>

NewZealand EvolBiol

PhD Studentships in New Zealand on offer:

The Allan Wilson Centre is seeking candidates for seven PhD studentships. The titles of the projects for which candidates are sought are:

* Population-Genetic Models for the Maintenance of Genetic Variation * Discrete random models in evolutionary biology * The evolution of sex pheromone receptors and speciation in New Zealand endemic leafroller moths * Biodiversity science: biogeoinformatics * Mathematical and statistical analysis of SNP data * Visualising evolution * New Combinatorial and Algorithmic Tools for Network Reconstruction * Population genetics of tetrodotoxin-producing sea slugs

To make application for a studentship please contact the academic listed in the first instance. This information is at http://www.allanwilsoncentre.ac.nz/ hamish.spencer@otago.ac.nz

Norway SalmonLouse NaturalSelection

START OF PhD STUDENTSHIP ADVERT

PhD studentship: studying natural selection and evolutionary processes in the salmon louse, Lepeophtheirus salmonis

The Institute of Marine Research (IMR) has a three-year PhD studentship available in the Population Genetics and Ecology research group in Bergen to work on experimental studies of natural selection, evolution and genetics in the parasitic copepod, L. salmonis. The position will be linked to a work-package within the Norwegian Research Council funded project “PrevenT” which is a large inter-institute project studying molecular, epidemiology and evolutionary processes in L. salmonis.

The IMR has a long history of conducting experiments with L. salmonis, and supports a well equipped laboratory in Bergen that includes a rearing facility for conducting experiments on this parasite. Technological advances have provided us with the ability to produce strains of lice (inbred, outbred, drug-resistant and mutant), and family groups. When combined with DNA parentage testing, this system provides the ability to study and manipulate how genotype (individual, family or strain) and environment (temperature, salinity, chemicals, host type) interact for this parasite.

The studentship will be based upon planning and execution of biological experiments in the facility above. Lice family groups will be established by the student and challenged by environmental variables in order to study and quantify selection. These experiments will require meticulous planning and attention to detail. Individual lice surviving the experiments will be identified by parentage testing using microsatellites. Thus, the position will include a mixture of experimental, and some DNA laboratory work.

We wish to appoint a highly motivated person with a masters degree in a biological discipline. The ideal candidate will be able to document first-hand experience of designing, planning and executing biological experiments, preferably with sea lice, and has experience of basic molecular techniques such as DNA isolations and PCR. However, candidates showing relevant experience with other experimental systems will be considered.

The Institute emphasizes personal qualities such as good communication and cooperative skills, the ability to work independently and as part of an active research team.

We offer:

* a positive, challenging and creative work environment * the opportunity to work in a national institute with a high level of international contact * flexible hours, a good pension scheme and a wide range of welfare services.

The Institute offers governmental regulated salaries as PhD student (code 1017).

For more information, please contact Research Group Leader Terje Svaasand,

Email: Terje.Svaasand@imr.no, tel: +47 55236891 or Project leader Kevin Glover, Email: Kevin.glover@imr.no, tel: +47 4755236357, or visit our web-site at http://www.imr.no/ The Institute of Marine Research is an "inclusive work-life" employer that encourages diversity, and we encourage all qualified candidates to apply for this position. Women are particularly encouraged to apply.

Please apply in writing, enclosing a CV, copies of relevant recommendations and academic transcripts together with a set of publications, to: Institute of Marine Research, Personnel Division, P.O. Box 1870 Nordnes, NO-5817 Bergen, Norway. Application number: "30-10". Closing date for applications: 01.07.2010.

Dr Kevin Glover Senior Scientist Institute of Marine Research Bergen 55236357 48040035 Scientific presentation: http://www.imr.no/om_havforskningsinstituttet/ansatte/g/kevin_glover/nb-no "Glover, Kevin" <kevin.glover@imr.no>

OregonStateU SystematicsBiodiversity

GRADUATE OPPORTUNITY (MSc) FALL 2010

SYSTEMATICS, BIODIVERSITY and CONSERVATION of NATIVE FISHES in the OREGON DESERT

As part of a new research program on the biodiversity of fishes in the Department of Fisheries and Wildlife at Oregon State University, Dr. Brian Sidlauskas is searching for a talented, highly motivated masters student to investigate the systematics, population structure and conservation status of daces (genus Rhinichthys) in the arid drainages of eastern Oregon. The planned project will combine phylogenetics, microsatellites and geometric morphometrics to test the distinctiveness and diagnosability of dace populations throughout Oregon's desert rivers and lakes. Particular attention will be paid to assessing the taxonomic status, evolutionary relationships and population structure of the threatened and federally listed Foskett Spring Dace (Rhinichthys osculus ssp.). The project will also examine dace populations from adjacent drainages, including the Warner, Goose Lake, Harney and Malheur systems.

Minimum requirements for the position include strong interest in the systematics and conservation of fishes and a solid background in organismal biology as demonstrated by a bachelor's degree in biology, fisheries and wildlife, zoology, evolution, ecology, or a related field. Prior experience in a molecular lab (DNA extraction, PCR, sequencing, phylogenetics, microsatellite genotyping in Genemapper or similar) is highly desirable. The ideal candidate will also have prior classwork in ichthyology, anatomy, genetics, evolution and statistics and possibly work experience in an ichthyology collection.

Seven quarters of support including tuition, stipend and health insurance are available from a combination of research assistantships and online teaching assistantships (Principles of Fish and Wildlife Conservation, Ichthyology), as are funds to support initial field and lab work. Applications for additional grant support are pending.

The successful candidate would need to relocate to Corvallis, OR by September 1, 2010 in order to participate in planned fieldwork in early and mid September. Classes begin September 27, 2010.

To apply: Please send a cover letter describing your specific interest in this position, your resume or CV, GRE scores (unofficial is fine), undergraduate transcript (a scan or unofficial copies are fine), and contact information for three references to brian.sidlauskas@oregonstate.edu in .doc or .pdf format by June 30, 2010. Official applications to the graduate school are processed on a rolling basis and will be requested of the top candidate in July.

About the Sidlauskas Lab: We research the systematics, biodiversity and conservation of freshwater fishes with a combined morphological and molecular approach. Ongoing projects range from local to global and include research in North America, South America and Africa. Our facilities include a newly renovated molecular lab, a top-of-the line Zeiss V20 stereomicroscope, morphometric, x-ray and photography equipment, and an ichthyology collection of more than 20,000 lots of fishes from the Pacific Northwest and beyond. For more information, see http://people.oregonstate.edu/~sidlausb/ –

Brian Sidlauskas Assistant Professor Department of Fisheries and Wildlife 104 Nash Hall Oregon State University Corvallis, OR 97331-3803

Voice: 541-737-1939 Fax: 541-737-3590 Email: brian.sidlauskas@oregonstate.edu Web: http://people.oregonstate.edu/~sidlausb/ brian.sidlauskas@oregonstate.edu

SwanseaU SalmonConservationGenetics

Optimization of captive breeding systems for salmonid stock enhancement using molecular tags Fully-funded KESS PhD Scholarship 2010/2011 entry

Closing date: 23 July 2010

Supervisors: Dr Carlos Garcia de Leaniz (Swansea University, Pure & Applied Ecology) Dr Sofia Consuegra (Aberystwyth University, IBERS) Dr John Taylor and Dr Peter Gough (Environment Agency Wales)

Project Description: Aquatic ecosystems provide key resources for humans but tend to be less resilient than terrestrial environments, being home to endangered organisms that are often easily damaged by anthropogenic activities. Developments such as tidal barrages can have catastrophic consequences for aquatic fauna (particularly for migratory species) and demonstrate the need for knowledge on a range of aquatic issues. Molecular tags are increasingly being used to assign fish to their population of origin, to determine paternity and establish pedigrees, and to distinguish hatchery from wild fish. In salmonid restoration programs, the use of molecular tags for mark-and-recapture will dispense with the need to physically tag hatchery fish and will allow for identification of stocked juveniles and returning adults. This will result in considerable savings and improved management of endangered salmonid stocks, and will also permit the estimation of fitness parameters of relevance for conservation

The objectives of this research project are: 1. To assess the contribution of stocked (hatchery-reared) and wild Atlantic salmon using inherent, non-intrusive molecular tags to the River Taff; 2. To estimate the genetic diversity and effective populations sizes of the wild and stocked salmon populations; 3. To assess the effects of multiple paternity and breeding design on survival and fitness of juvenile salmon; 4. To develop guidelines for improved breeding designs in salmonid stock enhancement.

The project is part-funded by the European Social Fund (ESF) through the European Union's Convergence programme administered by the Welsh Assembly Government. KESS PhD scholarships are collaborative awards with external partners. The successful candidate will work with academic staff at Swansea and Aberystwyth Universities, in collaboration with an industry partner, the Environment Agency Wales, based in Llandarcy.

Applicant requirements: We are looking for a highly motivated student with a First or Upper Second Class Honours degree in Biological Sciences or related field. Knowledge of fish biology, molecular ecology, and conservation biology is desirable. Acquaintance with salmonid conservation, evolutionary ecology and population genetics will also be an advantage.

Scholarship value: The scholarship covers University tuition fees (3440 in 2010/2011) for three years and a stipend of 13,290 per annum for three years. Generous support for consumables, equipment and travel is also available.

Training: The achievement of a Higher-level Skills Development Award (HSDA) is compulsory for each KESS scholar. The HSDA is based on a 60 credit award, which is an additional award to the PhD.

Eligibility: - Applicants must be UK/EU citizens. - Applicants must reside in the Convergence Area of Wales at the time of enrolment, and must also be able to take paid employment in the Convergence Area on completion of the scholarship. The Convergence Area means the following counties of Wales: Blaenau Gwent, Bridgend, Caerphilly, Carmarthenshire, Ceredigion, Conwy, Denbighshire, Gwynedd, Isle of Anglesey, Merthyr Tydfil, Neath Port Talbot, Pembrokeshire, Rhondda Cynon Taff, Swansea and Torfaen.

How to apply: To apply, please send the following to Dr. Carlos Garcia de Leaniz (address below) by 23 July 2010: - A completed KESS application form - The names of two personal referees - An up to date CV - A covering letter, in which you expand on the relevant contents in your CV and wider experience, and why you consider yourself a good candidate. - KESS applications forms can be obtained from Mrs Sandra Kramcha (s.kramcha@swansea.ac.uk) or from Carlos Garcia de Leaniz (c.garciadeleaniz@swansea.ac.uk)

Contact details: Dr Carlos Garcia de Leaniz School of the Environment & Society Pure & Applied Ecology Wallace Building Swansea University Swansea SA2 8PP c.garciadeleaniz@swansea.ac.uk

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

TexasTechU PlantEvolution

I am soliciting an outstanding Ph.D. Graduate Research Assistant for Fall 2010 (or Spring 2011) to investigate plant evolutionary ecology, field ecology, and/or mycorrhizal evolutionary ecology. The research program focuses on molecular and field ecology of natural populations of orchids and their fungal associates.

REQUIREMENTS

1. An M.S. degree (or equivalent) in an ecology-based discipline in Plant or Biological Sciences, or a closely related field.

2. Background or strong interest in techniques and data analysis methods in molecular biology, i.e., DNA extraction, selecting suitable markers, PCR, molecular data analyses, sequencing, constructing and interpreting phylogenies, etc., for application toward plant population genetics and mycorrhizal diversity studies.

3. Keen attention to detail, organizational and coordination skills, and ability to communicate effectively.

4. Ability to complete all admission requirements for beginning the program for the intended term. International students, too, can apply if all required documents are available.

SALARY and BENEFITS

Competitive salary. Varies with status (i.e., assistantship vs. fellowship).

APPLICATION

Please submit:

1. A one-page letter of application describing interests and qualifications. The applicant should specifically address how their skills match the position description and requirements;

1. Curriculum Vitae, including names, complete address, phone, and e- mail for three references;

1. GRE scores; and

1. TOEFL scores (if applicable) to:

jyotsna.sharma@ttu.edu

Please also see: http://www.depts.ttu.edu/gradschool/admissions/how.php Dr. Jyotsna Sharma Department of Plant and Soil Science MS 42122, Texas Tech University Lubbock, Texas 79409; USA

jyotsna.sharma@ttu.edu 806.742.2637 (office); 806.742.1697 (labs)

jyotsna.sharma@ttu.edu

“Sharma, Jyotsna” <jyotsna.sharma@ttu.edu>

Tours France VirusEvolution

PhD Studentship

Adaptation and Genomics of Viral Populations In response to Ecological Changes

Funding : European Research Council ERC-Starting Grant GENOVIR : Adaptation of Viral Genomes to insect Immunity

Supervisor : Dr Elisabeth HERNIOU UMR 6035 - Institut de Recherche sur la Biologie de l^{1}Insecte (IRBI) Université François Rabelais, Parc Grandmont, 37200 Tours, France

How organisms adapt to environmental changes? Genomics has revealed the complexity of gene networks underpinning cellular processes. So far we know little on how ecological adaptation affects genomes, because of the difficulty of simultaneously studying evolution at both ecological and whole genome levels. If natural selection is indeed a key mechanism at the interplay between genes and environment, the targeted genetic factors remain to be uncovered. Baculoviruses open a new perspective to understand at the genomic level how organisms adapt to their environment. Viruses have to evolve in well-defined and constrained niches: the hosts they infect. Moreover, their 150kb genomes are readily accessible by high throughput sequencing technology. The transmission of baculoviruses as groups of genomes sets them further apart for studying the effect of niches on populations. Their molecular biology is also well understood, a key to investigating the genetic and functional details of adaptation. They are ideal for linking genome changes to ecological changes.

At the frontier of ecology and genomics the project takes on the challenge of studying ecological adaptation at the level of whole genomes. Combining experimental evolution with comparative genomics, the specific goal is to characterise the phenotypic and genotypic adaptation of a baculovirus population to diverse host species.

We seek a candidate with strong interests in evolutionary biology, experimental evolution and bioinformatics. Please contact Dr Elisabeth Herniou (elisabeth.herniou@univ-tours.fr) for more information. Application consisting of cover letter, curriculum vitae and the name and contact details of three referees should be sent by e-mail to elisabeth.herniou@univ-tours.fr . Closing date 20 June 2010. Interviews to be held between the 28/06/10 and 02/07/10.

elisabeth.herniou@univ-tours.fr

UBritishColumbia EvolGenomics

A Graduate Assistantship (Ph.D. preferred, but M.Sc. possible too) is available in the lab of Dr. Keith Adams at the University of British Columbia in genome evolution and the evolution of gene expression starting in January 2011. My lab's research combines evolutionary biology with molecular genetics and genomics to study how gene expression, regulation, structures, and sequences evolve. We use lab experiments and computational analyses of gene sequence and expression data, including ultra-high throughput data (Illumina, 454), to test hypotheses and answer questions. See my web page at http://www.botany.ubc.ca/people/-kadams.html for a description of current research. I am looking for a highly motivated graduate student to help develop and work on a project about the evolution of duplicate gene expression, alternative splicing, and/ or function in plants. Candidates should have a strong undergraduate background in biology, with course work in molecular genetics and evolutionary biology. Prior molecular or computational research experience with any organism is required. For more information and inquiries about the research area please contact Keith Adams at keitha@interchange.ubc.ca

Keith Adams Botany Department and Centre for Plant Research University of British Columbia Vancouver, Canada

keitha@interchange.ubc.ca

UKiel NematodeMicrobialDiversity

PhD position in Kiel: Microbial Diversity associated with Nematodes

The PhD project aims at a characterization of the microbes associated with the nematode Caenorhabditis elegans and related species across different locations in Germany. This nematode is one of the best studied organisms under laboratory conditions; yet we still lack understanding of the conditions under which it lives in nature, including its microbial associates. Such information is essential for full understanding of the biology of this organism, including the exact function of its generally well characterized genes. The project is part of the European ESF Eurocores initiative on Ecological and Evolutionary Functional Genomics and it involves direct collaboration with research groups in The Netherlands, Belgium, and France. This specific PhD position (payment through the DFG according to 13 TV-L/2) will be based in the recently founded Department of Evolutionary Ecology and Genetics at the University of Kiel (Northern Germany), headed by Prof. Dr. Hinrich Schulenburg. The department itself provides an international and interactive atmosphere, while Kiel University and connected institutes (e.g., Max Planck Institute in Ploen) offer a stimulating research environment with a particular focus on evolutionary biology and also C. elegans genetics. The city of Kiel is a medium-sized pleasant town located at the coast of the Baltic Sea. It is the capital of the most Northern state of Germany, Schleswig-Holstein. It offers many opportunities for leisure activities, including theatres, an opera, the Schleswig-Holstein classical music festival, the heavy metal festival in Wacken, sailing, surfing, cycling, and the famous festivities of the "Kieler Woche" - one of the largest sailing events in Europe.

Requirements for the position: Master or Diploma in Biology, high motivation, excellent background in microbiology and/or ecology and/or evolutionary biology, good knowledge of statistics, handling of complex experimental set-up, teamwork, fluency in English.

Please send applications with CV, one-page statement of research interests, and the names and addresses of two referees as a single pdf-file by email to hschulenburg<at>zoologie.uni-kiel.de. Deadline for applications: 1st July 2010. Start of position: September 2010 or soon afterwards. Women are especially encouraged to apply. Severely handicapped people will be preferentially considered in case of equivalent qualifications. For further details + questions, send an email to hschulenburg<at>zoologie.uni-kiel.de. Otherwise see: http://www.uni-kiel.de/zoologie/evoecogen/ – Hinrich Schulenburg

Department of Evolutionary Ecology and Genetics Zoological Institute Christian-Albrechts-Universitaet zu Kiel Am Botanischen Garten 1-9 24118 Kiel Germany Tel: +49-431-880-4143 Fax: +49-431-880-2403 Email: hschulenburg@zoologie.uni-kiel.de Web: www.uni-kiel.de/zoologie/evoecogen/ Hinrich Schulenburg <hschulenburg@zoologie.uni-kiel.de>

ULaval Molecular basis of behaviour variation

Our laboratory is eager to receive application from highly motivated scientists with an excellent record to apply to a Quebec government fellowship available for non-Canadian candidates to study in a Quebec- based laboratory. Doctoral fellowships are available. Furthermore, internships are available for a visit to our laboratory (3000$can/ month, up to 4 months) during graduate studies in another laboratory. Pre-selection by the host university and our laboratory is mandatory.

Candidates from all over the world are invited to apply. Additionally, specific fellowships are available for candidates from Mexico, Brazil, China and Wallonie.

We are in the Department of Biology at Laval University, located in Quebec City, Quebec, Canada. Our laboratory is part of the Institute of Integrative and Systems Biology (IBIS). We study the underlying molecular and hormonal causes of variation in behaviour in vertebrates. We are interested in personality with an emphasis on the stress response and correlation among behaviours, as well as in reproductive tactics. We are also interested by the effects of the environment on development of behaviour, such as environmental enrichment in captive animals, maternal/paternal and social group effects, and endocrine disrupters. We therefore have a strong interest for phenotypic plasticity, along with the effects of genetic variation. We favour an integrative approach by linking data from the same individual: neuropeptides, neurotransmitters and their receptors (quantitative Real-Time PCR, microarrays, in situ hybridization, HPLC), hormones (EIA, HPLC), physiology and behaviour. Our model system is the threespine stickleback Gasterosteus aculeatus, a small fish studied in behavioural biology, which can be kept easily in the lab and whose genome is sequenced.

Laval University is one of the ten main Canadian universities. Quebec City is dynamic with all the advantages of a large city while still allowing for very easy access to wilderness and very reasonable cost of living. The chosen candidates that are successful at obtaining a fellowship will be part of the Institute of Integrative and Systems Biology. They will have access to core genomics and molecular biology facilities, lab meetings and Institute-wide group meetings, journal clubs and weekly seminars at the Institute and in the Biology Department. Several ecological genomics laboratories are part of the Institute and the Biology department, allowing for enriched interactions with members of the other laboratories working in this field. DEADLINES: Our laboratory must receive applications before July 23, 2010. We will then proceed to select candidates that will be able to apply to the University pre-selection committee with a deadline of August 9th 2010. Candidates selected by the university will then be allowed to apply to the general competition in Fall 2010, with results given in April 2011. Start date can be between May and December 2011.

Contact me directly by email for more information about the program and opportunities in our laboratory.

Nadia.Aubin-Horth@bio.ulaval.ca

Nadia Aubin-Horth

Assistant professor

Department of Biology

Institute of Integrative and Systems Biology

Pavillon Charles-Eugene-Marchand

1030, Avenue de la Medecine

Laval University

Quebec city (Quebec) G1V 0A6

Canada

Nadia.Aubin-Horth@bio.ulaval.ca

ULethbridge EvolDynamics

Graduate position in Evolutionary Dynamics, Department of Biological Sciences, University of Lethbridge

An NSERC-funded graduate student position (MSc or PhD) is available in the Department of Biological Sciences at the University of Lethbridge (Alberta, Canada). The focus of this position is evolutionary dynamics. Potential project topics include, but are not limited to, (1) evolution of senescence, (2) evolution of cooperation, and (3) non-transitive competition. Interested candidates should visit http://people.uleth.ca/~robert.laird/ for lab details, and then email me (Dr. Rob Laird: robert.laird@uleth.ca). In your email, please include your CV and a brief statement of your research interests.

laird.robert@gmail.com

UStirling SaltmarshGeneticBiodiversity

Does the recovery of genetic diversity within species parallel the recovery of species diversity in restored saltmarsh systems?

Saltmarshes are highly important for biodiversity, supporting a high density of invertebrates, and large numbers of wading birds and wildfowl. In addition to their biodiversity value, saltmarshes provide essential ecosystem services to human communities, such as flood defence and control of estuarine nutrient pollution. However, a combination of anthropogenic pressures has resulted in ongoing loss and degradation of saltmarsh in the UK. Saltmarshes are now a priority habitat under the UK Biodiversity Action Plan, under which restoration and creation of new saltmarsh is a key objective.

Saltmarsh plant biodiversity is key to ecosystem function. In these low plant diversity communities, diversity within species (genetic diversity) may compensate for low species diversity, resisting disturbance and invasion and maintaining high diversity of the saltmarsh fauna. This project will assess the temporal development of biodiversity in restored saltmarsh, focussing on the recovery of genetic diversity in key plant species and invertebrate and bird species recovery. The work will include a theoretical focus on community development as well as having application to saltmarsh restoration practice. The project will include a substantial component of population genetic analysis of samples to be collected during fieldwork throughout the UK, together with additional analyses of existing biodiversity data.

The successful candidate will work with Alistair Jump at the University of Stirling in association with Toby Wilson of RSPB Scotland. The ideal candidate will have a strong interest in restoration ecology. He or she should have broad ecological knowledge and be independent and highly self-motivated. Experience of conducting ecological sampling and survey work is essential and a high degree of competence in laboratory-based (particularly population genetic) analyses will be an advantage. The successful applicant will be required to liaise with reserve managers and relevant NGO staff and to work with minimum supervision whilst undertaking fieldwork.

Informal enquiries are encouraged. Applicants should submit a CV, covering letter and two letters of recommendation from academic referees. Your covering letter should clearly set out why you are suited to this project, with reference to your relevant experience, and your motivation for undertaking research leading to a PhD.

Applications should be sent by mail to Dr Alistair Jump, SBES, University of Stirling, Stirling, FK9 4LA or emailed to a.s.jump@stir.ac.uk.

Applications must be received by June 24thth 2010 for an expected start date of October 1st 2010. Shortlisted candidates will be interviewed during the week beginning July 5th. Due to funding restrictions, applicants must be a national of a country within the European Union.

Dr Alistair Jump

Lecturer in Plant Ecology School of Biological and Environmental Sciences University of Stirling Stirling FK9 4LA UK

Tel: +44 1786 467848 Fax: +44 1786 467843 www.biogeo.org www.sbes.stir.ac.uk Alistair Jump <a.s.jump@stir.ac.uk>

UTurku TropicalBiodiversity

UNIVERSITY OF TURKU, FINLAND

PHD STUDENT POSITION - TROPICAL BIODIVERSITY

One three-year PhD student position (2011-13) is available in the newly funded project “Biodiversity and multiple trophic interactions” lead by PhD Ilari E. Sääksjärvi (Zoological Museum, Department of Biology, University of Turku) and PhD Juha-Pekka Salminen (Department of Chemistry, University of Turku). The project is funded by the Kone Foundation, Finland.

The project aims to study biodiversity of selected key faunal elements and trophic interactions in Peruvian Amazonia (The National Reserve of Allpahuayo-Mishana). The team has studied the parasitoid insect diversity (taxonomy, systematics and ecology) of Allpahuayo-Mishana since 1998. The new project will assess biodiversity patterns of Amazonian insects using a novel combination of study methodologies (including biodiversity research; natural compound chemistry; DNA barcoding, rearing lepidopteran larvae and insect parasitoids). In summary, we aim to link tropical biodiversity to tritrophic tropical plant-herbivore-parasitoid interactions in an environment whose present-day environmental conditions are governed by the Andean-Amazonian landscape history.

The work description involves both extensive fieldwork in Peruvian Amazonia and laboratory works taking place at the University of Turku. Salary euro 1,900 per month (non-negotiable) will be paid as a tax free stipend up to euro 18,300 per year, with euro 4,500 per year subject to taxes. Successful applicants should have a M.Sc. in biological sciences with expertise in biodiversity research, tropical biology and/or entomology. Experience of tropical fieldwork and sampling of natural insect populations is essential. Besides of English, a successful applicant should also speak Spanish. The graduate student will coordinate part of the field work alone with local field assistants who do not speak English.

The applications should be sent to Ilari E. Sääksjärvi (ilari.saaksjarvi@utu.fi or by mail to the address below). We kindly ask you to attach a Curriculum vitae to your application (with possible publication list included), contact information of two references and a max. one-paged letter of motivation. In the motivation letter you should provide a description of your research interests, language skills and state why you would be a suitable candidate for the present project.

The work is scheduled to start in Turku, Finland, in January, 2011. The field work in Peru will be initiated in April, 2011. The new PhD student will be positioned to work in the Zoological Museum, Section of Biodiversity and Environmental Research, Department of Biology, University of Turku.

Closing date for applications is 30th July, 2010. We look forward to welcoming a new enthusiastic student to our young and positive minded research team!

Relevant references e.g.:

Sääksjärvi, I.E., Haataja, S., Neuvonen, S., Gauld, I.D., Jussila, R., Salo, J. & Marmol Burgos, A. (2004) High local species richness of parasitic wasps (Hymenoptera: Ichneumonidae; Pimplinae and Rhyssinae) from the lowland rain forests of Peruvian Amazonia. Ecological Entomology 29: 735-743.

Sääksjärvi, I.E., Ruokolainen, K., Tuomisto, H., Haataja, S., Fine, P., Cárdenas, G., Mesones, I. & Vargas, V. (2006) Comparing composition and diversity of parasitoid wasps and plants in an Amazonian rain forest mosaic. Journal of Tropical Ecology 22: 167-176.

Dr. Ilari E. Sääksjärvi

Zoological Museum Section of Biodiversity and Environmental Science Department of Biology FIN-20014 University of Turku, Finland E-mail. ilari.saaksjarvi@utu.fi University of Turku Amazon Research Team (UTU-ART): http://www.sci.utu.fi/projects/amazon/ ileesa@utu.fi

---

UZurich PlantEvolution

Ph.D or post-doc assistantship in plant evolution/biogeography at the University of Zurich

Position description: Applications are open for one 3-yr Ph.D. assistantship (or a part-time post-doctoral assistantship) to study the origin and evolution of island endemics in the Mediterranean Region. Our first studies on Rutaceae, Araceae and Boraginaceae used chloroplast DNA sequences and geological data to reconstruct the temporal and spatial frameworks for the origin of plants endemic to the continental fragment islands of Corsica and Sardinia and the oceanic islands of the Canarian archipelago (Salvo, G., S. Ho, G. Rosenbaum, R. Ree, E. Conti. 2010. Tracing the temporal and spatial origins of island endemics in the Mediterranean region: A case study from the citrus family (Ruta L., Rutaceae). In Press Systematic Biology; Mansion, G., F. Selvi, E. Conti. 2009. Origin of Mediterranean insular endemics in the Boraginaceae: Integrative evidence from molecular dating and ancestral area reconstruction. Journal of Biogeography 36:1282-1296; Mansion G., G. Rosenbaum, G. Bacchetta, J Rossello, E. Conti. 2008. Phylogenetic analysis informed by geological history supports multiple, sequential invasions of the Mediterranean basin by the angiosperm family Araceae. Systematic Biology 57:269-285). Some of the open questions include the following: i) Are species in the selected Mediterranean groups monophyletic? ii) What are the origins of the polyploid species? iii) Is there variation of ploidy level within species? iv) Was island colonization associated with a shift of the ecological niche? The successful applicant will choose one or more of these plant families to: generate flow cytometry data aimed at determining ploidy levels; generate nuclear DNA sequences and infer species trees; incorporate ecological data to investigate issues of niche conservatism vs. niche evolution in the selected groups.

Requirements: Demonstrated experience in molecular, phylogenetic and flow-cytometry methods and/or ecological niche modeling will be highly valued in the selection process. Excellent knowledge of the English language, written and oral, required. Familiarity with additional European languages would be useful for fieldwork in the Mediterranean Region and living in Switzerland.

Facilities: Our research group offers a very supportive working atmosphere and excellent research facilities in a highly international scientific environment. Several opportunities for collaborations and participation at international meetings are available.

How to apply: Send the following documents by email AS A SINGLE PDF FILE to Prof. Elena Conti, ContiElena@access.uzh.ch: I) a one- to two- page application letter clearly addressing the following questions: a) Why are you interested in a Ph.D. or post-doc position in this research topic? b) What are your career goals?; II) your detailed curriculum vitae, including a list of field collecting, molecular, analytical, and linguistic skills, presentations at scientific meetings, and publications (if applicable); III) a copy of your undergraduate and graduate academic record; IV) names and full addresses of two or three referees selected from your academic advisors.

Finally, ask your referees to send reference letters directly to Prof. Conti by email addressing: i) your intellectual and academic skills, ii) your dedication to science, and iii) your ability to work cooperatively in a team.

Deadline for application: June 30, 2010. Positions will remain open until a suitable candidate is found.

Starting date: As soon as a suitable candidate is selected.

Prof. Elena Conti, Ph.D. University of Zurich, Institute for Systematic Botany Zollikerstrasse 107, 8008 Zuerich, SWITZERLAND Ph: 0041 44 634 8424 Fax: 0041 44 634 84 03 email: ContiElena@access.unizh.ch http://www.systbot.uzh.ch/Personen/ProfessorenundDozenten/ElenaConti.html

Special issue on Mediterranean Biogeography, Journal of Biogeography 2009: http://www3.interscience.wiley.com/journal/122463450/issue?CRETRY=1&SRETRY=0 .

DIVERSITAS-BioGENESIS program: http://www.diversitas-international.org/?page=core_biogen
Elena Conti <ContiElena@access.uzh.ch>

Jobs

AlbertEinstein SystemsBiology

Multiple Tenure Track Faculty Positions

Albert Einstein College of Medicine of Yeshiva University

Bronx, NY 10451

The Albert Einstein College of Medicine, one of the leading medical schools in New York City, is seeking to fill multiple tenure track faculty positions in the newly formed Department of Systems and Computational Biology. Established in April 2008, the main goal of the new department is to advance our understanding of living systems by developing theoretical, computational and experimental approaches to study complex biological systems.

The College has 750 medical students, 325 graduate students and 360 post-doctoral fellows in training and boasts a strong research faculty covering broad areas of experimental biology, offering outstanding opportunities for collaborative interactions. The 200,000 square foot Center for Genetic and Translational Medicine at Einstein, which opened in late 2007, locates computational, systems and experimental scientists in physical proximity to foster interdisciplinary communication and collaboration. Highly competitive start-up packages are available.

We seek outstanding scientists with broad experience and demonstrated collaborative interactions with experimental or clinical investigators. Candidates should have strength in a physical, mathematical or computational field at the Ph.D. or equivalent level. Experience applying these skills to a biological or biomedical area (demonstrated through publications or support) is also required. Areas of interest include, but are not limited to: Modeling cellular processes, such as signaling, transcriptional regulation and immune response; Pathway analysis; Genetic networks; Functional proteomics and genomics; Evolution of structure and function; Computational neuroscience; Mathematical and computational modeling of complex traits and diseases.

Applicants should send a letter of interest, C.V., statement of research and teaching interests, and names of three referees, in electronic format to:

Systems and Computational Biology Search Committee

Albert Einstein College of Medicine

Jack and Pearl Resnick Campus

1300 Morris Park Ave. Price Center, Rm. 153

Bronx, New York 10461

E-mail Address: sysbio@einstein.yu.edu

Subject line should be: SCB Faculty Search

Yeshiva University is an equal opportunity employer committed to workforce diversity

d.russell@jobtarget.com

IGFL Lyon JuniorSeniorGroupLeaders

JUNIOR/SENIOR GROUP LEADER POSITIONS

LYON, FRANCE

The Institut de Génomique Fonctionnelle de Lyon (IGFL) is a research institute run by the French Centre National de la Recherche Scientifique (CNRS), the Ecole Normale Supérieure de Lyon (ENS Lyon), the Institut National de la Recherche Agronomique (INRA) and the Université Claude Bernard Lyon 1 (UCBL). The IGFL will be moving during autumn 2011 to a new 3200 m2 building located next to the ENS Lyon, within a multidisciplinary campus which includes more than 1000 scientists, carrying out research in all areas of biology.

The IGFL currently consists of 10 research groups and will eventually bring together 18 research groups, representing a total of approx. 200 persons who will conduct fundamental (basic) research in integrative biology, developmental biology, evolutionary sciences and bioinformatics/modelling at the genomic scale. The research groups strongly interact with medical and agronomical research via regional, national and international networks (see http://igfl.ens-lyon.fr/).

The IGFL, in view of its new facilities, is recruiting outstanding scientists for junior/senior group leader positions. The IGFL welcomes projects addressing whole-organism level research, with a special focus on animal-based research.

Groups will benefit from easy access to state-of-the-art core services, including cell and small animal imaging, transgenic animal facilities (mouse, fish, drosophila), paleogenomics, bioinformatics, mass spectrometry, proteomics, transcriptomics, FACS sorting, histology and electron microscopy.

Applications (in English) should include curriculum vitae, a short description of achievements and records of self-financing, a proposed research program of approx. 10 pages and contact details of 3 professional references. The deadline for applications is July 10th 2010. Please send as a single PDF named LASTNAME_IGFL_2010.pdf to direction.igfl@ens-lyon.fr . Enquiries should also be directed to this address.

Frederic Brunet <Frederic.Brunet@ens-lyon.fr>

MuseumVictoria SeniorCuratorBirds Mammals

Dear all,

We are seeking a new Senior Curator of Birds and/or Mammals at Museum Victoria in Melbourne, Australia.

We are seeking an enthusiastic and skilled researcher in the fields of ornithology and/or mammalogy to join our active science department of 40 research staff and 27 postgraduate students. Museum Victoria is home to a natural sciences collection of more than 16 million lots dating back to 1854. It is also a modern research institution with excellent laboratory and field research capabilities including molecular and ancient DNA laboratories.

The position is full time and ongoing.

JOB DETAILS:

MV/0025 - Senior Curator Terrestrial Vertebrates (Birds/Mammals) Grade 5, Value Range 1

Applications close: Wednesday 30 June 2010 COB

Applicants are advised to refer to the Museum Victoria website link:

http://www.museumvictoria.com.au/About/Work-Opportunities/Employment/ If you need any more information regarding the post, feel free to contact me,

Jane Melville

Senior Curator, Terrestrial Vertebrates Museum Victoria Department of Sciences GPO Box 666 Melbourne, VIC 3001 Australia

Email: jmelv@museum.vic.gov.au PH: INT + 61 3 8341 7444 FAX: INT + 61 3 8341 7442

jmelv@museum.vic.gov.au

Netherlands GenomicSelection

Breeder for genomic selection

For our glasshouse vegetable crops in De Lier (NL) Rijk Zwaan is looking for a Breeder for genomic selection.The field of breeding has changed rapidly with the coming of new marker and sequencing technologies. The implementation of these technologies and use of genotypic information requires new specialisations. For this reason we open this new position.

As a Breeder for genomic selection you will support breeders and prebreeders of our fruit crops (tomato, pepper, cucumber, melon and* *eggplant) and lead them in the process of optimal application of genomics information and large scale marker usage. You will be responsible for developing protocols and methodologies for integrating genotypic data in breeding as well as the development of decision-support tools for breeders to link and* *interpret genotypic and phenotypic information.

You will work with teams of highly motivated breeders. Also you will co-operate with other research teams, e.g. in the field of bio-informatics, quantitative genetics*, *molecular genetics and with our high throughput* *genotyping laboratory.

Your education at university level is followed by a PhD in the field of bio-informatics and/or quantitative genetics or relevant work experience in this field. You have experience in the design and use of genetic studies, knowledge of statistical software, bio-informatics, MAS, advanced QTL mapping, genome wide selection and association mapping. You are a creative and practical personality, who is able to identify and iniate new projects and lead them to readily-usable tools or information. Your good communication skills are required to integrate cross-functional projects and to bring state-of-the-art research to practical breeding. Besides being fluent in English, also being able to communicate in Dutch would be beneficial.

For more information about this vacancy and our company please contact Jair Haanstra, telephone number: +31 174 532300. You may send your CV and covering letter to Rijk Zwaan, f.a.o. Emilie ten Bokkel Huinink to: work@rijkzwaan.nl.

We prefer an e-mail, but you can also send your letter and CV by mail:

Rijk Zwaan f.a.o. Emilie ten Bokkel Huinink

P.O. Box 40 2678 ZG De Lier The Netherlands

Evert Gutteling <eurogene_inc@hotmail.com>

OkinawaInstSciTech EvolutionaryBiol

The Okinawa Institute of Science and Technology (OIST http://www.oist.jp) invites applications for new faculty positions as it enters a period of growth in preparation for transition to an international graduate university in 2012. Approximately 15 faculty positions will be filled during this search. OIST provides a world-class research environment in newly completed facilities in an area of distinctive culture, unique ecology, and outstanding natural beauty.

Successful candidates will be given the opportunity to excel in their chosen area of research, and will be expected to contribute to graduate teaching, research supervision and other academic activities. Applicants should have a PhD or equivalent degree, and demonstrate excellence in research.

The initial appointment will be as Principal Investigator (PI) or Independent New Investigator (INI) for a term of five years. When the transition to a graduate university is completed in 2012, it is planned that PI and INI positions will change to a tenure track system with Assistant Professors, Associate Professors, and Professors. Some appointments will be made on a joint or part-time basis. Substantial internal funding will be provided to support the faculty member's research, based on a 5-year research plan, which is renewable after scientific review.

This search is targeted broadly. The non-departmental structure of OIST and orientation toward interdisciplinary research permits flexibility in appointing applicants who are able to introduce new research areas or enhance existing areas. Established research areas include genomics, developmental biology, mathematical and computational biology, molecular and cell sciences and neuroscience. New research areas include structural biology, biological physics, biological chemistry, marine sciences, ecology and evolutionary biology, and microbial and plant genetics.

At a time when worldwide support for research is increasingly risk-averse, and grant funding places an ever-growing burden on faculty, OIST promotes innovative research in a highly facilitating and supportive environment. This is achievable because OIST has internal research funding, offers outstanding central research facilities, and consults faculty on the design of new laboratory space. Central research facilities at OIST include core facilities for genomics, rodent vivarium, radioisotope use, electron microscopy, and supercomputing facilities.

OIST is committed to being international with more than 50% of faculty and researchers from outside Japan. The official language of OIST is English. OIST is an equal opportunity, affirmative action employer and encourages applications from women. More details regarding the aims of the search and advantages of working at OIST are available in the Information for Applicants in the application package that is downloadable from the website (http://www.oist.jp/en/newsevent/careers/542-faculty-positions.html). Applications should be submitted in accordance with the instructions in the application package. Applications for the current search close 31, July 2010. Interviews will take place in late August/September, with a view to making appointments early in 2011.

Please don't hesitate to contact me with any questions. Alexander Mikheyev Principal Investigator Okinawa Institute of Science and Technology < http://www.oist.jp/ > Research Lab 1, Level D 1919-1 Tancha, Onna-son, Kunigami Okinawa 904-2234 Japan

mikheyev@gmail.com

OxfordBrookesU EvolutionLecturer

Dear everybody,

We are looking for a senior lecturer in biology, to strengthen our evolutionary ecology department here at Oxford Brookes University. The full details of the job can be found here: https://edm.brookes.ac.uk/hr/hr/vacancies.do;jsessionid=d3289131a45a949f530f07cf59b2e7cc6da1c723bc30ab34894f49e81193b5f
7522048 In summary,

Salary scale: Â£36,716, rising annually to Â£45,156

Qualifications required for post: A higher degree (PhD) in a relevant biological or related subject.

Experience required for post: at least 3 years relevant postdoctoral research experience.

Overall purpose of post: To undertake academic and academic related responsibilities in the area of evolutionary ecology or conservation biology that complements existing research in the School. To undertake and support interdisciplinary research across the research groupings of the School. To contribute to teaching quantitative skills across the UG and PG curriculum, and in particular to take the lead in developing MSc provision with a focus on ecological and evolutionary informatics.

Main duties:

1. To teach UG and PGT students using appropriate instruction methods such as lectures, tutorials, lab-

oratory practical classes, seminars and other formal pedagogic work, particularly in the fields of ecological informatics (candidates with expertise that extends from traditional (molecular) bioinformatics to the level of biogeographic analysis and evolutionary ecological models would be particularly welcome). 2. To supervise UG and PGT student projects and dissertations. 3. To supervise students engaged on higher degree work by research. 4. To mark and assess studentsâ work and to invigilate. 5. To establish a research group that complements existing areas of expertise in the School or to contribute to an existing research group; to attract external funding and publish work of a quality suitable for return in the REF. 6. To undertake and support interdisciplinary infomatics across the research groupings in the School. 7. To undertake other forms of scholarly activity and to take part in School Academic Development activities related to enhancing the standard of teaching and student experience. 8. To undertake curriculum development work including identification of consumer requirements, planning, development and evaluation of courses and course materials and supervise course provision. In particular the appointee will be expected to contribute to the development of an MSc course that builds on existing MSc courses in Conservation Biology. 9. To manage and administer education processes including the administration and management of education and training programmes, and publicity and public relations work. 10. To participate in the administrative processes of the institution including committee membership, quality assurance procedures, recruitment and admission of students. 11. To represent the institution on or to appropriate external bodies. 12. To participate in staff development and appraisal processes and in service training. 13. To undertake such other duties as may reasonably be required by the University having regard to the general principles used in the above descriptions.

The closing date is fairly soon, 22nd of June 2010.

If you need any more information regarding the post, feel free to contact me (Casper J. Breuker - cbreuker@brookes.ac.uk) or Dr Tim Shreeve (tgshreeve@brookes.ac.uk).

Casper J. Breuker

Dr Casper J. Breuker Senior Lecturer in Biology Evolutionary Developmental Biology Research Group, Sinclair Building, School of Life Sciences, Oxford Brookes University, Gipsy Lane, Headington, Oxford, OX3 0BP, UK

Office: GIP-S1.08 tel: +44(0)1865483244 fax: +44(0)1865483242

e-mail: cbreuker@brookes.ac.uk

SouthernCrossU PlantConservationGenetics

Seeking outstanding Plant Geneticist

Southern Cross University, located on the picturesque east coast of Australia, is seeking a visionary Scientific Director for its Centre for Plant Conservation Genetics. The Centre delivers internationally significant, innovative solutions in research, education and commercialisation of Plant Molecular Genetics.

Full details of the position can be found at www.scu.edu.au/jobs . For further information contact Emeritus Professor Peter e-mail peter.baverstock@scu.edu.au or phone +61(0)421491353

Emma Evans <emma.evans@scu.edu.au>

TUMunchen PopulationGenetics

Technische Universität München

The Faculty Center of Life and Food Sciences Weihenstephan at the Technische Universität München invites applications for the position of

Full Professor of Population Genetics (W3)

to be filled by the winter semester 2010.

Applications are invited from candidates with an excellent international academic record in population genetics. The successful candidate is expected to bridge theoretical and experimental population genetics and genomics by implementing novel molecular methods such as next-generation sequencing, statistical and stochastic methods and to interface effectively with the existing strengths of the faculty. The tenure track position will be established within the TUM research cluster âSynbreedâ (www.synbreed.tum.de) dedicated to genome based research on crop and livestock breeding. Active involvement in the interdisciplinary research consortium âMunich Centre of Advanced Computingâ (www.mac.tum.de) is expected.

The position requires a firm commitment to teaching at undergraduate and graduate levels in the bioscience curricula, such as agricultural sciences, biology and molecular biotechnology.

Preconditions for employment are a degree from a university or an accredited college of applied science, pedagogical aptitude, Ph.D./doctorate and a postdoctoral lecturing qualification or certification of an equivalent academic achievement, which may have been obtained as a junior professor or outside a university environment. At the time of appointment applicants should not be older than 52 years. Under certain circumstances the age limit may be lifted.

As part of the excellence initiative of the German federal and state governments, the Technische Universität München pursues the strategic goal of substantially increasing the proportion of women in research and education and thus expressly invites qualified female scientists to apply for this position.

The Technische Universität München provides support for Dual Career Couples and their families via the TUM Munich Dual Career Office.

In cases of substantially equal eligibility, preferential consideration will be given to disabled candidates.

Applications with the usual supporting information (CV, certificates, credentials, etc., list of publications including reprints of the most important papers) should be submitted by 15.08.2010 to:

Dekan der Fakultät Wissenschaftszentrum Weihenstephan für Ernährung, Landnutzung und Umwelt der TU München, Alte Akademie 8, D-85354 Freising-Weihenstephan, e-mail: dekanat@wzw.tum.de. For more detailed information please contact Prof. Dr. Chris-Carolin Schoen, e-mail: chris.schoen@wzw.tum.de.

Natalie Ohl <natalie.ohl@wzw.tum.de>

UArizona PlantTree of life analyst

iPlant Tree of Life Engagement Team Analyst

The iPlant Tree of Life (iPToL) project (http://-iptol.iplantcollaborative.org) is seeking an engagement team analyst (ETA) to work at the BIO5 Institute at the University of Arizona in Tucson. The ETA serves as a liaison between scientific working groups the iPlant software development team. This involves active discussion with the scientists, research into appropriate supporting technologies, and the judicious application of technical judgment to convert working group conversation into practical design requirements.

The primary responsibilities of the iPToL Engagement Team Analyst include:

- Tool research and evaluation, prototype software development - Translation of working group discussions into formal software requirements - Attending working group meetings and leading technical discussions - Working with scientific collaborators to develop workflows and narratives - Performing related duties as assigned by the iPToL Scientific Lead and Project Manager

REQUIRED QUALIFICATIONS - Advanced degree (MS or Ph.D) in a life science discipline (biology, genetics, biochemistry, etc.). Candidates with a degree in another natural science, computer science, information technology or a related discipline will also be considered with a demonstrated track record of research experience in the life sciences; - 2-3 years work experience conducting computational biology research and/or collaborative scientific software development (academic, government, or industry); - interest in science and technology and ability to rapidly adapt to new technologies; - excellent oral presentation and communications skills; - advanced ability to work independently under established deadlines and as part of a team; - ability to travel as required to partner/collaborator institutions, relevant conferences, etc.

PREFERRED QUALIFICATIONS - A research background in evolutionary biology or phylogenetics - experience in projects involving advanced computing and information technologies used in life science research in academia, government laboratories, and/or industry; - strong programming skills - proven ability to promote and support the use of high-performance computing, visualization, networking, and massive data storage systems to scientists to expand their research impact.

To apply for this position please visit http://www.uacareertrack.com/applicants/-Central?quickFind=3D197806 Sheldon McKay, PhD Scientific Lead, iPlant Collaborative BIO5 Institute, University of Arizona Email: mckays@email.arizona.edu Google Voice: (203) 701-9204

sheldon.mckay@gmail.com

UArizona PlantTree of life analyst correction

The iPlant Tree of Life (iPToL) project (http://iptol.iplantcollaborative.org) is seeking an engagement team analyst (ETA) to work at the BIO5 Institute at the University of Arizona in Tucson. ÂThe ETA serves as a liaison between scientific working groups the iPlant software development team. This involves active discussion with the scientists, research into appropriate supporting technologies, and the judicious application of technical judgment to convert working group conversation into practical design requirements.

The primary responsibilities of the iPToL Engagement Team Analyst include:

- Tool research and evaluation, prototype software development - Translation of working group discussions into formal software requirements - Attending working group meetings and leading technical discussions - Working with scientific collaborators to develop workflows and narratives - Performing related duties as assigned by the iPToL Scientific Lead and Project Manager

REQUIRED QUALIFICATIONS - Advanced degree (MS or Ph.D) in a life science discipline (biology, genetics, biochemistry, etc.). Candidates with a degree in another natural science, computer science, information technology or a related discipline will also be considered with a demonstrated track record of research experience in the life sciences; - 2-3 years work experience conducting computational biology research and/or collaborative scientific software development (academic, government, or industry); - interest in science and technology and ability to rapidly adapt to new technologies; â Â Âexcellent oral presentation and communications skills; â Â Âadvanced ability to work independently under established deadlines and as part of a team; â Â Âability to travel as required to partner/collaborator institutions, relevant conferences, etc.

PREFERRED QUALIFICATIONS - A research background in evolutionary biology or phylogenetics â experience in projects involving advanced computing and information technologies used in life science research in academia, government laboratories, and/or industry; - strong programming skills - proven ability to promote and support the use of high-performance computing, visualization, networking, and massive data storage systems to scientists to expand their research impact.

To apply for this position please visit https://www.uacareertrack.com/applicants/Central?quickFind=197806 or contact Sheldon Mckay (mckays@email.arizona.edu)

Sheldon McKay, PhD Scientific Lead, iPlant Collaborative BIO5 Institute, University of Arizona Email: mckays@email.arizona.edu Google Voice: (203) 701-9204

Sheldon McKay <sheldon.mckay@gmail.com>

UCapeTown AvianEvolution

Opportunity to join the University of Cape Town

Position: Senior Lecturer - Percy FitzPatrick Institute of African Ornithology, Department of Zoology (Ref. 2205).

We invite applications for the above permanent position in the Percy FitzPatrick Institute of African Ornithology, a world-renowned, national Centre of Excellence in ornithological research with a strong emphasis on postgraduate supervision.

The Institute is seeking a person with strengths in modern approaches to avian conservation or avian evolutionary/behavioural ecology and with competence in biostatistics. Applicants must have a PhD, with at least five years postdoctoral experience, a sound publication record in ornithology and experience in postgraduate supervision.

The successful candidate will be expected to work as part of a research team, but to pursue his/her own research, publish research findings in journals of high international standing, recruit and supervise postgraduate students, and attract research funding. The annual remuneration package, including benefits, is R433 117 (w.e.f. 1 July 2010: R446 898). Closing date: 30 June 2010

To view the full advertisements and application requirements, please visit www.uct.ac.za and click on Vacancies.

UCT is committed to the pursuit of excellence, diversity and redress. Our Employment Equity Policy is available at http://hr.uct.ac.za/policies/ee.php .

Jacqueline.Bishop@uct.ac.za

UCollegeDublin 1year VertebrateEvolution

Applications are invited for the post of Temporary Lecturer in Vertebrate Biology in the UCD School of Biology & Environmental Science. The person employed should have a particular interest in birds"and/or" reptiles. Their interests should lie in the area of evolution/evolutionary ecology and preferably have experience with vertebrate morphology and/or comparative physiology.

Candidates should have a PhD in an appropriate discipline and will be expected to provide teaching of vertebrate biology to undergraduates primarily in the Zoology programme, together with more advanced topics which would be available to students from other programmes. This is a temporary one year post.

Salary: 50,807 - 81,452 p.a. Appointment on scale will be made commensurate with qualification and experience.

To apply, go to: https://hrweb.ucd.ie/pls/corehrrecruit/erq_jobspec_details_form.display_form stefano.mariani@ucd.ie

---

UdelosAndes BotanistPlantPhysiologist

Dear Dr. Restrepo

The EvolDir is aimed specifically at evolutionary biologists, systematists, etc. I do not see that your advert is directed toward this audience. If I am in error, please rewrite your advert to indicate why evolutionary biologists specifically are targeted and I would be happy to post it.

Thank you, Brian

UNIVERSIDAD DE LOS ANDES Botanist/Plant Physiologist

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

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

The Universidad de los Andes is among the most renowned universities in Latin America. The Biological Sciences department hosts 27 full-time professors with internationally recognized research programs in evolution, ecology, genetics, microbiology, botany and zoology. For more information visit: http://cienciasbiologicas.uniandes.edu.co/ Interested candidates should send curriculum vitae, copies of recent publications, a brief description of research and teaching program, and two letters of recommendation before September 15, 2010 to the following address. Electronic submissions are preferred.

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

UNIVERSIDAD DE LOS ANDES Botánico(a) / Fisiólogo(a) Vegetal

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

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

La Universidad de los Andes se encuentra dentro de las mejores universidades de Latinoamérica. Su Departamento de Ciencias Biológicas alberga 27 profesores de tiempo completo quienes lideran programas de investigación de la más alta calidad en evolución, ecología, genética, microbiología, botánica y zoología. Para mayor información visitar: http://cienciasbiologicas.uniandes.edu.co/ Candidatos interesados, favor enviar hoja de vida, copia de publicaciones, una breve descripción del programa de investigación y docencia, y dos cartas de recomendación antes del 15 de septiembre de 2010 a la siguiente dirección. Aplicaciones por medio electrónico son bienvenidas.

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

ULiverpool Evolution

A permanent teaching position (0.8 FTE) is available at the School of Biological Sciences, University of Liverpool. Applicants from areas of quantitative biology, behaviour, evolution and ecology are especially encouraged to apply. Further details can be found below.

http://www.liv.ac.uk/working/job_vacancies/-academic/A-570918.htm Informal enquiries to our Head of School, Prof. Steve Edwards, biolhos@liv.ac.uk

Dr Steve Paterson School of Biological Sciences University of Liverpool Liverpool L69 7ZB, UK Tel (+44) 151 795 4521 Mob (+44) 151 794 7668 Fax (+44) 151 795 4408 Email s.paterson@liv.ac.uk

S.Paterson@liverpool.ac.uk

USouthCarolina GenomicsPopulationGenetics

Lab Manager and Post Doctoral Associates - Genomics/Population Genetics

The Department of Biology at the University of South Carolina is seeking applicants for the positions of laboratory manager and post doctoral research associates in the areas of comparative genomics and population genetics. We are seeking researchers with expertise in comparative, evolutionary, and population genomics, applications of high-throughput genomic technologies, and interests in diversity analyses across a range of economically important animal and plant species. This research initiative will focus on discovering, characterizing, and benefiting (both academically and economically) from unique and important organisms of South Carolina, including terrestrial, aquatic, and marine animals, microbes, and plants (including those used for agriculture, horticulture, forestry, and pharmaceutical/industrial use).

The ideal candidates will be highly motivated, creative, and energized by working in an interdisciplinary environment, and have a record of distinguished performance. The positions are to be located in the Department of Biology on the University of South Carolina, Columbia campus. This Postdoctoral Fellow will be supervised and work closely with Stephen Kresovich, South Carolina Center of Economic Excellence Endowed Chair of Genomics and Vice President for Research and Graduate Education at the University of South Carolina.

A Ph.D. degree is required, and salary is commensurate with experience. Specific requests for information may be sent to Stephen Kresovich at sk@sc.edu. Submit applications via the University of South Carolina employment job site (https://uscjobs.sc.edu), and also please send application letter, including a CV, statement of research interests, and names and addresses of three references to: Dr. Stephen Kresovich, Office of Research and Graduate Education, Osborne Administration Building, Suite 202, University of South Carolina, Columbia, SC 29208. Applications should be received immediately with the positions ready to be occupied as soon as possible.

The University of South Carolina is an affirmative action, equal opportunity employers. Minorities and women are encouraged to apply. The University of South Carolina does not discriminate in educational or employment opportunities or decisions for qualified persons on the basis of race, color, religion, sex, national origin, age, disability, sexual orientation or veteran status.

“CAFFEE, AMY” <CAFFEEA@mailbox.sc.edu>

UTennessee NIMBios EducationOutreach

I think this job posting (which I pasted below) might be of interest to the EvolDir folks.

Thank you,

Catherine

– Catherine Crawley, Ph.D. Communications Coordinator National Institute for Mathematical and Biological Synthesis (NIMBioS) University of Tennessee 1534 White Avenue Knoxville, TN 37996-1527 Phone: (865) 974-9350 Fax: (865) 974-9461 Email: ccrawley@nimbios.org http://www.nimbios.org http:/-/twitter.com/nimbios Staff Position - Education and Outreach Coordinator - National Institute for Mathematical and Biological Synthesis (NIMBioS) This full-time position is responsible for coordinating all outreach and education research activities of NIMBioS in collaboration with the Director and the Associate Director for Education, Outreach and Diversity. This position develops the array of outreach activities of NIMBioS including activities with the general public, K-12 programs at schools, collaboration networks for high school teachers, coordination of summer undergraduate research programs, mentoring networks for undergraduates, coordination of outreach-linked-to-research with the staff of Great Smoky Mountains National Park, and organization of workshops and conferences related to education and outreach. A MS in a quantitative scientific field (e.g., Mathematics, Statistics or Computer Science) or an area of the Life Sciences or equivalent experience is required; a PhD is a plus. Applicants should also have experience working in collaboration with researchers with BS, MS and PhD degrees to meet project tasks and the ability to communicate scientific topics to diverse audiences. Position Title: Research Associate II. Pay Grade 41. To apply, submit a CV with cover letter and names of two references to: Dr. Chris Welsh via email to cwelsh@utk.edu. The University of Tennessee is an EEO/AA/Title VI/Title IX/Section 504/ADA/ADEA institution in the provision of its education and employment programs and services. All qualified applicants will receive equal consideration for employment without regard to race, color, national origin, religion, sex, pregnancy, marital status, sexual orientation, gender identity, age, physical or mental disability, or covered veteran status.

Catherine Crawley <ccrawley@nimbios.org>

UTexasAustin LabTech SticklebackParasites

Position Title: Research Technician 1

Employer: Howard Hughes Medical Institute

Where: Section of Integrative Biology, University of Texas at Austin, Austin, TX

Classification: Full-time

Starting Salary: $33,000 to $40,000 annually depending on qualifications, plus benefits.

Start date: August 1 or later

Duration: Renewable annually depending on performance, with an expected duration of three years.

Job summary:

The Bolnick lab in the Section of Integrative Biology at the University of Texas at Austin, is seeking a highly motivated research technician to assist with a study of the ecology and evolution of stickleback fish (Gasterosteus aculeatus) and their macroparasites. The technician's job will focus on documenting geographic variation in parasite communities of the threespine stickleback and corresponding variation in stickleback immunogenetics. For more information on the Bolnick lab, visit:

https://webspace.utexas.edu/dib73/Bolnicklab/-Bolnicklab.html The research associate will be an employee of the Howard Hughes Medical Institute.

Responsibilities will include:

Quantifying parasite incidence and identity in wild-caught fish specimens, measurements of fish morphology and diet, DNA extraction, PCR, and next-gen sequencing. Training will be provided as needed. The technician will have the opportunity to assist with periodic field work on Vancouver Island, Canada, to obtain specimens. The technician may also assist with daily management of the laboratory, including purchasing, equipment maintenance, database management, and animal care.

Minimum qualifications:

A Bachelor's degree in biology or equivalent field. A strong work ethic, an ability to work independently and meticulously, and good organizational skills.

Preferred qualifications:

Experience with one or more of the following: fish parasitology, morphometrics, immunology, DNA sequencing, and/or population genetic analyses of DNA sequence data. Ideal candidates would have a Masters degree in an appropriate subfield of biology, including but not limited to evolution, ecology, immunology, parasitology, ichthyology, molecular genetics, or bioinformatics. Experience with field research is also a plus.

To apply:

Applications will be reviewed as they are received, and the position will remain open until filled. The application should include:

1) a letter of application with a description of past research experience and education (degree, institution, GPA, courses taken)

2) a curriculum vitae

3) the names of three references

The application may be sent via email as a pdf file (preferred) or word file to:

danbolnick@mail.utexas.edu

Or, applications may be sent via mail to:

Dr. Daniel Bolnick Section of Integrative Biology One University Station C0930 University of Texas at Austin Austin TX 78712, USA

danbolnick@mail.utexas.edu

UWesternAustralia BeeEvolutionaryProteomics

POSTDOCTORAL POSITION (REF: 3163) ARC CENTRE OF EXCELLENCE IN PLANT ENERGY BIOLOGY and COLLABORATIVE INITIATIVE FOR BEE RESEARCH (CIBER)

A key opportunity to explore proteomics of honeybees:

â 2 year appointment, available immediately Salary range: Level A $53,542 - $72,537 p.a. - minimum starting salary for appointee with PhD will be $70,058 p.a. â Closing date: Friday, 16 July 2010

The Collaborative Initiative for Bee Research (CIBER) is dedicated to facilitate interdisciplinary research on honeybees. The ultimate goal is to better understand honeybees and counter the dramatic losses currently occurring. To achieve this, CIBER combines expertise from beekeepers with decades of experience, sociobiologists and their insights into the functioning of bee societies, evolutionary ecologists and their understanding of evolutionary processes and molecular biologists that provide expertise to harness the honeybee genome and proteome. The latter occurs in conjunction with ARC Centre of Excellence in Plant Energy Biology (CPEB) which houses state-of-the-art equipment for proteomics and metabolomics approaches and major resources for microarray analysis, imaging and computing.

Applications are invited from a suitably qualified postdoctoral Research Associate to work in a team environment in CIBER on quantitative proteomics and mass spectrometry of honeybees. The project aims to study male bee fertility to understand molecular determinants of sperm survival that influence paternity success in managed as well as feral bees in Western Australia, which will also generate information important for future bee breeding in Australia. A PhD in protein biochemistry or molecular biology or related discipline is essential. The position is available immediately.

For further information see CIBER*: http://-www.ciber.science.uwa.edu.au or CPEB http://-www.plantenergy.uwa.edu.au or contact Professor Harvey Millar, emailhmillar@cyllene.uwa.edu.au or Associate Professor Boris Baer, email bcbaer@cyllene.uwa.edu.au for more information on the project.

Application Details*: The position description follows. Written applications quoting the reference number, personal contact details, qualifications and experience, along with contact details of three referees should be sent to Director, Human Resources, The University of Western Australia, M350, 35 Stirling Highway, Crawley WA 6009 or emailed tojobs@uwa.edu.au by the closing date.

ROLE STATEMENT As the appointee you will undertake innovative laboratory-based research in a team environment to study male bee fertility to understand molecular determinants of sperm survival that influence paternity success in bees which will also generate information important for future bee breeding in Australia. Your primary aim will be to use proteomic approaches in collaborative projects, aimed at publication in international research journals. You will be supervised by Assoc. Prof. Baer and collaborate closely with the other chief investigators on the project and personnel from the Industry Partner.

KEY RESPONSIBILITIES 1. Design, execute and analyse research on proteomic approaches to understanding honeybee male fertility. 2. Set up reliable and reproducible experimental systems to extract samples from honeybees sourced from UWA or from collaborators to use in experiments. 3. Work closely with CIBER scientists in designing the use of proteomics in projects and troubleshooting protein separation, quantification and analysis. 4. Keep records and follow procedures required by the partners in an ARC Linkage project. 5. Help maintain and troubleshoot issues in the mass spectrometry facility in collaboration with other researchers and the manufactures. 6. Other duties as directed.

A/ Prof. Boris Baer CIBER: The Collaborative Initiative for Bee Research Website: www.ciber.science.uwa.edu.au MCS Building M 310 The University of Western Australia Crawley WA 6009 Australia phone: +61 8 6488 4495 fax: +61 8 6488 4401 E-mail: bcbaer@cyllene.uwa.edu.au

Boris Baer <bcbaer@bi.ku.dk>

Vienna DrosophilaGenetics

PART-TIME TECHNICIAN POSITION IN DROSOPHILA GENETICS

A part-time technician position in the biology of Drosophila aging is available in the group of Thomas Flatt at the University of Veterinary Medicine (Department of Biomedical Research, Institute of Population Genetics), Vienna, Austria. The position is funded by a grant from the Austrian Science Foundation (FWF) and will be for at least two years, part-time (3 days per week).

We are seeking a well trained and self-motivated technician with good social, management, and organizational skills. The successful applicant should have prior laboratory experience with basic molecular biology techniques and genetics, a strong work ethic, and the ability to work independently. A degree in biology or a related field would be a plus. Applicants with experience in Drosophila maintenance and genetics would be highly desirable and will be given preference. The working language in the laboratory is English, so the candidate should be proficient in spoken and written English. German skills, although helpful, are not essential. The initial appointment will be made for 6 months, with a possible extension to up to two years. The annual salary is 17,016 Euro (before tax) for part-time work (3 week days). The position is available as of September or October 2010.

The responsabilities of the research assistant/technician will include: assisting in the daily operation and maintenance of the lab; ordering supplies; preparing reagents and fly food media; maintaining fly stocks; assisting with and performing experiments. Bench and lab work will include standard molecular biology procedures such DNA and RNA extraction, PCR, RT-PCR, cloning, fly genetics, and immunohistology. Prior experience in performing Western and Northern blots would be a plus.

In a 2009 world-wide survey by the William M. Mercer Institute, Vienna ranked first world-wide in terms of standards of living. Vienna is a beautiful, historical yet modern city, located in the heart of Europe, close to the Alps and to major cities like Munich, Zurich, Prague, and Budapest. Being famous for its concert sites, opera houses, theathers, museums, and coffee shops, Vienna also provides great outdoor activities, such as sailing on the Neusiedler See, ice skating, biking and hiking in the Viennese woods and the nearby Alps. Moreover, the city has a wide range of great restaurants, bars, wineries, cinemas, clubs, libraries, galleries, and art collections. The Vienna area is also an exceptional and highly international research environment. Four major life science universities and three world-class research institutes (GMI, IMBA, IMP) provide a dynamic and interactive setting. Vienna hosts an active Drosophila community, and the onsite availability of the Drosophila RNAi center (VDRC) provides a great opportunity for functional Drosophila work.

To apply for this position, please send your application, including a cover letter, as a single pdf file to the following email address: thomas.flatt@vetmeduni.ac.at

Informal inquiries are welcome and should be sent to the same e-mail address. For further information see (http://i122server.vu-wien.ac.at/pop/-Flatt_website/flatt_home.html).

The deadline for submission is 15 August 2010.

Dr. Thomas Flatt Institute of Population Genetics Department of Biomedical Sciences University of Veterinary Medicine Vienna Veterinärplatz 1 A-1210 Wien Austria/Europe

VOX +43-1-25077-4334 FAX +43-1-25077-4390 E-mail: thomas.flatt@vetmeduni.ac.at

Lab Website: http://i122server.vu-wien.ac.at/pop/-Flatt_website/flatt_home.html Vienna Graduate School of Population Genetics: http://www.popgen-vienna.at Thomas Flatt <flatt.thomas@gmail.com>

WoodsHole EvoDevo

Position Title: Postdoctoral Scientist, Evo-Devo of Gene Regulatory Networks, Bay Paul Center

Description: An anticipated postdoctoral position in the Evo-Devo of Gene Regulatory Networks will be available in Joel Smith's lab at the Marine Biological Laboratory in Woods Hole.

We seek a talented and enthusiastic researcher to contribute to funded investigations into the evolution of developmental Gene Regulatory Networks (GRNs). The successful candidate will conduct molecular biology and functional genomics studies in non-vertebrate model organisms, including the sea urchin, Strongylocentrotus purpuratus - the pioneering system for GRN research

- and the starlet sea anemone, Nematostella vectensis, to determine the regulatory mechanisms governing axis specification and pattern formation during early stages of embryogenesis. The Postdoctoral Scientist will be part of a collaborative team, sharing expertise in gene regulation, cell and evolutionary biology and working to gain a deep mechanistic understanding of the origins of the bilaterian body plan.

The successful applicant will hold a Ph.D. in one of the biological sciences. Necessary skills include standard molecular biology techniques, with experience in embryology, stem cell biology, and gene regulation a plus.

Special Instructions to Applicants:

Required Applicant Documents -Resume/CV -Cover Letter -References (3)

Please submit three items: (i) a cover letter describing your research goals and your specific motivation to join our lab, (ii) a CV, and (iii) contact information for three references, including your Ph.D. supervisor by completing an application using the MBL website: http://-www.mbl.edu/hr/employment.html . Please email Joel Smith (joelsmith@mbl.edu) with any questions about the position.

Posting Number: 0000320

Deadline: Until a suitable candidate is found.

The MBL is an Equal Opportunity/Affirmative Action Employer/Non- smoking workplace.

“Katie K. Newhall” <knewhall@mbl.edu>

Katie K. Newhall | Center Research Administrator | Marine Biological Laboratory Josephine Bay Paul Center for Comparative Molecular Biology and Evolution 7 MBL Street, Woods Hole, MA 02543 508-289-7137 (direct) 508-457-4727 (fax) knewhall@mbl.edu Please consider the environment before printing this email.

knewhall@mbl.edu

Other

Biotechniques reprint

Dear all,

If anybody has:

Walsh, P.S., Metzger, D.A. & Higuchi, R., 1991. Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. BioTechniques, 10, 506-513.

I would be very thankful if you could email me a copy as a pdf please. Our library seems to have 'filed' everything older than 1996 now.

Best,

Mark.

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

Senior Lecturer (Affiliate), University of Adelaide, School of Earth and Environmental Sciences, Faculty of Sciences, SA 5000 Australia, http://ees.adelaide.edu.au/disciplines/eeb/ "Stevens, Mark (SAM)" <Mark.Stevens@samuseum.sa.gov.au>

CallInterest FourthIntlBarcodeConference

The Consortium for the Barcode of Life (CBOL) will be holding the Fourth International Barcode of Life Conference in late 2011 and invites expressions of interest from organizations interested in hosting the conference. Previous conferences have been hosted by The Natural History Museum, London (February 2005), Academia Sinica (September 2007) and Universidad Nacional Autonoma de Mexico (November 2009) and preference will be given to organizations in regions that have not previously hosted a barcode conference.

The host organization will be asked to designate a conference chair and local organizing committee who will work closely with CBOL in planning the conference. The committee will be responsible for: providing a meeting venue that will be of interest to scientists; hiring a conference management company with which logistical arrangements will be made; and obtaining partial funding of the conference from co-sponsors. The conference chair will be a member of the technical program committee that will plan the conference agenda and select speakers.

CBOL Member Organizations are invited to express their interest in hosting the conference by contacting David Schindel (schindeld@si.edu). Please include the name and contact information for the proposed conference chair.

Expressions of interest are requested by 15 July 2010. Organizations that respond to this call will receive guidelines for preparing their proposals to CBOL's Executive Committee which must be received by 1 September 2010. The final selection of the conference venue will be made by CBOL's Executive Committee by 1 October 2010.

David E. Schindel, Executive Secretary

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

National Museum of Natural History Room CE-119 10th & Constitution Avenue, NW Washington, DC 20560

Postal mailing address:

National Museum of Natural History Smithsonian Institution P.O. Box 37012, MRC-105 Washington, DC 20013-7012

"Schindel, David" <schindeld@SI.EDU>

Cichlid evolution

Cichlid Evolution: Lessons in Diversification Call for Papers

With an estimated 3000 species, distributed from Central and South America, across Africa to Madagascar, the Middle East, and southern India, cichlid fishes (Cichlidae) represent the most species-rich family of vertebrates, accounting for about 10% of extant teleost diversity. Throughout their distributional range, cichlids have repeatedly demonstrated their capacity for undergoing adaptive radiation, generating an outstanding variation of body shapes, colour patterns, and behaviour, and an enormous diversity of trophic and ecological specializations, making them an important model system for evolutionary biology. With the completion of the first cichlid genomes in the foreseeable future, cichlid fishes will receive even more attention in evolutionary research. We invite investigators to contribute original research as well as tutorial or review articles that seek to advance our knowledge of mechanisms underlying processes generating and maintaining the tremendous diversity of cichlid fishes. Potential topics include, but are not limited to:

* Advances in phylogenetics, phylogeography, and population genetics * Genomic and transcriptomic research * Role of behavioral and ecological specializations in cichlid diversification * Physiological/morphological adaptations to particular environments * Importance of hybridization for generating diversity * Sexual versus natural selection * Evolution of developmental mechanisms

Before submission authors should carefully read over the journal's Author Guidelines, which are located at http://www.sage-hindawi.com/journals/ijeb/guidelines.html. Prospective authors should submit an electronic copy of their complete manuscript through the journal Manuscript Tracking System at http://mts.sage-hindawi.com/ according to the following timetable:

Manuscript Due November 15, 2010 First Round of Reviews February 15, 2011 Publication Date May 15, 2011 Lead Guest Editor

* Stephan Koblmueller stephan.koblmueller@uni-graz.at, Department of Zoology, Karl-Franzens-University Graz, Universitätsplatz 2, 8010 Graz, Austria

Guest Editors

* R. Craig Albertson rcalbert@syr.edu, Department of Biology, Syracuse University, Syracuse, NY 13244, USA * Martin J. Genner m.genner@bristol.ac.uk, School of Biological Sciences, University of Bristol, Woodland Road, Bristol BS8 1UG, UK * Kristina M. Sefc kristina.sefc@uni-graz.at, Department of Zoology, Karl-Franzens-University Graz, Universitätsplatz 2, 8010 Graz, Austria * Tetsumi Takahashi tetsumi@terra.zool.kyoto-u.ac.jp, Graduate School of Science, Kyoto University, Kitashirakawa-Oiwake Sakyo, Kyoto 606-8502, Japan

Stephan Koblmüller Department of Zoology; Karl-Franzens-University Graz Universitätsplatz 2; 8010 Graz Austria phone: +43 (0)316 3803978 fax: +43 (0)316 3809875 homepage: http://www.kfunigraz.ac.at/zoowww/personal/kobl/kobl.htm stephan.koblmueller@uni-graz.at

---

Clustering PhylogeneticTree

Dear all,

I have a phylogenetic tree of 695 phoB proteins, now I want to estimate the the optimal number of clusters on this tree. However, before choosing any statistic to estimate the number of clusters I have to slide a vertical line along the phylogenetic tree in order the decide the current number of clusters. If this could be done automatically, it means we have to handle the newick string of this tree. How should I write the code dealing with the newick string, which amounts to slide a vertical line to decide the subgroups. Thanks in advance!

Sincerely,

shan

– Shan Li Bioinformatics UNC Charlotte

Shan Li <lishan989@gmail.com>

Divergence rate To Mutation rate conversion

I would like to calculate a mutation rate per site, per generation, from a mtDNA control region divergence rate reported in the literature in units of divergence per million years. In my calculation, I am assuming that each species diverges at an equal rate, and I have a generation time of 5 years. The reported divergence rate is 4.8% per million years. To get the mutation rate, I divide 0.048/1,000,000, multiply by 5 for my generation time and divide by 2 to account for the fact that I have two lineages going different directions. This gives me a lineage-specific mutation rate of 1.2 x 10(-7) per-site, per-generation.

That seems like an awfully slow rate for the control region. Where am I going wrong? I feel like my math is off somehow but I can't figure out where.

Joel Anderson <Joel.Anderson@tpwd.state.tx.us>

Dmelanogaster samples

I am looking for old Drosophila melanogaster population samples. Specifically, I am looking for Drosophila melanogaster that are collected from one geographic locations before 1970s and maintained since then in laboratory.

Any possible source/information will be greatly appreciated.

Grace Yuh Chwen Lee <grylee@ucdavis.edu>

Invasive species survey

Dear Colleagues, I would like to draw your attention to the world's largest collaborative project on invasive species. The Global Garlic Mustard Field Survey is just entering its second field season and we already have demographic data and seed collections from 65 populations – more than any published study on invasive species. This year we are hoping to double that number and we are particularly keen to have more North American contributors.

The project is an international collaboration aimed at obtaining much-needed data on the abundance and distribution of /Alliaria petiolata/ (Garlic Mustard). It involves a very basic sampling protocol that standardizes sampling across sites, making it ideal for incorporation into field courses, nature surveys, and long-term monitoring and management efforts. The estimated duration of sampling for a team of two people is 2-4 hours per population.

For academics who substantially contribute to this endeavor, we anticipate the possibility of authorship on manuscripts resulting from the work. Our plan for the future includes development of teaching modules and expanding to similar surveys for other key invasive species. The sampling protocol and additional information are available at the following website: www.GarlicMustard.org. Please contact us directly if would like to participate or if you have any questions or concerns.

Dr. Robert Colautti Biology Department Duke University rob.colautti@duke.edu

Dr. Oliver Bossdorf Biology Department University of Bern bossdorf@ips.unibe.ch

Dr. Steven Franks Biology Department Fordham University franks@fordham.edu

rob.colautti@duke.edu

London SpeakersCorner June14

Dear Evoldir user,

We'd like to invite you to attend/contribute to an exciting, innovative science communication event taking place in London this month.

On 14th June, distinguished scientists will commandeer Speaker's Corner in Hyde Park to address the public on burning scientific issues such as evolution, biodiversity and climate change. We are providing the public with the opportunity to engage first-hand with some of the UK's most eminent scientists. In effect, we're removing the -middle man'. The event will consist of three themes: Evolution of the Earth (e.g., biodiversity, evolution, palaeontology, geology), Earth Challenges (e.g., climate change, population growth, biodiversity loss), Earth Solutions (e.g., sustainable energy, GM crops, biodiversity conservation). Speakers include Armand Leroi (of 'Mutants'), Robin Dunbar (Univ. Liverpool), Sandy Knapp (NHM), Alun Anderson (science writer and former editor-in-chief of New Scientist), Jonathan Baillie (ZSL)...and many more!

See speaker biogs, and post your own questions at: www.zsl.org/speakerscorner The event aims to complement the 2010 theme of International Year of Biodiversity. We are turning Speaker's Corner into an arena for public (and scientific) learning and debate centred around the theme of Biodiversity 2010. We feel this is important and timely, given recent public distrust of scientists and evident gaps in the public's knowledge and understanding of the key scientific issues facing the world today. Speaker's Corner is internationally renowned as a public arena for free speech, and is therefore a very natural setting to encourage public engagement in science.

Come and join in the heckling, discussions and fun!

Best wishes

Seirian Sumner, Kate Jones & Charlotte Walters (Organisers)

Dr Seirian Sumner Research Fellow Institute of Zoology Zoological Society of London Regent's Park London, NW1 4RY

Tel: +44 (0) 207 449 6617 Fax: +44 (0) 207 586 2870 Home: +44 (0) 1491 652 882

Web: www.zsl.org/seiriansumner ZOOLOGICAL SOCIETY OF LONDON LIVING CONSERVATION Registered Charity no. 208728

seirian.sumner@googlemail.com

London SystematicsAssociationLecture 7thJuly

The Systematics Association Sir Julian Huxley lecture

Species for Macroevolution

Prof. Andy Purvis, Imperial College, London.

The Linnean Society, Burlington House, Piccadilly, London Wednesday 7th July 2010, 6 pm

The meeting is open to visitors. Wine will be served after the lecture to members and guests. Please advertise this lecture as widely as you can.

Abstract: Species are fundamental units for evolutionary biology. Alone among the levels of classifications into which we place individuals, the species level has the potential to have an objective reality: when we count them, we think we are counting something meaningful. If we compare number of species in different taxa, regions, or times, we are led to try to understand why the numbers are different or similar. Incomplete knowledge may lead us to use higher taxa, such as genera or families, instead, but we do so in the hope and expectation that they will reflect what good species-level data would show. I will argue: 1. That this hope is misplaced - analysing higher taxa conflates processes that should be kept separate; 2. That analysing temporal patterns in numbers of higher taxa might be particularly problematic when using large, multi-author databases; 3. That even species cannot be used uncritically in macroevolutionary analyses - even with good data (a complete phylogeny of present-day species, or a complete record of fossil species) - but that 4. The best fossil records can let us come close to the ideal species for macroevolution, letting us tackle questions that cannot be addressed any other way.

James Cotton School of Biological and Chemical Sciences Queen Mary, University of London +44 (0)207 882 3645 j.a.cotton@qmul.ac.uk http://webspace.qmul.ac.uk/jacotton/index.html http://www.sbcs.qmul.ac.uk/staff/jamescotton.html
j.a.cotton@qmul.ac.uk

Mediterranean Flora

Origin of the Flora in the Mediterranean Basin: A Window on Plant Evolution in Mediterranean Climate Zones

Call for Papers

To date, many published biogeographic studies focused on the spatial and temporal origin of particular floristic regions, including the Holarctic, the Neotropics, South-Africa, Macaronesia, or Hawaii, but only a few were devoted to the Mediterranean Basin (MB). Indeed, the relative contribution of geological processes and long-distance dispersal (LDD) to the contemporary composition of this plant diversity hotspot remains largely unknown. Main hypotheses on the geographic sources of the MB flora were mainly derived from qualitative assessments of similarities with adjacent floristic regions such as North Africa or the Middle-East, but not with other Mediterranean floras. Indeed, despite the great general resemblance between the five existing Mediterranean areas worldwide, only a few works have systematically investigated the Mediterranean disjunctions using integrative approaches. Overall, questions dealing with the origin, evolution, and affinities of the respective Mediterranean floras remain largely unanswered for example, (i) is the MB a cradle for other Mediterranean regions? (ii) do these regions appear almost simultaneously under some general abiotic constraints or do they have their own history?

In this issue, papers testing the congruence between estimated ages and geographic sources of some Mediterranean groups with independently derived paleogeological/climatic models are highly welcome. We particularly take interest in manuscripts that report relevance of (i) disjunct patterns within the MB or between the MB and other Mediterranean regions, (ii) floristic exchanges between the Mediterranean areas via dispersal routes or long distance dispersal (LDD), and (iii) abiotic/biotic events as drivers of speciation in these diversity hotspots.

Main topics include, but are not limited to: - Importance of vicariance, geodispersal, or LDD in the origin of Mediterranean floras - Role of key innovations/key opportunities in explaining the current high plant diversity in the MB - Testing correlates of diversification in the MB flora - Testing the existence of a Mediterranean niche conservatism - Testing biogeographic methods allowing an a priori implementation of probabilistic models

Before submission authors should carefully read over the journal's Author Guidelines, which are located at http://www.hindawi.com/journals/jb/guidelines.html. Prospective authors should submit an electronic copy of their complete manuscript through the journal Manuscript Tracking System at http://mts.hindawi.com/ according to the following timetable:

Manuscript Due October 1, 2010 First Round of Reviews January 1, 2011 Publication Date April 1, 2011

Lead Guest Editor - Guilhem Mansion, Botanischer Garten und Botanisches Museum Berlin- Dahlem, Freie Universität Berlin, Königin-Luise-Straße 6-8, 14195 Berlin, Germany Guest Editors - Isabel Sanmartin, Department of Biodiversity and Conservation, Real Jardin Botanica, CSIC, Plaza de Murillo 2, 28014 Madrid, Spain - John Thompson, DÃ©partement Centre d'Ecologie Fonctionnelle et Evolutive CEFE CNRS UMR 5175, 1919 Route de Mende, 34293 Montpellier Cedex 5, France

Link to pdf version: http://www.hindawi.com/journals/jb/osi.html For further information, please contact directly: g.mansion@bgbm.org (restricted email access between 10.06.2010-01.07.2010)

Dr Guilhem Mansion

Botanischer Garten und Botanisches Museum Berlin-Dahlem Freie Universität Berlin Königin-Luise-Straße 6 - 8 14195 Berlin

http://www.bgbm.fu-berlin.de/bgbm/STAFF/wiss/Mansion/default.htm Email: g.mansion@bgbm.org Tel.: +49 30 838 50 121 Fax: +49 30 838 50 218 Fax: +49 30 838 50 218

Micro examples

I am looking for microsatellite electropherograms with their alleles as well as stutters identified to get an idea of allele scoring, very simple to complex ones all are welcome; and also microsatellite electropherograms from polyploid plants with alleles/ stutters designated.

AVIK RAY avik.ray.kol@gmail.com National Centre of Biological Sciences Bangalore-65, India

avik.ray.kol@gmail.com

MrBayes aarevmatpr parameters

Dear EvolDir members, my name is Federico and I am a PhD student currently working on mitochondrial genome phylogenetics. Among other analyses, I wanted to enforce MtArt and MtPan matrices for my protein alignments: therefore, I used the MrBayes 3.1.2 command

prset aamodelpr=fixed(gtr) aarevmatpr=fixed(<190 comma-separated values>);

However, when the MCMC run is over and I proceed with sump command, I see amino acid substitution rates as free parameters in the STAT file. This was obviously not expected, because they should be fixed parameters and not allowed to vary, thanks to aarevmatpr set to fixed. In the similar case of nucleotide analyses, indeed, substitution rates are not listed into the STAT file if I use the prset revmatpr=fixed command.

Through the showmodel command, I could see that MrBayes acknowledges that I set up a fixing prior on substitution rates, but then lists them among free parameters and considers amino acids frequencies (!) as not allowed to vary.

Did anyone come across the same problem? Can someone explain this behaviour of MrBayes 3.1.2? I am very grateful in advance to each of you for the help to come!

Best regards, Federico Plazzi Dipartimento di Biologia Evoluzionistica Sperimentale Via Selmi, 3 40126 Bologna (BO) - Italy federico.plazzi@unibo.it

LA RICERCA CâÃ E SI VEDE: 5 per mille all'UniversitÃ di Bologna - C.F.: 80007010376 http://www.unibo.it/Vademecum5permille.htm Questa informativa Ã inserita in automatico dal sistema al fine esclusivo della realizzazione dei fini istituzionali dellâente.

federico.plazzi@unibo.it

MrBayes problem

Dear MrBayes users and experts,

I am getting stuck in ONE parameter of MrBayes.

Many thanks in advance for your help.

I suspect a bug with prset pinvarpr parameter : there is always an error message whatever are the options i fixed.

Here are the command lines : the two last ones fail.

MrBayes > execute TestBSprotAli.nex .... Successfully read matrix Exiting data block Reached end of file MrBayes > lset rates=invgamma Setting Rates to Invgamma Successfully set likelihood model parameters MrBayes > lset ngammacat=4 Setting Ngammacat to 4 Successfully set likelihood model parameters MrBayes > prset aamodelpr=fixed(gtr) Setting Aamodelpr to Fixed(Gtr) Successfully set prior model parameters *MrBayes > prset Pinvarpr = Fixed (0.3) Expecting <number> Instead found ')' in command 'Prset' or MrBayes > prset Pinvarpr=uniform(0,0.2) Expecting <number> Instead found ',' in command 'Prset'

*Again many thanks for your help.

Xavier

– Xavier Bailly, PhD

Developmental Marine Genomics and Phylogenomics

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

tel: + 33 2 98 29 23 29 fax: + 33 2 98 29 23 24

email: bailly@sb-roscoff.fr http://www.sb-roscoff.fr/ Xavier Bailly <xavier.bailly@sb-roscoff.fr>

MrBayes taxon names

Hello,

I have run a large single-gene mtDNA matrix, with more than one sequence per species, in Mr Bayes. The matrix was built using data downloaded from GenBank and to identify the terminals I used shortened species names followed by the accession numbers. When the run had converged I used the sum t command to obtain the consensus tree, however for several species the name is cut short and most of the accession number is no longer included but rather replaced by suspension points (ie ...). Thus I can no longer identify specific sequences because the accession numbers have been cut short. Strangely, the names are complete in the two tree files, and they appear to be cut short only when the sum t command is executed.

Is there a command that would allow me to tell MrBayes not to cut taxon names? The names I have are not longer than those that appear in the example files of MrBayes, nor do I have other symbols other than alphanumeric and the underscore to replace a space.

Any suggestions are welcome!

Thank you,

Alejandro

Alejandro Gonzalez Voyer Post-doc

NEW ADDRESS & NEW E-MAIL

Estación Biológica de Doñana (CSIC) Avenida Américo Vespucio s/n 41092 Sevilla Spain

E-mail: alejandro.gonzalez@ebd.csic.es

Tel: +34- 954 466700, ext 1749

Website (From my previous position): http://www.iee.uu.se/zooekol/default.php?type=personalpage&lang=en&id=146 Alejandro Gonzalez V <alejandro.gonzalez@ebd.csic.es>

NationalScienceFoundation forum

Dear Colleagues,

We are now in the season when most of us who applied for NSF funding in January of 2010 are receiving word that our grants will not be funded. In spite of many weeks of grant writing and many years of field and lab research, as many as 75% of applicants are opening emails that characterize our work as “Not Competitive.”

And yet this is the same work that we routinely publish in peer-reviewed journals and books, that got us jobs at top-flight institutions and positions on respected editorial boards and advisory panels, and that we present and discuss passionately at professional meetings.

Something is wrong with a system that does not recognize quality science, that is discouraging to new and experienced researchers alike, and that offers no appeals process and little transparency.

In order to address these issues, several of us have created a new discussion forum dedicated to debating the current state of NSF and proposing solutions for its challenges. We invite you to contribute to this critical discussion.

This forum is located at http://nsfisbroken.proboards.com/index.cgi What problems have you had with NSF? What creative solutions have you come up with to these problems? The forum is designed to address such issues. Let's bring out our best ideas, and hope that NSF pays attention.

Anonymous posting is supported, registration is possible but not required. Ad hominem attacks and vulgar or base language are not tolerated.

The forum creators began with the premise that the mission of NSF is critically important and that its employees are bright, hard working, and well meaning. But we argue that the current funding system has become opaque and out of touch with reality, and in many cases serves to hinder rather than advance science.

This forum is NOT affiliated with NSF or any other institution.

Please forward this email to all interested colleagues.

Sincerely,

Aureliano Buendia Private State University

aurel.buendia@gmail.com

NCBI to Wikipedia taxon mapping

Some 52,956 taxa that have sequences in GenBank are linked to Wikipedia. These links appear in the NCBI taxonomy pages under the heading "External Information Resources (NCBI LinkOut)". For example, the NCBI page for "Mammuthus primigenius"

http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id7349 shows a link to Wikipedia page for "Woolly Mammoth"

http://en.wikipedia.org/wiki/index.html?curid369680 My motivation in creating this link was to provide an easy way for someone visiting a NCBI taxonomy page to get a quick sense of what we know about that taxon (even if it's simply to answer "what on Earth is this?").

For some details on how this mapping was created please see my blog post: http://tinyurl.com/35cljpv. Thanks to Scott Federhen and Kathy Kwan at NCBI for all their assistance in getting this into NCBI Linkout. There are inevitably going to be errors and ommissions in this mapping. These can be updated at http://iphylo.org/linkout . Regards

Rod

Roderic Page Professor of Taxonomy DEEB, FBLS Graham Kerr Building University of Glasgow Glasgow G12 8QQ, UK

Email: r.page@bio.gla.ac.uk Tel: +44 141 330 4778 Fax: +44 141 330 2792 AIM: rodpage1962@aim.com Facebook: http://www.facebook.com/profile.php?id12517192 Twitter: http://twitter.com/rdmpage Blog: http://iphylo.blogspot.com Home page: http://taxonomy.zoology.gla.ac.uk/rod/rod.html r.page@bio.gla.ac.uk

Pacific Symposium

We invite high quality manuscripts for publication and presentation at a special session on Microbiome Studies at the Pacific Symposium on Biocomputing, 3-7 January in Hawaii. Papers will be refereed by top names in the field, and accepted papers will be published in the PSB proceedings, which are indexed in Medline.

For details: http://psb.stanford.edu/cfp-microbiome.html james a. foster university of Idaho

"James A. Foster" <foster@uidaho.edu>

PhilTheoryBiol

Philosophy & Theory in Biology, an online open access journal devoted to bringing together the philosophy of science and theoretical biology communities, seeks submissions for two special ongoing features: Trends and Crosstalk. "Trends" are in depth review (as opposed to original scholarship) papers on topics of current interest within the areas covered by the journal, while "Crosstalk" entries provide technical yet accessible articles written by biologists on topics of interest to philosophers, or by philosophers on topics of interest to biologists.

Submissions for ideas for Trends or Crosstalk papers can be sent to editors@philosophyandtheoryinbiology.org, and more information about the journal (including how to submit regular papers and book essays) can be found at philosophyandtheoryinbiology.org

Massimo Pigliucci Editor, Philosophy & Theory in Biology massimo@platofootnote.org

Prof. Massimo Pigliucci The Graduate Center & Lehman College City University of New York www.platofootnote.org www.rationallyspeaking.org "I love deadlines. I like the whooshing sound they make as they fly by..." -Douglas Adams

Predicting PathogenEvolution funding

Sent on behalf of Michael Callahan, M.D., DTM&H, Program Manager for Prophecy: Predicting Pathogen Evolution.

Dear Members,

I am contacting you in regard to a novel funding opportunity which may be of interest to subscribers of the EVOLDIR emailing list.

DARPA's viral pathogen surveillance program known as "Prophecy" is based on a multi-year investment in the preemptive prediction of emerging viruses using in-silica models validated by high-throughput biological validation systems, all of which are corrected by the real-time reporting of mutations in animal reservoirs or humans. A Broad Agency Announcement (BAA) will soon be released for Prophecy which will seek integrated multi-disciplinary solutions to predicting viral pathogens before emergence in natural ecologies.

Talented scientists and engineers will be critical to the success of this program. It is our belief that the members of the EVOLDIR emailing list may offer novel approaches, methodologies and trans-discipline solutions which would greatly assist DARPA in this challenging program. As you are likely aware, this belief is supported by the successes of DARPA's Fundamentals of Biology program which brought biologists, mathematicians, and physicists together to challenge conventional biological paradigms.

Due to the interdisciplinary nature of the program Prophecy and its goal of predicting pathogen evolution, collaborations will be necessary and we envision that it may take time to formulate productive teams. To this end DARPA will be holding teaming meetings to introduce potential responders to the Prophecy BAA and encourage their collaboration in the pursuit of multidisciplinary approaches to the program. There will be 2 meetings which are described in the attached Special Notice (DARPA-SN-10-48).

We hope that you will forward this Special Notice to the Society membership and that the expertise of your community will help DARPA in achieving these challenging objectives. Please note that there are two meetings over the next six weeks that will precede the publication of the BAA.

Regards,

Michael Callahan MD Program Manager, Prophecy

Christopher Houchens <chouchens@sainc.com>

RepublicCapeVerde VoluntaryFieldAssist

Field assistant wanted ? Republic of Cape Verde ? Sept to Dec 2010

Can you: 1. Work long hours unsupervised 7 days per week? 2. Find nest, and capture and ring shorebirds? 3. Contribute to your own expenses?

The project We are investigating breeding ecology and behaviour of Kentish plover Charadrius alexandrinus in Cape Verde by monitoring colour-ringed individuals. This is an all-year resident population and many individuals are already ringed from previous years.

The place The study sites are in Maio Island, Cape Verde, at the Salina Porto Ingles and nearby lagoons (see the Bradt Guide to Cape Verde Islands). Accommodation on the islands is in an apartment, with occasional water and electricity. The island has spectacular wildlife, including endemic birds, corals and marine mammals; it is a beautiful and inspiring place to work. However, the island is a small and isolated place with basic commodities, the weather can be harsh and a great deal of walking is required.

The job The fieldwork will run from 1 September to mid December 2010. It will be unsupervised, and will involve ? among other tasks ? searching for plover nests and marked plovers and their families, taking behavioural observations and monitoring nest survival. It will also involve capturing, ringing and bleeding adults and young.

The candidate This is a volunteer post ? applicants must be willing to pay for their own transport to Maio, and to contribute to their expenses once there. However, we are applying for funding elsewhere and if successful, these funds would cover the majority of expenses.

You will be a keen birder with sharp eyes and plenty of experience of trapping, handling and ringing birds. Clean driving licence is essential. You must be personable and happy to engage with locals to explain the project; some Spanish or Portuguese is helpful. You must be physically fit, hard-working and meticulous, and have a proven ability to work independently. As you will appreciate from its description, the project will involve many different challenges. A proven ability to collect high-quality data is essential (i.e. a good degree in a biological subject or equivalent experience), and you should be prepared to type up your data in the evenings! You must have a positive attitude and an ability to look after yourself ? this means cooking your own meals, dealing with logistics (such as ordering food), and most importantly being capable of organising your own work for a substantial period of time. If you like chatting on the phone, or feel the need to text and email people all the time, this position is not for you. The cost of living is high, and food is expensive.

Costs It is possible to fly through Lisbon from the UK that costs about £700. Internal flights from Praia to Maio should be under £100, and accommodation is £5 per night. I expect that a budget of £2000 would cover your flights and expenses for the whole field season.

Interested? Please send a current CV with an email stating why you feel you are a strong candidate to me (Professor Tamás Székely) at bssts@bath.ac.uk. Application deadline: 16 July 2010.

I will also need the contact details (email and telephone) of two referees. If you have any questions, please direct them to me at the same email address, or call me on UK 01225 383 676.

bssts@bath.ac.uk

Scaleboot use

Dear All:

I try to learn how to use Scaleboot according to the manual as follows:

“

```
> library(scaleboot)
> mam15.mt <- read.mt(”mam15.mt“)
> mam15.ass <- read.ass(”mam15.ass“)
> mam15.relltest <- relltest(mam15.mt, ass = mam15.ass)
> summary(mam15.relltest)”
> library(scaleboot)
```

it is ok

```
> mam15.mt <- read.mt(“mam15.mt”)
Error in file(file, “r”) : cannot open the connection
In addition: Warning message:
In file(file, “r”) : cannot open file ’man15.mt’: No such file or directory
```

Did you experience this error before?

If so, could please you give me some advice?

Thank you very much,

I appreciate your time.

Best regards,

Runhua

Runhua Lei, Ph.D. Conservation Geneticist Omaha’s Henry Doorly Zoo 3701 South 10th Street Omaha, NE 68107

1-402-557-6924 (O) 1-402-738-2095 (Lab) 1-402-733-0490 (Fax)

leir@omahazoo.com

ShortCourses YouWouldLike 3

Call for Full Proposals for NESCent Courses

NESCent (The National Evolutionary Synthesis Center) recently had an open call for suggestions for new 1-2 week summer courses to be offered at our center in Durham, NC. This open call was followed by open, anonymous voting to collect feedback from the evolution community on perceived need/value of the proposed courses. See the top vote-getters here: www.nescent.org/courses/proposals . We appreciate all of the enthusiastic responses we received, and are now soliciting full proposals. While the five topics listed at the link, above, are of particular interest to us (based on community voting) anyone is welcome to submit a full proposal to deliver a course on any evolutionary topic.

Full proposals are due by July 10th, 2010.

For information on how to prepare and submit a full proposal, see www.nescent.org/courses/proposals/ . NESCent also co-sponsors existing short courses. If you currently teach a short course and would like to apply for NESCent support to cover instructor expenses or fellowships for underrepresented minority students, please see www.nescent.org/courses/proposals/-cosponsorship .Applications for co-sponsorship are also due by July 10th, 2010.

For questions or more information, please contact Jory Weintraub (jory@nescent.org).

Jory Weintraub <jory@unc.edu>

Small scale SNPs

Hi,

Has anyone got experience in (very) small scale SNP genotyping? We'd like to quickly and cheaply type a couple of SNPs in less than 100 genomic DNA samples, but most of the popular technologies don't seem to be cost-effective for such small project. A quick internet search suggests that a service company might do it for ~£200, and DIY PCR + sequencing doesn't seem to be any cheaper. I also found some PCR-based methods but quite a bit of optimisation needs to be done?

Thanks, Maureen Liu

Maureen Liu Postdoc Research Fellow

School of Biology University of Nottingham University Park Nottingham, NG7 2RD UK

telephone: +44 (0) 115 8230 354 fax: +44 (0) 115 8313 128 email: maureen.liu@nottingham.ac.uk

Maureen.Liu@nottingham.ac.uk

Software NewVersionFLOCKProgram

FLOCK is designed to unravel genetic structure within a collection of genotypes, whether pure or admixed. It is assumed that pure, "source", samples are not available. The program may be used to solve the "number (K) of populations" problem, separate pure and admixed specimens into K groups (K is known), picture structural relationships between samples. FLOCK is a non- Bayesian method and therefore differs substantially from previous clustering algorithms. Its working principle is repeated re-allocation of all collected specimens (total sample) to the k subsamples. The number of re-allocations until convergence typically stands between five and ten. The method was published as:

Duchesne P, Turgeon J (2009) FLOCK: a method for quick mapping of admixture without source samples. Molecular Ecology Resources 9: 1333-1344

A new version (2.0) is currently available. FLOCK now signals by red printing all P Values that exceed the Bonferroni corrected threshold (0.05/ number of runs) so that runs that are not validated by allocation number tables are easily identified. Also, FLOCK 2.0 may be run for a sequence of values of k in a single batch process. A separate output file, named the plateau record, is now automatically generated to facilitate plateau analysis, a powerful tool to estimate K.

FLOCK 2.0 can be downloaded at:

http://www.bio.ulaval.ca/no_cache/departement/-professeurs/fiche_des_professeurs/professeur/11/13/
Julie Turgeon (julie.turgeon@bio.ulaval.ca)

and

Pierre Duchesne (pierre.duchesne@bio.ulaval.ca)

Département de biologie

Université Laval

Québec, Québec

CANADA G1V 0A6

julie.turgeon@bio.ulaval.ca

Software PhyRe PhyloRepresentativeness

Dear EvolDir members, we are glad to inform you that a new program evaluating phylogenetic coverage has been released and is freely available on our lab website at

http://www.mozoolab.net . We called our package PhyRe, standing for PHYlogenetic REpresentativeness. It is composed by three Python scripts; therefore, it is platform-independent. Our idea is to deal with taxon sampling issue with a completely a priori approach: in this way, we can answer to the question "Did I sample taxa in my ingroup enough to conduct a phylogenetic study?" before starting the lab work. Phylogenetic Representativeness develops Taxonomic Distinctness for phylogenetic purposes: only a reference taxonomy is needed, then the ingroup is compared to the complete master list of organisms it stands for. Several tests of randomization and shuffling have been introduced to assess statistical confidence. We hope this concept can be useful to phylogeneticists planning their work and conducting their research project. A paper has been published on this topic:

Plazzi, F., Ferrucci, R. R., and Passamonti, M. (2010). Phylogenetic Representativeness: A New Method for Evaluating Taxon Sampling in Evolutionary Studies. BMC Bioinformatics 11:209.

Best regards, Federico Plazzi Dipartimento di Biologia Evoluzionistica Sperimentale Via Selmi, 3 40126 Bologna (BO) - Italy

– LA RICERCA CâÃ E SI VEDE: 5 per mille all'UniversitÃ di Bologna - C.F.: 80007010376 http://www.unibo.it/Vademecum5permille.htm Questa informativa Ã inserita in automatico dal sistema al fine esclusivo della realizzazione dei fini istituzionali dellâente.

federico.plazzi@unibo.it

Software TreeSnatcher Plus

We have finished a new version of our TreeSnatcher Plus application. This is the link to the new website: http://www.cs.uni-duesseldorf.de/AG/BI/Software/treesnatcher Abstract (from the website): TreeSnatcher Plus is a GUI-driven Java application for the semi-automatic recognition of multifurcating phylogenetic trees in pixel images. The program accepts an image file as input and analyzes the topology and the metrics of a tree depicted with user assistance. The analysis is carried out in a multiple-stage process using basic algorithms from the field of image analysis. It yields a Newick expression that represents the tree structure optionally including branch lengths.

Due to some differences between the JAVA versions for the three major OSes there is currently only a Mac OS X version. However, the versions for Windows and Linux will be available pretty soon.

We believe that the new application is much more flexible and usable now. as we have re-conceptualized and extended our program from 2007. You can now preprocess an image directly in TreeSnatcher Plus with a large selection of tools. The program now recognizes rectangular topologies and can therefore deal with branch lengths correctly.

Colleagues who like to try TreeSnatcher Plus for Mac OS X are kindly encouraged to study the tutorials from the website in detail. The tutorials serve as a substitute for a manual.

We would be very grateful for comments, ideas, bug reports, advice, or criticism and are happy to answer any questions.

The source code will be made available on request.

Best regards, Thomas Laubach

Thomas Laubach <tlaubach@gmx.de>

SouthAfrica Volunteers MammalEvol

Volunteers needed as field assistants for the project:

Evolution and Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

1 male volunteer from July on, one female volunteer from September onwards and more open positions afterwards

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work relating to evolution, ecology and behavior before starting an

MsC or PhD project.

Project: We study the evolutionary and ecological reasons as well as physiological mechanisms of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o‘ clock), and stops its activity with dusk (19 o‘ clock). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small social group.

Work of field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers are also expected to help with maintenance of the research station (water pump, solar power, etc.)

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1000 (around 105 Euro) must be paid for accommodation at the research station. For students with their own undergraduate project, a fee of Rand 1250 (approx. 130 Euro) per month applies. Students must buy their own food etc in Springbok (costs of about R 2000 or 210 Euro/month). Including extras, you should expect costs of about 300 - 400 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: At the moment we are looking for one male volunteer starting as soon as possible and one female volunteer starting in September (this is due to space constraints in the dorms). The volunteer project is ongoing, i.e. positions will also be available in 2011. Volunteers are expected to stay at least 2 months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to carsten.schradin@ieu.uzh.ch.

Please send your application BEFORE the 10th of July or after the 10th of August (no emails will be replied to that are send between 10th July and 10th August).

More information under www.stripedmouse.com Contact via e-mail: carsten.schradin@zool.uzh.ch

Dr. Carsten Schradin Research Assistant, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel: +41 -(0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

Working as a field assistant in Goegap Nature Reserve

A report by Romy Höppli, student at the University of Zurich, who staid in Goegap June to August 2008

Blue skies without a single cloud for six weeks - rocky mountains with little vegetation - yellow, orange and pink fields of flowers in whatever direction you look - small mammals, lizards and birds in our front yard and Mountain Zebras, Springbok and Ostrich right next door...

This was my time at the Succulent Karoo Research Station in Goegap Nature Reserve in South Africa! During six weeks from the beginning of July until the middle of August I’ve been living here, studying mice, experiencing nature like never before and being part of a small community where there was always something to laugh and joke about!

After arriving in Goegap, right the next morning my scientific adventure in South Africa began: Setting and checking traps, nest observations and radio-tracking were our daily routine. While I got bitten by the mice quite often in the beginning and my right middle finger was scarred all over, I

— / —

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

SwedishUAgric FieldVolunteer LifeHistoryEvolution

Field Volunteer for project investigating nest predation in Brown Thornbills

For the upcoming breeding season (Oct.-Dec. 2010) we are looking for a highly motivated volunteer to join our field project investigating nest predation in Brown Thornbills Acanthiza pusilla. The study population is located at Trevallyn Reserve next to Launceston, Tasmania (Australia). Our project researches the influence of nest predation and habitat quality on life-history strategies. The project of Dr. Michael Griesser is based at the Swedish University of Agricultural Sciences and is a collaboration withDr. Erik Wapstra the University of Tasmania.

The work of the volunteer will be to help in carrying out field experiments, locating nests, assisting the ringer in catching and banding of birds, and data management. We will work 5-6 days per week in the field. Observe that temperatures at the beginning of the breeding season can be below zero degree.

Qualifications: (1) BSc in Biology, Ecology or similar qualification (2) Previous field experience (3) Ability to work in small teams and sociable personality (4) Knowledge in observing & handling birds would be a plus (5) Driving licence would be helpful

Expenses of up to 800 Euro for travel to and from Launceston, as well as accommodation and food will be covered by the project.

Applications V including a CV, a letter of motivation (1 page) and the name of two referees V should be send to: Nicole Schneider (Nicole.Schneider@ekol.slu.se) and Michael Griesser (Michael.Griesser@ekol.slu.se).

Applications received until 15th July 2010 will be given full consideration.

Nicole Schneider Department of Ecology Swedish University of Agricultural Sciences PO Box 7044 75005 Uppsala Sweden

Nicole Schneider <nick.schnei@googlemail.com>

TravelGrants SpeciationResearch

Dear colleagues,

The European Research Networking Programme “Frontiers of Speciation Research”, supported by National Funding Organizations in16 member countries of the European Science Foundation,isinviting applications for travel grants intended to foster collaborations between European researchers working on topics related to the Programme.

Support is available for short visits (up to 2 weeks) and exchange grants (up to 3 months), with preference given to junior researchers at a graduate or postdoctoral level.

Applications are reviewed quarterly after a submission deadline of 24:00 CET on 15 March, 15 June, 15 September, and 15 December. About 4-6 weeks after each deadline, the ESF will inform applicantsabout the outcome of evaluations.

Further information and instructions on how to aplyare available at www.iiasa.ac.at/Research/EEP/-FroSpects/Travel_Grants.html .

For general information about the FroSpects Research Networking Programme, please see www.iiasa.ac.at/-Research/EEP/FroSpects .

With best wishes,

Åke Brännström & Ulf Dieckmann, on behalf of the FroSpects Steering Committee

Ulf Dieckmann <dieckmann@iiasa.ac.at>

Tropical bird feather DNA

Dear all,

I have a technical question and hope some of you are willing to share their experience with me. We are writing a grant proposal to work on a large bird species, from tropical South America.

Our experience working with feathers of (smaller) birds from colder climates has been good. - What is the feasibility of using feathers that may have been in the hot and humid tropics for several weeks? Would this have a bad effect on the quality of the DNA? - Would it be better to store the tip of the feather in ethanol or 5M NaCl as soon as possible, or would that make no difference (or even make it worse)? - What is the best/most economical extraction method: Qiagen animal kit, Chelex, or basic SDS/NaAc extraction?

Any advice welcome.

Best wishes, Kirsten

Dr Kirsten Wolff Reader in Evolutionary Genetics Newcastle University, School of Biology Newcastle NE1 7RU, UK Phone: 0191 222 5626 email: kirsten.wolff@ncl.ac.uk

Kirsten Wolff <kirsten.wolff@newcastle.ac.uk>

Viral qRT-PCR

Dear evoldir members and qRT-PCR experts,

I have started a new project and one of the techniques I want to use is the qRT-PCR.

First of all let me explain the research topic:

The barley yellow dwarf virus (BYDV, ssRNA-virus) and the wheat dwarf virus (WDV, (DNA-Virus) are widely distributed viral diseases of cereals. The virus BYDV is transmitted by aphids and WDV is transmitted by the leaf-hopper Psammotettix alienus. With the qRT-PCR I want to know which aphid or leaf-hopper carry the virus and maybe how many virus-particles.

Now my question:

What do you think is the best strategy: absolute or relative quantification? What should I use as a calibrator? Do you think I should synthesize the standards (synthetic genes)?

Thank you in advance for any advise or help!

Kind regards Nadine

Chromi@women-at-work.org

"Nadine A. Gund" <blue2.gundula@gmx.de>

Yasuni diversity

This CNN report shows the on-going struggle between advocates for preservation of the most diverse place on the planet, the impending drive for oil development, and the difficult economic choices developing countries need to make for themselves within a climate of international pressure from both companies and developed governments. The deal Ecuador has proposed could serve as an economic model of development for so many other places - please watch this at the very least to be aware. Plus, these presentations would be a great educational tool. Dr. Kelly Swing was my professor 10 years ago for an undergrad Tropical Ecology semester, for which we spent a month in Yasuni. That program was the most influential part of my entire (on-going) education, Yasuni is my favorite place in the world, and Kelly dedication continues to amaze me. http://www.cnn.com/video/data/2.0/video/international/2010/05/27/ef.amazon.research.bk.b.cnn.html If you liked that, check this out, but don't be put off by the lack of sound - it gets better as it progresses: http://www.youtube.com/watch?v=gdJhvbvjOnk Pamela Woods Ph.C.

University of Iceland University of Washington

Pamela Woods <pamelajwoods@gmail.com>

PostDocs

Belgium EvolutionaryComputation

Three open positions for 2 PhD students and 1 postdoc in the area of evolutionary computation / bio-inspired computing Interdisciplinary research project "Bio-inspired computing for coordination and control in large-scale and dynamic systems (BioCo3)"

In this interdisciplinary project (involving computer science, biology, operations research and logistics expertise) we will study decentralized approaches for controlling large-scale, dynamic systems - e.g. for controlling a large number of vehicles that need to accomplish transport tasks for clients (package delivery service). Achieving efficient and effective collective behavior is known to be quite a challenge, esp. if the systems are large in scale and submitted to changing operating conditions. Complex collective behaviour occurs in many socio-biological systems. Social insects, e.g., are able to find the shortest path to food sources without any central control, or can build enormously complex nests with built-in ventilation systems, or divide the work such that the chances of survival are optimal.

Some socio-biological mechanisms for collective behavior have already been studied in the context of computing (e.g. stigmergy and digital pheromones, or in discrete optimization techniques, such as ant colony optimization, artificial immune systems, genetic algorithms). It becomes apparent, however, that (1) large-scale and dynamic systems still hold major challenges, and (2) many socio-biological concepts and techniques have been unexplored.

The project therefore aims to study advanced concepts and mechanisms, known from social biological systems, and their applicability in decentralized control systems. To guide the research, the project will use concrete application scenarios, based on decentralized control in pickup-and-delivery problems (PDPs), and evolutionary algorithms to evolve more efficient control strategies.

Keywords: Multi-agent systems, Discrete optimization, Sociobiology, Social Insects, Biologically-inspired computing, Pickup-and-delivery problems, Ant Colony Optimisation, Evolutionary Algorithms, Genetic Algorithms

The partners in this project are Dept. of computer science, DistriNet labs Prof. Tom Holvoet

http://distrinet.cs.kuleuven.be/ Dept. of biology, Laboratory of entomology Prof. Tom Wenseleers http://bio.kuleuven.be/ento/ Dept. of mechanics, Center for industrial management Dr. Paul Valckenaers

http://www.mech.kuleuven.be/en/cib/ Saint-Lieven College, IT department Dr. Greet Vanden Berghe

http://ingenieur.kahosl.be/personeel/greet.vandenberghe/ Requirements For this ambitious project, two PhD positions and one position for a postdoctoral researcher are open. We invite applications from:

either people who have a strong computer science background (master degree for PhD positions, PhD degree for the postdoc position) with a strong affinity and interest in biology,

or people who have a strong a biological background (master degree for PhD positions, PhD degree for the postdoc position) and strong affinity and interest in computer science. The positions are available from October 1, 2010 (negotiable). Further requirements for candidates include

having a scientific, critical attitude being ambitious having good communication and social skills, team player having an independent working style being proficient in English experience as a researcher is welcome but not mandatory for the PhD positions.

For more information and for applying... For more information about the project and the positions, and for applying for a position, please contact the project coordinator:

Prof. Tom Holvoet

DistriNet Labs - Dept. of Computer Science, KULeuven, Belgium

http://people.cs.kuleuven.be/Tom.Holvoet For more information about the KULeuven:

http://www.kuleuven.be/ The deadline for application is

July 15, 2010.

When applying, make sure to include (pdf versions of):

a detailed resume (with publications, if you have any) a motivational letter specifically referring to the open positions copies of marks and degrees/certificates a list of 3 references that we can contact your MSc thesis in English (or a 5-page summary in English).

Please forward this message to interested staff/students... – Prof. Dr. Tom Holvoet DistriNet labs Dept. of Computer Science KULeuven

http://people.cs.kuleuven.be/Tom.Holvoet Celestijnenlaan, 200A B-3001 Leuven Belgium +32 16 32.76.38

Dr. T. Wenseleers Dept. of Biology Zoological Institute K.U.Leuven Naamsestraat 59 B-3000 Leuven Belgium tel. +32 (0)16 32 39 64 mobile +32 (0)472 40 45 96 e-mail tom.wenseleers@bio.kuleuven.be web

— / —

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

---

Bergen Norway FishPopulationGenetics

The Institute of Marine Research has a two-year post doctoral research position available to work with modeling genetic interactions between wild and farmed fish. The position will be connected to the Population Genetics and Ecology research group in Bergen, Norway.

Closing date for applications: 10.07.10.

The position will be linked to the modeling workpackage in the Strategic Institute Project “INTERACT”, financed by the Norwegian research council. Building upon published data, current models and state-of the art, the work-package aims to advance models to quantify the interactions between wild and farmed fishes, for both Atlantic cod and Atlantic salmon. The ultimate aim is to identify “break points” for tolerance of genetic introgression in wild populations.

Together with members of the research team, the appointee will have responsibility for establishing, testing and publishing new models that shed light onto the consequences of farmed escapees and tolerable levels of introgression in wild populations. This will be achieved through developing models describing dynamics of wild salmon and cod populations that are interacting and potentially interbreeding with conspecific fish of aquaculture origin. Important parameters to be tested include numbers of escapees, fitness of hybrids, and behavioural interactions between wild and cultured fish.

We wish to appoint a highly motivated person with a PhD in modeling, statistical genetics, population ecology or related discipline. The appointee will need to be able to document experience of programming and use of models to study dynamical systems in biology. Previous experience with modelling of fish population dynamics is not necessary but is considered advantageous.

The Institute emphasises personal qualities such as good communication and cooperative skills, the ability to work independently and as part of an active research team. A record of publishing in this field will be considered an advantage.

We offer:

* a positive, challenging and creative work environment * the opportunity to work in a national institute with a high level of international contact * flexible hours, a good pension scheme and a wide range of welfare services.

The Institute offers governmental regulated salaries as post doctor (code 1352 post doctor).

For more information, please contact project leader Kevin Glover or research group leader Terje Svaasand. The Institute of Marine Research is an "inclusive worklife" employer that encourages diversity, and we encourage all qualified candidates to apply for this position. Women are particularly encouraged to apply.

Please note that information about applicants may be made public even if an applicant has requested to be left off the list of applicants. Applicants will be notified about this in advance

Please apply in writing, enclosing a cover letter, full CV, copies of relevant recommendations and academic transcripts together with a set of publications, to: Institute of Marine Research, Personnel Division, P.O. Box 1870 Nordnes, NO-5817 Bergen, Norway. Application number: "31-10". Closing date for applications: 10.07.10.

mikko.heino@imr.no

BrighamYoungU FlowerEvoDevo

Postdoctoral position in evolution of plant development

A postdoctoral position is available in the laboratory of Clinton Whipple (whipplelab.byu.edu) at Brigham Young University to work on an NSF funded project investigating the evolution of interactions among proteins regulating flower development. The successful candidate will employ a variety of approaches to understand the function and evolution of dimerization properties among floral homeotic B class proteins in the grass family. The project will include functional characterization of a maize B class mutant, isolation of B class genes from diverse grasses and close relatives, and assays of DNA binding and protein interaction. The candidate must have a PhD in Plant Biology, Mol/Cell biology or related field. A strong background in molecular biology, including PCR, cloning and sequence analysis, excellent oral and written communication skills, and willingness to mentor undergraduate students are required. Familiarity with EMSA, site-directed mutagenesis, and knowledge of plant development and morphology are helpful but not required. Funding is available for three years beginning September 1, 2010.

Interested candidates should send a cover letter describing their research interests and background, reasons for interest in this project, a CV and contact information for at least two references to whipple@byu.edu.

Clinton Whipple Department of Biology 679 WIDB Brigham Young University Provo, UT 84602

Office: 801 422-9293 Fax: 801 422-0090 email: whipple@byu.edu website: whipplelab.byu.edu

whipple@byu.edu

BrownU ComputationalGenomics

Postdoctoral Position in computational/functional genomics at Brown University

A postdoctoral position is available in the Fairbrother lab, at Brown University. The research will involve detecting genetic variations within the human population that alter pre-mRNA splicing. The approaches used will include RNA CLIP and high throughput binding assays to accrue binding measurements and several downstream computational analysis.

Candidates with research experience in population genetics or RNA biology or splicing will be considered:

The position can begin as early as Summer, 2010.

Applications should email a CV and any other relevant information to

Will Fairbrother fairbrother@brown.edu

Will Fairbrother <william_fairbrother@brown.edu>

Brussels BeetlePopulationGenetics

We are seeking a postdoc with skills in population genetic analyses and molecular markers, to infer the current and past dispersal of bark beetles in Europe and Siberia. I believe this should be of interest to evolutionary biologists and population biologists and would appreciate if you could post this announcement.

Best wishes,

Patrick

Postdoctoral position in molecular ecology and forest entomology We are looking for a postdoctoral candidate for a 2 years position to work on the inference of contemporary and past dispersal of the bark beetle Dendroctonus micans using molecular markers. The candidate should have a strong experience in population genetic analyses and in working with molecular markers. Experience in forest entomology will also be valued, but is not essential. The candidate will contribute to a project (see description below) funded by the Belgian Fund for Scientific Research (FNRS), and work in the laboratory of Biological Control and Spatial Ecology (http://www.ulb.ac.be/sciences/lubies/indexuk.html) and in the laboratory of Evolutionary Biology and Ecology (http://ebe.ulb.ac.be/ebe/ebe-Welcome.html). To apply, please send a CV, a statement of research interests/ experiences, and names and contact information of two references that are familiar with your work, to Jean-Claude Grégoire (jcgregoi@ulb.ac.be), before June 21, 2010. We will eventually propose one candidate for a postdoctoral grant from the FNRS (only non-Belgian candidates, who received their PhD AFTER January 2005, are eligible). The grant can start in January 2011 and salary is ca. 2000 euros/month.

Project description:

Postdoctoral position Fonds National de la Recherche Scientifique - D. micans

The aim of the proposed research will be to complement a general study of the contemporary and past dispersal of the bark beetle Dendroctonus micans (Scolytine) by analyzing its population structure with molecular markers. D. micans is probably of Siberian origin and has been gradually moving into Western Europe since the late nineteenth century. The whole life cycle of this insect occurs within the phloem of living spruces, despite the presence of toxic monoterpenes in the resin. The larvae are gregarious. The sex ratio is unbalanced, ranging from 1:10 to 1:40 in favor of females. After metamorphosis, the young males mate with their sisters, so that 98% of the emerging females are fertilized by their brothers. Each female is then immediately able to colonize a new host. The adults are not gregarious and attack their host tree solitarily. For a long time, it was thought that the males never leave their natal gallery, because they mate within them. However, males have recently been trapped in the forest (passive interception traps) in ratios similar to those observed in the galleries. This raises questions over the fate of these males and over the function of their flights. Do the flying males enter other chambers containing preemergent broods, or do they join their sisters in their new galleries? Only one adult female is usually found in the newly formed egg galleries. A preliminary study of genetic variation suggests low levels of variation within populations, but has identified a couple of microsatellite loci for which different alleles are fixed in different populations sampled in France and Belgium. The proposed postdoc will focus on the indentification of additional molecular markers and their use for characterizing the genetic structure of D. micans populations. These molecular data will be combined with behavioral data and a field study directly assessing the movement of the beetles, in order to increase our understanding of the dispersal strategy of this insect pest.

Patrick Mardulyn Evolutionary Biology and ecology, CP 160/12 Free University of Brussels (ULB) av. FD Roosevelt 50 1050 Brussels Belgium

Phone: (32)(2)6502649 Fax: (32)(2)6502445 e-mail: pmarduly@ulb.ac.be

homepage: homepages.ulb.ac.be/~pmarduly/ lab website: www.ulb.ac.be/sciences/ecoevol/index_EN.html
Patrick <pmarduly@ulb.ac.be>

Cambridge KAUST-mosquito genomics

Applications are invited for two experienced and keen postdocs to work on genomic and transcriptomic variation in mosquitoes. The project will use Illumina sequencing to characterise natural variation in the genome and transcriptome of the disease vector Aedes aegypti, and to link this to variation in the ability of mosquitoes to transmit disease.

The project is a collaboration between Dr Arnab Pain (KAUST, Saudi Arabia) and Dr Frank Jiggins (Dept of Genetics, University of Cambridge, UK), which is funded for two years from 1 October 2010. There will be one position in each laboratory, with close collaboration and exchanges between the labs. Applicants must have a PhD or equivalent in genetics or bioinformatics and relevant research experience. The position at KAUST is for a bioinformatician and requires familiarity with handling large genomic datasets. The postdoc in Cambridge will involve analysis of the assembled genomes together with rearing of mosquitoes and molecular biology.

The positions come with a competitive salary and benefits package. Closing Date: 16 July 2010. Limit of tenure: 30 September 2012.

Applications for the position at KAUST should be made to Arnab Pain (arnab.pain@kaust.edu.sa).

For the position at Cambridge, please direct informal enquiries to Frank Jiggins (fmj1001@cam.ac.uk). Completed applications, which should consist of a completed CHRIS/6 application form (Parts I and III) - see http:/-/www.admin.cam.ac.uk/offices/hr/forms/chris6/ - and a full CV, should be sent to Ms Catherine Tinley, Dept of Genetics, Downing St, Cambridge CB2 3EH. e-mail: cjt59@hermes.cam.ac.uk

fmj1001@cam.ac.uk

ColoradoStateU SalamanderTransposableElements

Post-Doctoral Position Mueller Lab Department of Biology Colorado State University

An NSF-funded post-doctoral position in evolutionary genomics is available in the Biology Department at Colorado State University. The position is focused on genome evolution in plethodontid salamanders, which have among the largest vertebrate genomes: 15 to ~75 Gb. Although such genomes are known to consist largely of repetitive DNA, the repeat elements, their mutational dynamics, and the ways in which these dynamics translate into large and variable genome sizes remain almost completely uncharacterized. The postdoc will use next-gen sequencing data to study the mutational processes underlying this extreme genomic expansion.

The postdoc will interact with collaborators at UC Denver (David Pollock, the Consortium for Comparative Genomics) and UT Arlington (Cédric Feschotte) to 1) identify and characterize novel repeat elements from several species of plethodontids, which diverged ~40-90 mya, and 2) analyze the tempo and mode of repeat element evolution, and the relationship with genomic expansion, in a phylogenetic context. These results will be combined with ongoing comparative methods-based analyses of plethodontid genome size evolution.

A Ph.D. in evolutionary or comparative genomics, or in a closely-related field, is required by the position start-date. The position is available as soon as a suitable candidate is identified. Start-date is negotiable.

The Department of Biology at Colorado State University is an interdisciplinary group with a strong crew of evolutionary biologists. Fort Collins is a beautiful city of 120,000 people located at the base of the Rocky Mountains. We enjoy easy access to world-class outdoor recreation and 300+ days of sunshine each year.

To apply for the position, please e-mail the following application materials (as a single pdf file, if possible) to MuellerLabPostdoc@gmail.com: (1) CV, (2) one-page statement of research interests, (3) up to three recent publications (or, alternatively, include url's for paper downloads within your CV), and (4) contact information for three references. For full consideration, materials must be received no later than Wednesday, July 21, 2010. However, applications will be accepted until the position is filled.

For questions or informal inquiries about the position, please contact Rachel Mueller: Rachel.Mueller@colostate.edu (970) 491-6717 http:/-/rydberg.biology.colostate.edu/muellerlab/Home.html CSU is an EO/AA employer. CSU conducts background checks on all final candidates.

rlm@colostate.edu

ETH Zurich Entomology

Postdoctoral Research Assistant in Entomology

ETH Zurich, Applied Entomology

The project deals with effects of climate change, focusing on temperature-dependent flight characteristics and associated life history traits in an invasive fruit moth species. To predict further spread of this pest into hitherto uncolonized areas, we want to understand the magnitude of its potential to adapt to changing environments. Little is known about how insect flight characteristics change with ambient temperature conditions experienced during flight (acclimation), during development (developmental plasticity), and experienced over two generations (cross-generational effect). A computer-linked apparatus will be used for comparative assessment of insect flight performance.

Education: PhD with experience in insect behaviour

Entrance upon July 15, 2010, or upon agreement

Duration of appointment: 1 year, with option for extension based on performance and opportunity

Review of applications will start immediately and continue until a suitable candidate is found. Send Curriculum Vitae, a list of methods you are familiar with, indication of the earliest possible starting date, as well as addresses with phone numbers of three references to Prof. Dr. Silvia Dorn.

ETH Applied Entomology investigates insect-plant interactions, particularly as a basis for more sustainable pest and crop management. Main languages spoken are English and German.

For further information you may contact Dr. Dominique Mazzi (dominique.mazzi@ipw.agrl.ethz.ch)

Contact address:

Prof. Dr. Silvia Dorn ETH Zurich / Applied Entomology (Subject: Postdoc Insect Behaviour) Schmelzbergstrasse 9 / LFO CH-8092 Zurich

Email: silvia.dorn@ipw.agrl.ethz.ch Subject: Postdoc Insect Behaviour

http://www.em.ipw.agrl.ethz.ch

dominique.mazzi@ipw.agrl.ethz.ch

Finland 2 MolecularSystematics 2

Apologies, the deadline for applying for the recently advertised positions is 30 JUNE 2010, not July as in the original e-mail. My mistake. Here is the advertisement again (with the correct dates):

Two postdoctoral positions are available in the newly funded project “Diversification of plant-feeding insects over millions of years: what is the role of dramatic climate changes?” (funding from the Kone Foundation) headed by Niklas Wahlberg (University of Turku, Finland) and Tommi Nyman (University of Eastern Finland). A strong background in molecular systematics is required for both positions. The positions are available for one year starting in September 2010, with a possibility to extend for a second and third year. Salary will be 2100euro per month (non-negotiable) paid as a tax free stipend up to 18,800euro per year, with 6400euro per year subject to taxes (in practice, about 1900euro per month net income). One postdoc will work in Turku, Finland, the other in Joensuu, Finland, with active interaction planned between research groups.

The postdoc in Turku will work in the research group of Niklas Wahlberg (http://nymphalidae.utu.fi), expanding the work on Nymphalidae butterflies to other lepidopteran groups (Geometridae and Noctuoidea). The major focus of this postdoc will be to generate new molecular data for geometrid moths, assist in generating molecular data for noctuids, and take responsibility in analyzing resulting data using phylogenetic methods. The candidate should particularly be familiar with methods used to analyze changes in rates of diversification over evolutionary time (e.g., with algorithms in programs such as SymmeTree and Medusa). Interested persons should send their CV, a statement of why they are interested, and contact information of two references to Niklas Wahlberg (niklas.wahlberg@utu.fi) by the 30 JUNE 2010.

The postdoc in Joensuu will work in the research group of Tommi Nyman (www.joensuu.fi/biologia/nyman), and focus on the diversification history of sawflies (the mostly herbivorous basal grade of Hymenoptera). The first task of this postdoc will be to increase the number of easily amplifiable nuclear genes to be used for phylogenetic and timing of diversification analyses. The candidate should be familiar with whole-genome databases, publicly available EST libraries, primer design, and lab practices when developing new markers. The candidate will be expected to generate new molecular data for sawflies, and to take responsibility for analyzing the resulting data using phylogenetic methods. Interested persons should send their CV, a statement of why they are interested, and contact information of two references to Tommi Nyman (tommi.nyman@uef.fi) by the 30 JUNE 2010.

The project will facilitate numerous comparative analyses that will shed light on common patterns in the evolutionary radiations of two species-rich and ecologically important insect herbivore taxa. Both research groups are young, dynamic, and innovative; a perfect opportunity to take advantage of a robust background knowledge to find something new and exciting for science in a collegial atmosphere!

– Niklas Wahlberg Academy Research Fellow Laboratory of Genetics Department of Biology University of Turku 20014 Turku FINLAND

Phone: +358 2 333 5569 Fax: +358 2 333 6680 Skype: niklas_w2

Nymphalidae Systematics Group: http://nymphalidae.utu.fi niklas.wahlberg@utu.fi

FloridaStateU DrosophilaWing EvoDevo

A postdoctoral position is available to model the development of the Drosophila wing. This is part of a larger project to understand the relationship between genetic and phenotypic variation and evolutionary change using the Drosophila wing as a model organ. The position is part of a collaborative project involving David Houle (Florida State University), Isaac Salazar-Ciudad (Universitat Autonoma de Barcelona) and Ian Dworkin (Michigan State University). Primary responsibility of this position is construction of a cell-based model of morphogenesis, differentiation and growth that will interface with sub-cellular models of gene interactions. The winning candidate will also collaborate with a larger team to compare model to empirical results, to test and refine the model, and use the model to make evolutionary predictions. Preference will be given to candidates with experience in computational and analytical modeling , and a desire to fuse developmental, genetic and evolutionary approaches to fundamental questions about the relationship between genotype and phenotype.

The position is for an initial period of two years, and may be extended for an additional two years. It will be supervised by Houle and Salazar-Ciudad. Applications should be submitted as a single pdf file and include a curriculum vitae, a summary of research accomplishments and future research objectives, and the names and contact information for at least one professional reference (and preferably three). Review of applications will begin July 15, 2010 and continue until a suitable candidate is identified. Application materials should be sent electronically to David Houle (dhoule@bio.fsu.edu). Florida State University is an Affirmative Action / Equal Opportunity Employer.

Candidates who are attending the Society for the Study of Evolution meeting are encouraged to contact Houle (dhoule@bio.fsu.edu) to arrange an interview. Candidates who are attending the European Evo Devo meeting are encouraged to contact Salazar-Ciudad (Isaac.Salazar@uab.cat) to arrange an interview.

David Houle

Phone: 850-645-0388 FAX: 850-645-8447 http://bio.fsu.edu/~dhoule/ Department of Biological Science Florida State University 319 Stadium Drive Tallahassee, FL 32306-4295

dhoule@bio.fsu.edu

GhentU SystemsBiology

Postdoc position in Systems Biology

The Division of Bioinformatics and Systems Biology at the VIB Department of Plant Systems Biology, Ghent University invites applications for an Expert Scientist position in the field of Computational Systems Biology. We seek highly-motivated individuals with an interest in developing novel algorithms and software tools for the integration of high-throughput genomic data and the inference and modeling of regulatory networks. The ideal candidate should hold a doctoral degree in a relevant field (physics, computer science, applied mathematics, engineering or life sciences), with several years of postdoctoral experience, and have a proven record of its application for the life sciences.

Major duties include:

- Responsible for the functioning of a small group of researchers (PhD students and postdocs). - Develop new and innovative (breakthrough) projects in line with the strategic plan of the Department and VIB. - Provide scientists in the Department and VIB with transfer of in-depth knowledge. - Transfer science into publications in high impact journals. - Detect potential technology transfer possibilities.

The position will initially be available for 2 years (starting September 1st 2010), with the possibility of a 3 year extension depending on positive evaluation. For further information please consult our homepage (http://bioinformatics.psb.ugent.be/) or contact the Scientific Director Prof. Dr. Yves Van de Peer (yves.vandepeer@psb.vib-ugent.be).

Applications including a motivation letter, CV, list of publications, names and contact information of three references and a research proposal (2-3 pages) should be sent to Prof. Dr. Yves Van de Peer before July 1st 2010.

– Yves Van de Peer, PhD.

Professor in Bioinformatics and Genome Biology Associate Department Director, VIB Department of Plant Systems Biology Group Leader Bioinformatics and Systems Biology Ghent University Technologiepark 927 B-9052 Ghent Belgium

Phone: +32 (0)9 331 3807 Cell Phone: +32 (0)476 560 091 Fax: +32 (0)9 331 3809 email: yves.vandepeer@psb.vib-ugent.be

http://bioinformatics.psb.ugent.be/ Yves Van de Peer <yves.vandepeer@psb.vib-ugent.be>

ImperialCollegeLondon PopulationGenomics

Research Associate in Population Genomics at Imperial College London

The Research Associate in Population Genomics will join the Department of Infectious Disease Epidemiology based at St Mary's campus as well as be expected to interact with collaborating research groups in Cambridge. The successful candidate will additionally spend some time in Professor Mark Stoneking's laboratory in Leipzig.

The post holder will be closely involved in a long term project aiming at understanding the relative role of past demography and natural selection in shaping the human genome. More specifically, he/she will be focusing on high throughput sequencing and will be, in particular, responsible for generating about 2,000 complete human mitochondrial genomes. These sequences will allow quantifying to what extent past climate has shaped worldwide human mitochondrial sequence variation.

For informal enquiries please contact Francois Balloux f.balloux@imperial.ac.uk.

Applications should be submitted through the following URL:

< https://www4.ad.ic.ac.uk/-OA_HTML/OA.jsp?akRegionCode=-3DIRC_VIS_VAC_DISPLAY_PAGE&akRegionApplicationId=-800&OASF=IRC_VIS_VAC_DISPLAY&OAHP=-IRC_EXT_SITE_VISITOR_APPL&transactionid=-1826533789&retainAM=Y&addBreadCrumb=-RP&p_svid=17675&p_spid=898025&oapc=48&oas=-OSKPj4kLC0g_p2Eies1U2g >

Dr François Balloux MRC Centre for Outbreak Analysis and Modelling, Department of Infectious Disease Epidemiology, Faculty of Medicine, Imperial College, St Mary's Campus, Norfolk Place, London W2 1PG, United Kingdom Tel: 0044 (0)20 7594 3260 E-mail: fballoux@imperial.ac.uk Web: http://www1.imperial.ac.uk/medicine/people/-f.balloux/ f.balloux@imperial.ac.uk

IndianaU ReproductiveDiversity

Evolution is one of the 3 themes of this training grant (along with development and neuroscience).

The wording has been approved by our employment office so I am not free to modify it.

but I can tell you that the training faculty on this training grant includes a set of evolutionary biologists, e.g. Curt Lively, Mike Wade, Armin Moczek, Emilia Martins (and me too), and we hope to recruit post-docs who have trained with evolutionary biologists.

you will find the words evolution of development in the ad.

the reason I lead with sexual health and gender studies is that I am also trying to broaden the net since most of the people who have applied in the past have been evolution of behavior people and we are striving for interdisciplinary

This is a link to the faculty on this training grant.... we are a varied group, but we are firmly rooted in evolution studies.

http://www.indiana.edu/~reprodiv/faculty.htm Ellen Ketterson ketterso@indiana.edu Distinguished Professor of Biology

Indiana University invites applications for up to two post-doctoral traineeships to be supported by NICHD via an NIH T32 training grant entitled, 'Common Themes in Reproductive Diversity.' We offer broadly integrative training in the areas of sexual reproduction and development with a focus on the behavior of animals including humans. Research conducted by participants addresses key questions in the development and expression of sex differences, as well as maternal and paternal effects on morphological, sexual, and social development. Indiana University's excellent support for research and its globally recognized strengths in human sexual health, gender studies, animal behavior, endocrinology, and the evolution of development ensure high quality training. For more information see http://www.indiana.edu/~reprodiv/index.htm We welcome candidates interested in human as well as nonhuman behavior who wish to train across disciplinary lines.

Traineeships include a competitive salary based on current NIH pay scale commensurate with experience, and modest funds to support research and travel. The successful applicant will help foster collaborations among faculty and serve as a professional model for predoctoral trainees. A Ph.D. in gender studies, psychology, biology, neuroscience, chemistry, or a related field is required. Candidates are invited to make initial contacts with training faculty http://www.indiana.edu/~reprodiv/faculty.htm To apply, please visit the following website to find instructions and forms to download: http://www.indiana.edu/~reprodiv/apply/ Please e-mail your completed application to Linda Summers at lisummer@indiana.edu or (less desired) mail it to 402 N. Park Street, Bloomington, IN 47405. The email subject line should read: CTRD Post-doc Application. For full consideration, applications should arrive by 15 August 2010, although later applications will be considered. The search will continue until the positions are filled. Please note that one of the lines must begin on or before April 2011, and the second line would not become available before May 2011. If you have specific questions about the process or fellowships, please contact Ellen Ketterson (ketterso@indiana.edu) who will answer your questions or forward your inquiry to the appropriate person.

Minority applicants are especially encouraged to apply. Trainees must be citizens, non-citizen nationals, or permanent residents of the US. Indiana University is an Equal Opportunity / Affirmative Action Employer.

Ellen Ketterson ketterso@indiana.edu

IowaStateU EvolBiology

ISU is soliciting applications for a post-doctoral position for a scientist interested both in research and in pedagogy. This is a split position, about half "scientific pedagogy", and the remainder more traditional scientific research in a host laboratory. The latter can be with any faculty member at ISU willing to host the post-doc. The formal ad follows:

Science Teaching Fellow

The Howard Hughes Program for Innovation in Undergraduate Science Education at Iowa State University invites applications for two Post-doctoral Science Teaching Fellow positions in the fields of Biology and Chemistry. Specific responsibilities of these grant-funded positions will include working in coordination with science faculty to identify specific learning goals for core undergraduate courses, decide on assessments of student progress toward these goals, and develop and prototype innovative in-class and out-of-class course activities and laboratory materials to promote student learning. Fellows will have the opportunity to join a research group, providing additional opportunities for scholarship, publication, and professional development in the sciences. ISU is located in a vibrant college town and is committed to excellence and world-class diversity.

Qualified candidates must have a Ph.D. in the biological sciences, chemistry, or science education; excellent organizational and interpersonal communication skills; teaching experience; and have the potential for contributing to science education scholarship and research. To apply, send the following to cesmeestaff@iastate.edu: a cover letter briefly summarizing qualifications, curriculum vitae, a statement of scholarly interests and expertise, and contact information for three references. For questions regarding this position, please contact Prof. Ogilvie at cogilvie@iastate.edu. Review of applications will begin on June 28, 2010 and will continue until the position is filled.

Applications from women and members of under represented groups are strongly encouraged. Iowa State University is an EO/AA employer.

Jonathan F. Wendel, Professor and Chair Department of Ecology, Evolution, & Organismal Biology, Iowa State University Ames, IA 50011 Voice (515) 294-7172; FAX 515-294-1337; jfw@iastate.edu http://www.eeob.iastate.edu/faculty/WendelJ/ (Personal home page) http://www.eeob.iastate.edu/ (Department home page)

"Wendel, Jonathan F [EEOBS]" <jfw@iastate.edu>

LavalUniv Quebec SylvicultureAndCommunities

POST-DOCTORAL RESEARCH PROJECT RESEARCH CHAIR IN SYLVICULTURE AND

WILDLIFE

The NSERC-Université Laval Industrial Research Chair in Silviculture and Wildlife has research opportunities for one post-doctoral fellow to participate in its research program. This program seeks to develop silviculture systems suited for the sustainable management of uneven-aged boreal forests. The post-doctoral project should commence no later than August 2010, with a duration of 1-2 years. A fellowship of 35,000$ per year will be available.

* Research theme 1: Modelling animal communities in managed boreal forest. The project aims to model animal-habitat relationships in the managed forests of the Côte-Nord region of Québec. The study will integrate information on forest structure, composition, and management with data on animal communities that have been collected as part of the chair's studies. Species groups to be considered include invertebrates, forest birds, and small mammals. A number of indicator species have been identified in uncut forests. We now need to determine whether these species are also adequate indicators of local species assemblages in post-logging forests. The following article presents one way to analyse the data:

Azeria et al. 2009. Using null model analysis of species co-occurrences to deconstruct biodiversity patterns and select indicator species. Diversity and Distributions 15: 958-71.

The study should also evaluate the response of the indicator species to landscape characteristics in order to subsequently map broad-scale patterns of biodiversity.

* Research theme 2: Response of animal communities to various silvicultural practices. The post-doctoral fellow could characterize the impact of silvicultural practices on the foraging behaviour of small mammals. The results should reveal spatio-temporal variations in the perception of foragers to predation risk and competition intensity. The following paper presents a similar study:

Lemaître et al. 2010. Deer mice mediate red-backed vole behaviour and abundance along a gradient of habitat alteration. Evolutionary Ecology Research 12: 203-16.

The post-doctoral fellow could also become involved in other on-going studies. We are therefore looking for candidates with broad interests and skills. Please visit "www.sylvifaune.ulaval.ca" to find out more about the chair's studies.

The post-doctoral fellow will have administrative responsibilities, which include: 1. Writing scientific papers, progress reports, and posters. 2. Helping to plan and supervise fieldwork. 3. Maintaining the project's database; as well as supervising and verifying contributions from employees and students. 4. Developing and maintaining links with practitioners, managers and researchers in order to promote an exchange on chair-related work. 5. Advising and assisting researchers and students in their studies.

Qualifications: Hold a PhD in terrestrial ecology, forestry, biostatistics or related field. Have extensive research experience in animal or community ecology. Have in-depth knowledge of ecological modelling and contemporary multivariate statistical methods. Be familiar with the use of Geographic Information Systems. Université Laval is a French university and some basic French is an asset.

Documents to provide by email: Applicants for this position should forward me a short cover letter indicating their motivation, accompanied by a current CV and the names and contact information of three references. We will begin to review the applications on July 2nd 2010:

Daniel Fortin Département de biologie, Pavillon Alexandre-Vachon, 1045, av. de la Médecine, Université Laval, Québec (Qc) G1V 0A6, Canada Email: Daniel.Fortin@bio.ulaval.ca

basille@biomserv.univ-lyon1.fr

MaxPlanckInst Jena InsectBacteriaSymbioses

Postdoctoral Positions in the Insect Symbiosis Research Group

The Insect Symbiosis Research Group at the Max Planck Institute for Chemical Ecology in Jena (http://www.ice.mpg.de/kal/home/home_de.htm?mp=369) studies the evolution and chemical ecology of insect-bacteria symbioses. Two postdoctoral positions are available immediately.

Postdoctoral fellowship Molecular ecology of a defensive insect-bacteria symbiosis Solitary digger wasps of the genus Philanthus cultivate Streptomyces bacteria in specialized antennal glands that protect the wasp offspring in the cocoon against pathogen infestation by producing a cocktail of antibiotics. One postdoctoral position is available to study the benefits of the symbiosis for the bacterial partner as well as to elucidate the diversity and synergistic activity of antibiotic substances produced by the symbionts to protect the insect host. We are seeking a highly motivated candidate with strong communication and excellent organizational skills who can operate in an interdisciplinary research environment. The successful candidate should have a strong background in chemical-analytical techniques (e.g. GC-MS, HPLC-MS, proteomics, lipidomics, MALDI-imaging) as well as a profound interest to work in evolutionary ecology. Applicants should have a PhD in biochemistry, chemical ecology, evolutionary biology or a closely related field.

Postdoctoral fellowship Comparative Genomics of symbiotic Streptomyces strains in beewolves All digger wasp species of the genera Philanthus and Trachypus that have thus far been investigated cultivate bacteria of a specific group of Streptomyces in their antennal glands. The symbionts produce a diverse set of antibiotics to protect the wasp larvae against fungal and bacterial pathogens. One postdoctoral position is available to study the evolutionary history of the symbiotic interaction between digger wasps and Streptomyces and the genetic basis of antibiotic production by using a comparative genomics approach. We are seeking a highly motivated candidate with strong communication and excellent organizational skills who can operate in an interdisciplinary research environment. The successful candidate should have experience in whole-genome sequencing using next-generation sequencing technologies, a strong bioinformatics background to handle and analyze genome-scale datasets (including programming skills, e.g. Perl) as well as a profound interest in evolutionary ecology. Applicants should have a PhD in molecular ecology, evolutionary biology or a closely related field.

The Max Planck Institute is an equal-opportunity employer and especially encourages women to apply. Applications from handicapped persons will be favored when all other qualifications are equal.

Please send your applications (including cover letter with statement of purpose and previous research experience, CV, and contact information for 2 referees) until July 31, 2010 to:

Dr. Martin Kaltenpoth Max Planck Institute for Chemical Ecology Research Group Insect Symbiosis Hans-Knöll-Str. 8 07745 Jena Germany Email: mkaltenpoth@ice.mpg.de Fax: ++49-3641-571810

– Dr. Martin Kaltenpoth Max Planck Research Group Leader Max Planck Institute for Chemical Ecology Research Group Insect Symbiosis Hans-Knoell-Str. 8 07745 Jena Phone +49-3641-571800 Fax +49-3641-571810 Email: mkaltenpoth@ice.mpg.de

mkaltenpoth@ice.mpg.de

MichiganStateU EvolutionaryGenetics

Postdoc in Behavioral Ecology and Evolutionary Genetics Michigan State University

I am looking to fill a postdoc position in sexual selection and genetics of speciation, focused on measuring selection in the wild at the genetic level. The project uses a manipulative field experiment to directly test how sexual selection acts on genomic regions conferring sexual isolation. We work with the charismatic threespine stickleback, and are interested in selection through female choice and male competition, and both behavioral and morphological traits. We combine selection and genetic studies in nature to address several fundamental questions: 1) What is the genetic basis of sexual isolation in natural populations? 2) How does sexual selection act in nature on the genetic elements that underlie sexual isolation? 3) How is genetic variation maintained in sexually selected traits?

Responsibilities include conducting a large scale field behavior experiment, generating the mapping population, genotyping and genetic mapping, analyzing data, and preparing manuscripts. The ideal candidate has excellent field skills, including with field behavior experiments and/or facility with evolutionary genetics and genetic mapping. This is a rare combination, so expertise with one area and keen interest in the other is fine. I am looking for a scientist who is creative, collaborative, and committed, and who wants to train in an integrative lab that is passionate about behavioral evolution, its selective causes, and its genetic underpinnings. Good writing skills and strong publication record a definite plus. There will be opportunities to learn new techniques, to supervise students, and to do independent work. A PhD in Evolution, Behavior, Ecology or a related field is required.

Appointment initially for 1 year with possibility of renewal up to 3 years. Funding is through an NSF CAREER grant and BEACON (an NSF Science and Technology Center focused on evolution in action). As such, the postdoc will be part of a dynamic group of evolutionary biologists encompassing evolutionary ecology, evolutionary genetics, behavioral ecology, and evolutionary computing at Michigan State University. The group is stellar, and provides an exceptional scientific environment. http://www.zoology.msu.edu/all-faculty/janette-boughman.html http://www.zoology.wisc.edu/-faculty/Bou/index.htm http://www.beacon.msu.edu/ http://eebb.msu.edu/index.php Apply via email by sending a single pdf file with letter of interest including a summary of research accomplishments and future goals, CV, and 3 reference contacts to Jenny Boughman (boughman@msu.edu). Please use the following in the subject line: Postdoc MSU Sexual selection and speciation genetics

Start date is negotiable but available Aug 15. Applications will be considered until the position is filled. I will also be at the Evolution meeting in Portland Oregon June 25-29 and can arrange to meet there. Michigan State University is an Affirmative Action / Equal Opportunity Employer.

Jenny Boughman Associate Professor Zoology, Ecology Evolution & Behavioral Biology, BEACON Michigan State University boughman@msu.edu

Jenny Boughman <jboughman@wisc.edu>

MichiganStateU KBS MicrobialEvoEcol

A postdoctoral research position is available in the Lennon Lab at Michigan State University's W.K. Kellogg Biological Station (KBS). Applicants may propose their own research or collaborate on one of the ongoing projects in the lab that focuses on microbial dormancy, functional traits and microbial biodiversity, resource subsidies in aquatic food webs, the ecology and evolution of virus-bacteria interactions, and the evolutionary ecology of plant-soil feedbacks. For more details on the research conducted in the Lennon Lab see http://-/microbes.kbs.msu.edu . The primary responsibility of the postdoc will be to develop a new project or take the lead on one of the above-mentioned existing projects. This will include implementation of experiments, data analysis, and manuscript preparation. The postdoc will be in residence at KBS (http://www.kbs.msu.edu/), which has an excellent infrastructure for conducting microbial, evolutionary, community, and ecosystem ecology. The postdoc will also have the opportunity to collaborate with people in the Department of Microbiology & Molecular Genetics (www.mmg.msu.edu); the Ecology, Evolutionary Biology, and Behavior Program (www.eebb.msu.edu); and the KBS Long-Term Ecological Research (LTER) site (www.lter.kbs.msu.edu).

Highly qualified applicants will have experience in ecological and evolutionary theory; PCR-based microbial analyses, including phylogenetic and metagenomic analyses; quantitative methods, including statistics, simulation modeling, and bioinformatics; microbial physiology, including culture-based approaches; and fieldwork in aquatic and/or terrestrial ecosystems.

Applicants must have a Ph.D. in Ecology, Evolution, Microbiology or a related field. Two years of funding is available. The position is available immediately, although the start date is somewhat flexible. Interested parties should email a cover letter explaining why they are interested in the position, a CV, and a brief statement of research interests to Jay Lennon (lennonja@msu.edu). Applications will be evaluated as they are received and will continue until the position has been filled.

lennonja@msu.edu

MichiganStateU PlantAdaptationGenetics

Postdoctoral Position in Plant Ecological Genetics Michigan State University

A postdoctoral position is available to conduct research on the ecological genetics of adaptation in the model plant Arabidopsis thaliana. This is one of several positions associated with a multi-investigator, collaborative project to identify the traits, genes and gene networks involved in adaptation to natural environments. Team members include Doug Schemske (Michigan State University; evolutionary ecology, adaptation, speciation), Mike Thomashow (Michigan State University; gene regulatory networks, transcriptome, molecular genetic analysis of cold acclimation), John McKay (Colorado State University; physiological adaptation, drought tolerance), Barbara Demmig-Adams and William Adams (University of Colorado; photosynthesis and photoprotection) and Jon Agren (Uppsala University; adaptation, plant evolutionary ecology). Our research addresses the following questions: 1) What are the Quantitative Trait Loci (QTL) that contribute to adaptation in nature and to key traits involved in adaptation. 2) How does the substitution of adaptive QTL influence the phenotype, gene expression/regulation and plant fitness? 3) Are there adaptive tradeoffs between traits and/or pleiotropy between adaptive QTL? 4) What are the individual genes underlying adaptive QTL?

The research associated with this particular position will be conducted in close collaboration with Doug Schemske (MSU) and Jon Agren (Uppsala University). Responsibilities include fieldwork in Europe (Italy, Sweden) to establish and monitor large-scale field experiments, laboratory research in Michigan to conduct QTL mapping of Recombinant Inbred Lines and to produce Near Isogenic Lines, data analysis and the preparation of manuscripts for publication, and assistance in the organization of workshops on career development. Preference will be given to candidates with a background in ecology, population and/or evolutionary biology, experience with field experiments, familiarity with molecular techniques, and a basic understanding of techniques for genetic mapping and gene discovery. Nevertheless, the primary criteria for consideration are creativity, enthusiasm and the desire to fuse ecological and genetic approaches for addressing fundamental questions in evolutionary biology. A background in plants is desirable but not required.

Applications should be submitted as a single pdf file and include curriculum vitae, a summary of research accomplishments and future research objectives, and the names and contact information for three professional references. The review of applications will begin July 15, 20101 and continue until a suitable candidate is identified. This is a 12-month appointment with extension for one or more years contingent on performance. A Ph. D. is required. The start date is negotiable. Application materials should be sent electronically to Douglas Schemske (schem@msu.edu). Michigan State University is an Affirmative Action / Equal Opportunity Employer.

1. Candidates who are attending the June Evolution meetings are encouraged to contact Schemske to arrange an interview (available dates are June 25 and 26).

Douglas Schemske <schem@msu.edu>

MIchiganStateU SexualSelectionSpeciation

Postdoc in Behavioral Ecology and Evolutionary Genetics Michigan State University

I am looking to fill a postdoc position in sexual selection and genetics of speciation, focused on measuring selection in the wild at the genetic level. The project uses a manipulative field experiment to directly test how sexual selection acts on genomic regions conferring sexual isolation. We work with the charismatic threespine stickleback, and are interested in selection through female choice and male competition, and both behavioral and morphological traits. We combine selection and genetic studies in nature to address several fundamental questions: 1) What is the genetic basis of sexual isolation in natural populations? 2) How does sexual selection act in nature on the genetic elements that underlie sexual isolation? 3) How is genetic variation maintained in sexually selected traits?

Responsibilities include conducting a large scale field behavior experiment, generating the mapping population, genotyping and genetic mapping, analyzing data, and preparing manuscripts. The ideal candidate has excellent field skills, including with field behavior experiments and/or facility with evolutionary genetics and genetic mapping. This is a rare combination, so expertise with one area and keen interest in the other is fine. I am looking for a scientist who is creative, collaborative, and committed, and who wants to train in an integrative lab that is passionate about behavioral evolution, its selective causes, and its genetic underpinnings. Good writing skills and a strong publication record a definite plus. There will be opportunities to learn new techniques, to supervise students, and to do independent work. A PhD in Evolution, Behavior, Ecology or a related field is required.

Appointment initially for 1 year with possibility of renewal up to 3 years. Funding is through an NSF CAREER grant and BEACON (an NSF Science and Technology Center focused on evolution in action). As such, the postdoc will be part of a dynamic group of evolutionary biologists encompassing evolutionary ecology, evolutionary genetics, behavioral ecology, and evolutionary computing at Michigan State University. The group is stellar, and provides an exceptional scientific environment. http://www.zoology.msu.edu/all-faculty/janette-boughman.html http://www.zoology.wisc.edu/-faculty/Bou/index.htm http://www.beacon.msu.edu/ http://eebb.msu.edu/index.php Apply via email by sending a single pdf file with letter of interest including a summary of research accomplishments and future goals, CV, and 3 reference contacts to Jenny Boughman (boughman@msu.edu). Please use the following in the subject line: Postdoc MSU Sexual selection and speciation genetics

Start date is negotiable but available Aug 15. Applications will be considered until the position is filled.

I will also be at the Evolution meeting in Portland Oregon June 25-29 and can arrange to meet there.

Michigan State University is an Affirmative Action / Equal Opportunity Employer.

Jenny Boughman Associate Professor Zoology, Ecology Evolution & Behavioral Biololgy, BEACON Michigan State University boughman@msu.edu

Jenny Boughman <jboughman@wisc.edu>

Neustadt Germany ChickenGenomics

Post-doc position in chicken genomics and biodiversity available

A three year post-doc position in the field of chicken genomics and biodiversity is available at the Friedrich-Loeffler-Institute, Institute of Farm Animal Genetics Mariensee, 31535 Neustadt, Germany, to start 1st August 2010.

The postdoctoral researcher will be working on a project which is part of an interdisciplinary network for genome based research in plants and animals (Synbreed), funded by the German Ministry of Education and Research (BMBF). For more information regarding the project go to www.synbreed.tum.de . Description of Research Project: A wide range of chicken breeds will be genotyped with a high density chicken SNP array. The resulting data is a vital source for population genomic analysis to assess phylogenetic history and relationships between populations and individuals. Multivariate methods will be used for data analysis to identify new ways to combine molecular genetic and phenotypic information in biodiversity studies. The successful candidate will contribute to tasks associated with understanding of the importance of biodiversity in farm animal species and its molecular mechanisms based on next generation genotyping and sequencing as well as the application of sophisticated statistical methods. The post will be part of the Breeding and Genetics Research group at the Mariensee Institute (FLI) http://www.fli.bund.de/de/startseite/forschung-institute.html . Required qualifications of applicant: PhD degree in animal genetics or population biology; background and interest in animal domestication biology. Desirable skills include knowledge in molecular techniques as next generation genotyping and sequencing, solid statistical background (preferably including Bayesian methods, multivariate analyses, LD based methods) as well as experience in usage of statistical software packages, and skills in data analysis for genetic studies. The applicant should be enthusiastic and self- motivated.

A 1-page cover letter of interest, a CV and contact information with two references should be sent to Dr. Steffen Weigend (steffen.weigend@fli.bund.de). The application should be sent by 9th July 2010. Salary is based on grade EG13 for 39 hours per week for a period of 36 months.

Steffen Weigend Breeding and Genetic Resources Group, FLI

Institute of Farm Animal Genetics, Friedrich-Loeffler-Institut Hoeltystrasse 10 31535 Neustadt Germany

Tel: +49 (0) 5034 871 180 Fax: +49 (0) 5034 871 143 email: steffen.weigend@fli.bund.de Web site: http://www.fli.bund.de/ linn_groeneveld@eva.mpg.de

Norway FishGeneticInteractions

Post Doctoral position: Modeling genetic interactions between wild and farmed fish

The Institute of Marine Research has a two-year post doctoral research position available to work with modeling genetic interactions between wild and farmed fish. The position will be connected to the Population Genetics and Ecology research group in Bergen.

The position will be linked to the modeling work-package in the Strategic Institute Project “INTERACT”, financed by the Norwegian research council. Building upon published data, current models and state-of the art, the work-package aims to advance models to quantify the interactions between wild and farmed fishes, for both Atlantic cod and Atlantic salmon. The ultimate aim is to identify “break points” for tolerance of genetic introgression in wild populations.

Together with members of the research team, the appointee will have responsibility for establishing, testing and publishing new models that shed light onto the consequences of farmed escapees and tolerable levels of introgression in wild populations. This will be achieved through developing models describing dynamics of wild salmon and cod populations that are interacting and potentially interbreeding with conspecific fish of aquaculture origin. Important parameters to be tested include numbers of escapees, fitness of hybrids, and behavioural interactions between wild and cultured fish.

We wish to appoint a highly motivated person with a PhD in modeling, statistical genetics, population ecology or related discipline. The appointee will need to be able to document experience of programming and use of models to study dynamical systems in biology. Previous experience with modelling of fish population dynamics is not necessary but is considered advantageous.

The Institute emphasises personal qualities such as good communication and cooperative skills, the ability to work independently and as part of an active research team. A record of publishing in this field will be considered and advantage.

We offer:

* a positive, challenging and creative work environment * the opportunity to work in a national institute with a high level of international contact * flexible hours, a good pension scheme and a wide range of welfare services.

The Institute offers governmental regulated salaries as post doctor (code 1352 post doctor).

For more information, please contact project leader Kevin Glover, email: Kevin.glover@imr.no, Tel: +47 4755236357 or research group leader Terje Svaasand, email: Terje.svaasand@imr.no, Tel: +47 55236891, or visit our web-site at http://www.imr.no/ The Institute of Marine Research is an "inclusive work-life" employer that encourages diversity, and we encourage all qualified candidates to apply for this position. Women are particularly encouraged to apply. Please note that information about applicants may be made public even if an applicant has requested to be left off the list of applicants. Applicants will be notified about this in advance

Please apply in writing, enclosing a cover letter, full CV, copies of relevant recommendations and academic transcripts together with a set of publications, to: Institute of Marine Research, Personnel Division, P.O. Box 1870 Nordnes, NO-5817 Bergen, Norway. Application number: "31-10". Closing date for applications: 10.07.10.

Dr Kevin Glover Senior Scientist Institute of Marine Research Bergen 55236357 48040035 Scientific presentation: http://www.imr.no/om_havforskningsinstituttet/ansatte/g/kevin_glover/nb-no "Glover, Kevin" <kevin.glover@imr.no>

OhioStateU ComputationalBiology

Post-doctoral positions open immediately in computational biology, molecular biology and evolution in The Ohio State University Program in Pharmacogenomics. We invite applications from candidates with Ph.D. or equivalent degrees, to participate in the OSU Program in Pharmacogenomics (http://pharmacogenomics.osu.edu/). The Program is newly funded with a U01 from NIGMS titled ??Expression Genetics in Drug Therapy??, as part of the Pharmacogenomics Network (PGRN, http://www.nigms.nih.gov/Initiatives/PGRN). The OSU Program in Pharmacogenomics, directed by Wolfgang Sadée, is highly interactive, with multiple collaborators, affording unique opportunities for both fundamental genetics research and translation into clinical applications.

Send CV, statement of interest, names of three references and contact details to Sherry Ring, ring.32@osu.edu. The Ohio State University is an equal opportunity, affirmative action employer. Qualified women, minorities, veterans and individuals with disabilities are encouraged to apply.

Daniel Janies <danjanies@yahoo.com

Oslo Bioinformatics

Postdoctoral Fellowship in Bioinformatics, Ref.nr.: 2010/7507

Deadline: July 8, 2010

The Natural History Museum (NHM) is Norway's largest natural history museum, located in the beautiful Botanical Garden in central Oslo. The staff consists of about 150 people working with research, scientific collections, teaching, and public outreach in biology and geology (see http://www.nhm.uio.no/). The National Centre for Biosystematics (NCB) (see http://www.nhm.uio.no/forskning-samlinger/forskning/forskningsgrupper/ncb/) is a strategic, interdisciplinary research centre at the Museum, performing research and research training in modern biosystematics and biodiversity at a high international level. The NCB integrates research groups working with plants, fungi and animals. The Museum has well-equipped DNA laboratories, one of them assigned to ancient DNA work, as well as access to next-generation sequencing facilities at the UiO. The NCB offers an interdisciplinary, active and stimulating research environment with many postdocs, Ph.D. and Master students, and guest researchers.

At the NCB, we work with a wide variety of molecular data, including AFLPs, microsatellites, and Sanger and high-throughput next-generation sequencing. Our research encompasses phylogenetics, population genetics, phylogeography, biogeography, and traditional and environmental DNA barcoding. Several projects are based on ancient DNA.

In addition to his/her own research of relevance for the NCB, the successful applicant for this postdoctoral position in bioinformatics will work together with NCB scientists on the design, development and implementation of analytical pipelines for various research projects. The postdoc will provide the necessary bioinformatics-, database-, and software development competence to ensure efficient processing of data (e.g. from high-throughput sequencing platforms such as Roche 454 or Illumina/Solexa), automating of repetitive bioinformatics tasks, integrating and mining of diverse biological datasets, and development of custom data analysis tools and workflows. We envision a close and dynamic collaboration in which the successful applicant will have an important role in ongoing and future projects as well as have the opportunity to develop his/her own research.

The postdoc will also be involved in teaching (e.g. at the Research School in Biosystematics) and participate in supervision of PhD and Master students.

The candidate should either be a qualified bioinformatician with a strong background in phylogenetics/phylogenomics and/or population genetics, or a qualified phylogeneticist/population geneticist with very strong competence in bioinformatics and data analyses. Expert knowledge in bioinformatics with ability to design and implement analysis workflows is needed. Familiarity with or interest in learning necessary skills for the analyses of data produced by high-throughput sequencing is required. He/she should be a strong team worker and also be able to work independently.

The applicant must hold a Ph.D. degree in a relevant field, and document broad understanding of open source/commercially available phylogenetic/population genetic analyses software, bioinformatics tools and databases. Computational competence should preferably include OS (Unix/Linux, Windows), programming in R, Perl/Python (C++/ Java bonus), and the databases Oracle/SQL/mySQL/PostgreSQL. Candidates whose thesis is accepted for public defense can also apply. The procedures for employments are in general regulated by the rules for employment in post doctor positions/scientific positions at the University of Oslo, http://www.uio.no/-admhb/reglhb/personal/tilsettingvitenskapelig/-ansettelsesvilkar/guidelinespostdoctor.xml Female applicants are encouraged to apply. UiO has an agreement for all employees, aiming to secure rights to research results a.o.

For further information please contact NCB leader, Professor Christian Brochmann, phone +47 22851611, e-mail christian.brochmann@nhm.uio.no or Research Director Fridtjof Mehlum, phone +47-22851723, e-mail fridtjof.mehlum@nhm.uio.no Pay grade: 57-60 (NOK 448 400 - 472 800 per year) (Norwegian LTR scale, depending on qualifications)

To apply please provide four copies of CV and certificates of education, three sets of scientific publications, names and addresses of two reference persons, and a covering letter outlining relevant work experience, to the following address:

University of Oslo, Natural History Museum, P.O. Box 1172 Blindern, NO-0318 Oslo, Norway An extended applicant form must be completed and submitted together

— / —

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

---

PrincetonU OxytrichaEvolution

Postdoc Opportunity: Princeton University DNA Rearrangements, Recombination, Epigenetics, and Non-coding RNAs

PRINCETON UNIVERSITY

Postdoctoral Research Associate or senior research position in the Department of Ecology and Evolutionary Biology at Princeton University, with focus on DNA Rearrangements, Recombination, Epigenetics, Evolution, and non-coding RNAs in the unicellular eukaryote Oxytricha.

Professor Laura Landweber seeks a postdoctoral research associate to study the mechanism of scrambled gene and genome rearrangements in ciliates, particularly the role of non-coding RNAs or epigenetic factors, using experimental or bioinformatic research tools or both.

Requirements: PhD in molecular biology or relevant field. Strong experimental or computational training, experience, and publications from the PhD, ability to work independently and creatively, and strong research and written/oral communication skills are necessary.

For more information about the lab, see http://www.princeton.edu/ ˜ lfl and recent publications, such as Nature 2008, v451, p153 (http://www.ncbi.nlm.nih.gov/pubmed/18046331) or Science 2009, v324, p935 (http://www.ncbi.nlm.nih.gov/pubmed/19372392).

This is initially a one-year appointment with possibility of renewal based on satisfactory performance. Funding is currently available for three years. Apply online at http://jobs.princeton.edu/. Search for Requisition # 1000366 and include a letter, CV, statement of research interest, and email addresses of three references. Application review will begin immediately; start date is flexible.

Princeton University is an equal opportunity employer and complies with applicable EEO and affirmative action regulations.

–

Laura F. Landweber, Professor Ecology & Evolutionary Biology, Guyot Hall Princeton University, Princeton, NJ 08544 http://www.princeton.edu/˜lfl tel 609-258-1947 * fax 609-258-7892 * lfl@princeton.edu

Laura Landweber <lfl@princeton.edu>

QueenMaryU London open

Postdoctoral research opportunities at School of Biological and Chemical Sciences, Queen Mary University of London, UK

We are seeking candidates who are internationally competitive, taking into account the current stage of their career. The strongest candidates may be offered a short term departmental fellowship during which time they would be expected to seek external funding. We will provide other candidates with help in applying for appropriate fellowships that can be hosted at QMUL. For example, if you are interested in applying for a Marie Curie fellowship, it would increase your chances of success if you could contact the appropriate PI by 5ˆth July 2010, so we can provide you with advice on your application.

Current available projects in the School of Biological and Chemical Sciences are at http://www.sbcs.qmul.ac.uk/research/16201.html - please follow the project title link to find out details and contacts.

If you would like to apply for one or more projects, contact the PI with attaching a CV and two paragraphs describing your relevant background. More details might be obtained from the PI if required.

– Dr Anna Dulic-Sills School of Biological and Chemical Sciences Queen Mary, University of London Mile End Road, London E1 4NS

Tel: 0207 882 3053

a.dulic-sills@qmul.ac.uk

ReedCollege 2 CichlidEvolution

Reed_College.GenomeEvolution.GeneDuplication

A fulltime 2-year NSF funded research postdoc position is available in the Renn lab beginning September 1st at Reed College to study the pattern of Gene Duplication among African Cichlid Fishes.

Research duties will include: 1) quantification of gene duplicates using microarrays and qPCR. 2) Cloning and Sequence analysis of gene duplicates 3) Phylogenetic analysis of gene duplicates 4) Preparation of manuscripts

While there exists a well defined research agenda, I seek a creative and motivated postdoc able to take this project in interesting directions and develop novel approaches to do so. In addition to research work the position will require mentoring of undergraduate students and offers a possibility for teaching experience.

Applicants should have a PhD in Evolution or Genomics and in interest in the genomic architecture of adaptive radiations. Experience in molecular biology, phylogenetic analysis (e.g. MUSCLE, PHYML, PAML MrBayes), computer skills (e.g. Perl programming, statistical analysis with R-programming language, database management, Phyllup, MrBayes) and a demonstrated ability with scientific writing are required.

Applicants should make initial inquires by email: renns@reed.edu. Subject line: Postdoc Genome Evolution Letters of intent accompanied by a CV, including the names and phone numbers of at least three references, should also be sent by email. Reed College is an Equal Opportunity Employer. Interviews may be held during the Evolution meetings June25-29

——

ReedCollge.MolecularMechanisms.SocialBehavior An NSF/NIH funded position is available in the Renn lab at Reed College for a comparative study of genomic, neural, and endocrine mechanisms underlying social behavior cichlid fishes from Lake Tanganyika.

I seek a creative postdoctoral researcher who will take this project in interesting directions. We currently focus on questions related to the evolution of sex-biased behaviors and maternal aggression. We currently quantify gene expression and using microarrays and quantitative PCR, but we are moving to RNA-seq. Our projects include additional challenge due to their comparative nature using various species with limited genome sequence information. Therefore, in addition to a background in ethology/neuroscience/ or behavioral genetics, I seek a postdoc with experience/interest in bioinformatics and genome evolution. Gene expression work will be closely tied with measures and possible manipulation of hormone levels in parallel with behavioral observation. In addition to research the position will require mentoring of undergraduate students and holds the potential for teaching experience.

The position is open immediately and initial appointment will be for one year with the possibility of renewal. Interviews at the Evolution meeting are possible.

Applicants should make initial inquires by email: renns@reed.edu. Subject line: Postdoc Social Behavior Letters of intent accompanied by a CV, including the names and phone numbers of at least three references, should also be sent by email. Reed College is an Equal Opportunity Employer. Interviews may be held during the Evolution meetings June25-29

renns@reed.edu

RutgersU PopulationGenetics

Postdoctoral Position in Population Genetics at Rutgers University

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

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

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

The position can begin as early as Summer, 2010.

Applications should email a CV and any other relevant information to

Jody Hey hey@biology.rutgers.edu

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

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

732-445-5272 hey@biology.rutgers.edu http://genfaculty.rutgers.edu/hey/home "Hey, Jody" <Hey@Biology.Rutgers.Edu>

SanDiegoZoo Conservation

The San Diego Zoo's Institute for Conservation Research is seeking a highly qualified postdoctoral candidate to assist in the development of an emerging conservation science program for burrowing owls and the habitat on which they depend. Western burrowing owl populations appear to be in decline and may soon require federal or state listing as an Endangered Species. The successful candidate will develop a research program to address major conservation threats to the species in Southern California and begin to develop a comprehensive strategic regional conservation plan. Understanding the distribution and abundance patterns in relationship to habitat characteristics is critical for managing species across multiple habitat types fragmented over an extensive area. Also essential is identifying the population-genetic structure, or phylogeography, for the region, with the long-term goal of understanding population evolutionary history. For management, estimates of gene flow and genetic divergence, coupled with knowledge of geographic barriers and divergent ecological adaptation, is required. Understanding spatial ecology, including the distribution of burrowing owls on the landscape, dispersal and migration patterns, as well as fine-scale movements and habitat use within home ranges, is yet another pressing need. Active management strategies, such as translocation and habitat restoration, also require systematic testing to increase their efficacy.

Goals for the research program may include developing a spatially explicit model that addresses habitat needs, conservation threats, and genetic viability. This model will serve as a blueprint for conservation management, including translocation programs, when needed. An additional goal may be to develop optimal translocation strategies, using adaptive management methods. The successful candidate will work closely with conservation partners from governmental and nongovernmental agencies and with other researchers at the Institute.

The successful candidate will design and implement research; collect data and train others in data collection; organize and analyze data; create action plans for future conservation efforts; share results with relevant GO's and NGO's involved in implementing conservation measures, and at conferences and workshops; prepare manuscripts for publication; and become involved in outreach and education. The postdoctoral fellow is expected to build a collaborative research program with Institute scientists from several disciplines (for details see www.zooconservation.org . A Ph.D. in Ecology, Genetics, Conservation Biology, Wildlife Management, or related discipline is required. The following skills are desirable: ecological research methodology; scientific writing skills, as demonstrated in peer-reviewed publications; oral communication, teamwork and management abilities; fluency in English language; strong computer, data management, and statistical analysis skills

The position will be for three years. Salary commensurate with NIH postdoctoral fellow salary guidelines.

Application deadline is June 10, 2010 To apply, visit: https://www.hrapply.com/sandiegozoo/AppJobSearch.jsp Click on 'VIEW ALL JOBS'

oryder@sandiegozoo.org

SaudiaArabia SymbiodiniumEvolutionaryGenomics

Dear colleagues,

we have been recently awarded a grant to sequence the genome of a Symbiodinium species (dinoflagellates).

The group consists of Chris Voolstra, Tim Ravasi, and Vladimir Bajic at KAUST and Gos Micklem at University of Cambridge.

Briefly, we plan to employ an Illumina shotgun and mate pair sequencing approach. We plan to establish an email list that will provide updates on the status of the process.

Please email christian.voolstra@kaust.edu.sa should you wish to be on the email list, to participate in this project, or other queries related to the project.

The lab of Chris Voolstra and Gos Micklem both have a 2-year postdoctoral position to offer related to this project. Postdoc position for the Micklem lab will be announced in due course. Postdoc candidate for the Voolstra lab preferably has experience in evolutionary genomics and Symbiodinium physiology, ecology, and culturing methods as well as molecular methodologies.

To apply for postdoc in Voolstra lab: Please send cover letter summarizing your qualifications and interests, a curriculum vitae, and the names and contact information for 2-3 references to christian.voolstra@kaust.edu.sa . Projected start date: autumn 2010.

King Abdullah University of Science and Technology (KAUST) is a dynamic new university campus and campus community in Saudi Arabia that opened in September 2009. The campus is located directly at the Red Sea, near Jeddah. More information is available at www.kaust.edu.sa andhttp://faculty.kaust.edu.sa/sites/christianvoolstra/Pages/home.aspx Thank you and regards, Chris

Dr. Christian R. Voolstra Assistant Professor of Marine Science 4700 King Abdullah University of Science and Technology (KAUST) Building 2, office 4233 23955-6900 Thuwal, Kingdom of Saudi Arabia Tel.: +966 2 808 2377 http://web.kaust.edu.sa/faculty/christianvoolstra/ Chris Voolstra <chris.voolstra@googlemail.com>

SmithCollege MA EukaryoticPhylogeny

Postdoctoral Position in Eukaryotic Phylogeny and Genome Evolution

Smith College invites applications for a full-time postdoctoral research position focusing on the eukaryotic tree of life and genome evolution in microbial eukaryotes. The position will be in Laura Katz's laboratory (http://www.science.smith.edu/departments/Biology/lkatz/Research.htm). The initial appointment is for one year, with the possibility of extending for additional years.

Applicants should have skills in molecular systematics, bioinformatics, microbiology and/or molecular evolution. Potential projects include: 1) bioinformatic and/or experimental analyses of eukaryotic phylogeny and molecular evolution and 2) characterization of genome properties from microbial eukaryotes. Emphasis in the lab is on ciliates and amoeboid lineages. Research in the Katz lab aims to elucidate principles of the evolution in eukaryotes through analyses of microbial groups, and to assess how these principles apply (or fail to apply) to other organisms. Currently we focus on four interrelated areas: (1) Characterizing evolutionary relationships among eukaryotes; (2) Reconstructing the ciliate tree of life through multi-gene analyses; (3) Exploring the evolution of ciliate and foraminiferan genomes; (4) Describing the phylogeography of coastal marine ciliates.

To apply, submit application at http://jobs.smith.edu with uploaded letter of application, C.V., a statement of research interests, and the names and contact information of three references. Please also describe what interests you about this postdoctoral position and whether you have any particular ideas that you wish to pursue. Review of applications will begin June 30 and will continue until the position is filled.

Email Laura Katz (lkatz@smith.edu) with any questions about the position.

Smith College is a member of the Five College Consortium with Amherst, Hampshire, and Mount Holyoke Colleges and the University of Massachusetts Amherst. Smith College is an equal opportunity employer encouraging excellence through diversity.

lkatz@email.smith.edu

StanfordU TheoreticalEvolution

Stanford University, Biology Department, Theoretical Evolutionary Ecology. Postdoc position to work on the evolution of life histories with Shripad Tuljapurkar. The postdoc will interact with a group (at Stanford, Berkeley, Davis, Imperial College and Miami) working on aging and senescence, age-stage structured models, quantitative trait dynamics and evolution, coevolution of social behavior and life histories. We use and analyze data on birds, mammals, plants and humans. Applicants should have a background in theoretical ecology/evolution (or other quantitative field with knowledge of biology), strong analytical and numerical skills, familiarity with statistical methods and interest in working with data. See http://popstudies.stanford.edu for more info on past and ongoing research projects. Appointment is initially for one year, with the possibility of renewal. Flexible start date. Applications will be accepted through August 15, 2010. Send CV, copies of publications, and contact info for 3 references to Larry Bond, <larryb@charles.stanford.edu>, with a copy to <tulja@stanford.edu>.

–

Ulrich Steiner Post-doctoral associate 332 Herrin Hall Department of Biology/Morrison Institute for Population and Resource Studies Stanford CA 94305-5020 Phone (650) 725-7097 Fax (650) 724-3708 Email usteiner@stanford.edu http://www.stanford.edu/~usteiner/ Uli Steiner <usteiner@stanford.edu>

StellenboschU AbaloneGenomics

Postdoctoral positions available in the Department of Genetics (14 June 2010)

Two postdoctoral positions are available in the Aquaculture Division, Department of Genetics, Stellenbosch University with the project title “Genetic improvement of the abalone Haliotis midae.”

Haliotis midae, known locally as ’perlemoen’, occurs along the shores of South Africa and is the only one of the five endemic species that is commercially exploited.

Haliotis midae displays a very slow growth rate, taking two to five years to reach market size. This is an obstacle for profitable farming and global competitiveness. In order to increase the productivity and the profitability of the commercial abalone industry, a research program has been designed which makes use of modern technology currently applied to other aquaculture species. Two key outputs of this program for which two postdoctoral positions are available include: 1) The production of a transcriptome sequence of Haliotis midae utilizing next generation sequencing technologies including the Illumina Genome Analysis platform and the GS FLX platform and utilizing this for amongst others marker development. 2) The generation of comprehensive linkage maps and identification of QTLs utilizing microsatellite and SNP markers.

The successful candidate will be primarily responsible for: 1) Bioinformatic data analysis within this framework. This will include developing an in-depth understanding of tailored genomic analytical software packages for EST, transcriptome and gene expression analysis in order to conduct research and provide postgraduate students with bioinformatics support; keeping abreast of new developments in the areas of bioinformatics, transcriptome analysis and abalone research; the maintenance of a comprehensive sample tracking system; assisting laboratory staff and students with their research data output requirements. 2) Linkage and QTL mapping analysis within this framework. This will include utilizing currently available marker and data resources as well as initializing further linkage and QTL mapping design; providing postgraduate students with data analysis support; keeping abreast of new developments in the areas of linkage mapping, QTL mapping and abalone research in general; the maintenance of a comprehensive sample tracking system.

Minimum requirements: 1) PhD with specialization in Biotechnology, Bioinformatics, Genetics, Genomics or a closely related discipline. Candidates should have a strong computational background (DNA sequence analysis, evolutionary genetics/biology and gene expression data analysis) and proficiency in relevant software packages. 2) PhD with specialization in Biotechnology, Genetics, Genomics or a closely related discipline. Candidates should have a strong computational background (DNA sequence analysis, linkage mapping, QTL mapping) and proficiency in relevant software packages.

Recommended requirements: Proven experience with SNP analyses (bioinformatic or mapping analysis). Project management experience; excellent organizational and communication skills; proven ability to set deadlines and meet milestones.

These positions are available for 2 years with the possibility of extension. Commencement of duties as soon as possible but no later than November 2010.

Interested researchers are requested to send their CV including details of at least 2 references to Dr. Rouvay Roodt-Wilding at roodt@sun.ac.za or Dr Aletta Bester-van der Merwe at aeb@sun.ac.za

Closing date: 2 July 2010.

roodt@sun.ac.za

Stuttgart Germany PlantEvolution

Dear EvolDir readers,

we have an open position for a

POSTDOC IN ECOLOGICAL GENETICS AND EPIGENETICS OF PLANTS

to work on the role of genetic and epigenetic adaptation of the model plant Arabidopsis thaliana. The project involves common garden experiments in environmentally diverse field sites to measure the fitness of natural A. thaliana accessions and changes in epigenetic status over environments and time.

We are looking for an enthusiastic scientist with a Ph.D. in population or quantitative genetics, ecology or evolutionary biology, who has a genuine interest in plant ecology and evolution. The project is part of a collaborative European project funded by the European Science Foundation. The work includes the planning and analysis of field and growth chamber experiments, as well as the quantitative genetic analysis of genetic and epigenetic determinants of plant fitness, some molecular work and the analysis of sequence data together with project partners. Field trials will be carried out on experimental stations on the Suebian Alps and in the Rhine valley, therefore the ability to drive a car is required.

The successful applicant will be appointed for three years. Salary will be according to the German government salary scale (TV-L E13) and depends on previous experience, age and marital status.

The University of Hohenheim is located on a beautiful campus in the South German city of Stuttgart. There is a very good network of research groups on campus working on plant genetics, breeding and field trials. Further information about our group can be obtained from www.evoplant.uni-hohenheim.de or from the contact information below. The University of Hohenheim is an equal opportunity employer. Women and members of minority groups are strongly encouraged to apply.

Please send your application (Cover letter, CV, publication list, statement of research interests, addresses of at least two references) until 22 June 2010 by e-mail as a single PDF document to Bärbel Hessenauer (baerbel.hessenauer@uni-hohenheim.de). The starting date is flexible but 1st of September would be ideal.

Dr. Karl Schmid Professor Institute of Plant Breeding, Seed Science and Population Genetics Fruwirthstrasse 21 D-70599 Stuttgart Germany Phone: +49 711 459 23487 Email: karl.schmid@uni-hohenheim.de

karl.schmid@gmail.com

TexasAMU ComputationalGenomicsTexasAMU ComputationalGenomics

POSTDOCTORAL POSITION IN COMPUTATIONAL/EVOLUTIONARY GENOMICS

A postdoctoral position is available in the laboratory of Dr. James Cai in the Department of Veterinary Integrative Biosciences at the Texas A&M University (College Station, TX). The Cai lab (http://www.genomezoo.net/) focuses on computational research in population genomics and molecular evolution.

Candidates should have obtained a PhD degree in Biology, Bioinformatics, Computer Science, or a related discipline. Programming skills (ideally in Matlab and C) and experience in the application of computational methods to high-throughput genomic data are highly desirable. The successful candidate will work on a variety of projects to develop statistical tests and computational tools to investigate evolutionary processes shaping genome variability patterns. You will also have the opportunity to pursue independent research related to major research themes of the lab.

Interested applicants should submit a CV, a brief (2-3 paragraphs) statement of her/his research interests and experience, and contact information of three references by email to jcai@cvm.tamu.edu. Informal inquiries are welcome.

jcai@cvm.tamu.edu

TuftsU Speciation

POSTDOC: Genetics of temporal and behavioral isolation

A Postdoctoral Researcher position is available in the laboratory of Erik Dopman in the Department of Biology at Tufts University (http://ase.tufts.edu/biology/faculty/dopman/index.asp). Research in the lab focuses on the evolution of reproductive isolating barriers during the speciation process. Current aims are to identify the molecular genetic basis for traits contributing to reproductive isolation, to infer the evolutionary mechanisms shaping these loci, and to evaluate the consequences of barrier loci on genome- wide patterns of genetic variation.

We are applying a combination of comparative and experimental approaches to our studies of speciation, using Z and E pheromone strains of European corn borer as a model system. The ECB consists of multiple population types that vary in a suite of fitness-related characters that affect reproductive isolation, most notably, in the number of generations per year (voltinism), host-plant use, and reproductive behavior. PDFs of recent MSS can be found at http://ase.tufts.edu/biology/labs/dopman/publications/ . Highly relevant publications are Dopman et al. 2010, 2005, and 2004.

We seek a creative postdoctoral researcher who will join our group to study the genetics of temporal and behavioral isolation. Responsibilities of the successful applicant include assisting in or providing leadership with the following tasks: creation of BAC-tile paths, collection of next-generation sequence data, field work, and phenotyping of offspring from controlled crosses. A PhD in evolutionary biology, genetics/genomics, or in a related field, is required by the position start date. The successful candidate should have prior experience in molecular genetics, and proven skills acquiring and manipulating next-generation sequence data. Familiarity with whole genome analysis is preferred. The candidate will be expected to work independently, participate in group efforts with collaborators, and contribute to the supervision of PhD and undergraduate students. Opportunities for grant-writing will be available, and the potential to develop independent projects is high. See http://www.tufts.edu/central/research/postdoc/ for more information on postdoctoral scholars at Tufts.

This is a one-year appointment with possibility of renewal. Application review will begin immediately, but the start date is flexible. Interested individuals should contact Erik Dopman (erik.dopman@tufts.edu) and provide a CV (including date of availability), a 1-2 page statement of research interests, PDFs of relevant publications, and the names and contact information of three references. Informal inquiries are welcome.

Erik Dopman, Assistant Professor Department of Biology Tufts University 165 Packard Avenue Medford, MA 02155 t (617) 627-4890; f (617) 627-3805 http://ase.tufts.edu/biology/faculty/dopman/ erik.dopman@tufts.edu

---

TuftsU SpeciationGenomics

Postdoctoral Researcher Position Speciation Genomics in the European Corn Borer (Ostrinia nubilalis)

A Postdoctoral Researcher position in evolutionary genomics is available in the laboratory of Erik Dopman in the Department of Biology at Tufts University (http://ase.tufts.edu/biology/faculty/dopman/index.asp). Research in the lab focuses on the evolution of reproductive isolating barriers during the speciation process. Current aims are to identify the molecular genetic basis for traits contributing to reproductive isolation, to infer the evolutionary mechanisms shaping these loci, and to evaluate the consequences of barrier loci on genome-wide patterns of genetic variation.

We are applying a combination of comparative and experimental approaches to our studies of speciation, using Z and E pheromone strains of European corn borer as a model system. The ECB consists of multiple population types that vary in a suite of fitness-related characters that affect reproductive isolation, most notably, in the number of generations per year (voltinism), host-plant use, and reproductive behavior. PDFs of recent MSS can be found at http://ase.tufts.edu/biology/labs/dopman/publications/. Highly relevant publications are Dopman et al. 2010, 2005, and 2004.

We seek a creative postdoctoral researcher who will lead a genomic analysis of the ECB genome, using Illumina and 454 sequencing technologies. A PhD in evolutionary genetics or genomics, or in a related field, is required by the position start date. The successful candidate should have prior experience manipulating and analyzing high- throughput genomic data, and proven skills in at least one programing/ scripting language (Perl, Python). In addition, a strong background in molecular evolution and/or molecular biology is preferred. The candidate will be expected to work independently, participate in group efforts with collaborators (at Tufts and Cornell University), and contribute to the supervision of PhD and undergraduate theses. Opportunities for grant-writing will be available, and the potential to develop independent projects is high. See http://www.tufts.edu/central/research/postdoc/ for more information on postdoctoral scholars at Tufts.

This is a one-year appointment with possibility of renewal. Application review will begin immediately, but the start date is flexible. Interested individuals should contact Erik Dopman (erik.dopman@tufts.edu) and provide a CV (including date of availability), a 1-2 page statement of research interests, PDFs of relevant publications, and the names and contact information of three references. Informal inquiries are welcome.

Erik Dopman, Assistant Professor Department of Biology Tufts University 165 Packard Avenue Medford, MA 02155 t (617) 627-4890; f (617) 627-3805 http://ase.tufts.edu/biology/faculty/dopman/ erik.dopman@tufts.edu

---

UAberdeen MolecularEvolution

UNIVERSITY OF ABERDEEN

SCHOOL OF BIOLOGICAL SCIENCES

POSTDOCTORAL RESEARCH ASSISTANT - MOLECULAR ECOLOGY AND EVOLUTION (YZY201RX)

A postdoctoral researcher position is available within Dr Stuart Piertney's laboratory in the School of Biological Sciences at the University of Aberdeen.

The position is part of a NERC-funded project directed toward using QTL and eQTL mapping to identify genes affecting parasite resistance in red grouse, and examining patterns of population genetic structure of adaptive markers in natural populations.

The work will involve both fieldwork and laboratory components. Applicants must have a Ph.D. in biological sciences with expertise in molecular and/or evolutionary genetics, with experience of QTL mapping and/or SNP genotyping. Experience of fieldwork and the sampling and monitoring of natural populations is essential.

Informal enquiries may be made to Stuart Piertney at s.piertney@abdn.ac.uk

The post is available for three years, with salary at the appropriate point on the Grade 6 scale (£29,853-£30,747 per annum), with placement according to qualifications and experience.

Should you require a visa to undertake paid employment in the UK you will be required to fulfil the minimum points criteria to be granted a Certificate of Sponsorship and Tier 2 visa. As appropriate, at the time an offer of appointment is made you will be asked to demonstrate that you fulfil the criteria in respect of financial maintenance and competency in English. Please do not hesitate to contact Diane Norris, HR Adviser, for further information.

To apply online for this position visit www.abdn.ac.uk/jobs or alternatively you may request an application pack by emailing your name and contact details to jobs@abdn.ac.uk or by telephoning our 24 hour answer service on +44 (0)1224) 272727 quoting the job reference number 1142161.

The closing date for the receipt of applications is 24 June 2010

Dr Stuart B Piertney Institute of Biological and Environmental Sciences University of Aberdeen Zoology Building Tillydrone Avenue Aberdeen AB24 2TZ

Tel: +44 (0)1224 272864 (Office) Tel: +44 (0)1224 272892 (Lab) Fax: +44 (0)1224 272396

Personal web page http://www.abdn.ac.uk/biologicalsci/staff/details/s.piertney Ecology theme web page http://abdn.ac.uk/ibes/research/ecology/ s.piertney@abdn.ac.uk

UCaliforniaSanFrancisco HumanEvolution

POSTDOCTORAL POSITION

Evolutionary or Human Genetics

A postdoctoral position is available in the laboratory of Dr. Jeff Wall (Institute for Human Genetics, University of California San Francisco). The lab works on several projects in evolutionary and human genetics, including

– generation and analysis of large-scale sequence data in non-human primates

– methods for estimating local ancestry in admixed individuals

– methods for GWAS in admixed populations

– standard human population genetics

The successful candidate would be expected to work on one or more of these, but would have time to work on other projects if desired. We are looking for a candidate with experience in computer programming, bioinformatics, evolutionary genetics and/or next generation sequencing. Starting dates are flexible, and funding is available for at least 2 years.

Applicants should send a CV and the names and email addresses of at least two references to Jeff Wall <wallj@humgen.ucsf.edu>. Informal enquiries are also welcome.

Jeff Wall <wallj@humgen.ucsf.edu>

UGreifswald Germany ConservationGenetics

Job announcement

Applied Zoology and Conservation, Zoological Institute and Museum, University of Greifswald, Germany

Postdoctoral Researcher - Conservation Genetics

Application deadline: 01.08.2010

We are seeking a highly motivated team-oriented researcher with a strong background in Conservation/Population Genetics and good skills in statistics and modeling. The person appointed is expected to lead the DNA lab, teach (4 hours/week and semester) and supervise bachelor/ master students. Post-doc experience is of advantage.

Education: PhD with experience in Conservation and/or Population Genetics

Entrance: starting October 01, 2010

Duration of appointment: 3 years, with option for extension

Salary and benefits: according to a public service position in Germany (E 13)

Please send your application by email (all material in one attached file please) to Gerald Kerth (gkerth@orn.mpg.de). Include your CV, a short description of your research interests and research experience (including a list of methods you are familiar with), and names and email addresses of 2-3 references who could be contacted.

The newly established research group Applied Zoology and Conservation uses an integrative approach, combining behavioral, ecological, and molecular methods to investigate questions at the interface of evolutionary, behavioral, and conservation biology. Currently, we mainly study bats and species interacting with them, but our research is not restricted to a specific group of animals. Research interests include the causes and consequences of sociality (incl. cooperative behavior and host-parasite interactions), mate and habitat choice, dispersal, as well as applied and basic animal conservation. In the field, we apply automatic monitoring of animals marked with PIT-tags, radio-telemetry, thermography, and infrared- video. Genetic methods include analyses of nuclear and mitochondrial DNA microsatellites and sequences.

Greifswald, a lively town with 55.000 inhabitants and rich medieval architecture, is situated in Northern Germany at the Baltic Sea. It has good connections to the nearby islands of Usedom and Ruegen with their lovely beaches and is a train-ride of 2.5 hours away from Berlin. In its vicinity are several National Parks, harboring a diverse wildlife.

For further information contact gkerth@orn.mpg.de or see:

www.mnf.uni-greifswald.de/institute/fr-biologie/-zool-institut-museum/angewandte-zoologie-und-naturschutz.html PD Dr. Gerald Kerth

Max-Planck-Institute for Ornithology 82319 Seewiesen, Germany

phone: ++49 (0)8157-932-374 fax: ++49 (0)8157-932-344 email: gkerth@orn.mpg.de

gkerth <gkerth@orn.mpg.de>

UGroningen SpatialModelling

PostDoc position - Spatial Modelling

Modelling the ecological implications of the spread of genes from transgenic crop into wild relatives

Project information: In order to assess the ecological implications associated with the introduction of transgenic crops the Dutch Science Foundation (NWO) has launched the focal programme Ecology Regarding Genetically Modified Organisms (ERGO). The project “Introgression of crop (trans-)genes into wild relatives: hybrid fitness, background selection and hitchhiking” (for more info see vacancies at www.rug.nl/-biol/theobio) is a joint effort of the Universities of Groningen (Centre for Ecological and Evolutionary Studies,), Amsterdam (Institute for Biodiversity and Ecosystem Dynamics) and Wageningen (Laboratory for Plant Breeding,). The project comprises both various experimental studies (in which the wild lettuce species Lactuca serriola is used as a model) and a theoretical approach. This job offer concerns the subproject “The potential spread of crop genes in a crop/wild system: analysis and modelling of an invasive process.” It is the continuation of a previous project (for more info see vacancies at www.rug.nl/biol/theobio) and the models developed in this earlier project should serve as a point of departure.

Project description: Computer models will be developed for the spatial dispersal of transgenes (through pollen, seed, or vegetatively) in wild populations. The main objective is to predict the dispersal pattern and invasion prospects of a transgene on basis of the genetics and life history of the plant species involved. The potential effect of transgenes on dispersal characteristics will receive special attention. Model development will strongly reflect the developments in the related projects. The models developed in various subprojects will be integrated and validated with existing data, including those generated on L. serriola.

Profile: PhD with knowledge of population biology, population genetics and modelling. Extensive experience with programming and computer simulations. Good communication skills for interaction within a multidisciplinary programme.

Renumeration: Depending on age and experience, the gross salary per month will range between Euro 2861 and Euro 3088. Duration of the contract: 2.5 years (with an evaluation after the first year).

Location: Theoretical Biology Group at the Centre for Ecological and Evolutionary Studies (CEES) of the University of Groningen (The Netherlands). The group develops theory in two major research areas: evolutionary ecology and self-organization. Current research projects focus on evolutionary game theory, life history theory, evolutionary immunology, kin selection, sex determination, sex allocation, sexual selection, sexual conflict, metapopulation genetics, sympatric speciation, allometric scaling laws, resource and interference competition, host-parasite co-evolution, and the emergence of social structure. It offers a stimulating and exiting environment for doing research

Further information: Prof. Dr. Franjo Weissing (f.j.weissing@rug.nl; Tel: +31 50 363 2131) and Prof. Dr. Kuke Bijlsma (r.bijlsma@rug.nl; Tel: +31 50 363 2117).

Application: To apply for this position, send your application (including letter of motivation, detailed CV, PDFs of three most relevant publications, and the names and email addresses of three potential referees) in electronic form before 1 July to the office manager of the Theoretical Biology Group, Hinke Tjoelker (theobio@rug.nl). Please include the text 'ERGO PostDoc' in the subject line of your email.

joke.bakker@rug.nl

ULaval Molecular basis of behaviour variation

Our laboratory is eager to receive application from highly motivated scientists with an excellent record to apply to a Quebec government fellowship available for non-Canadian candidates to do research in a Quebec-based laboratory. Post-doctoral fellowships are available (1 year, 35,000 CAN$). Internships are also available for a visit to our laboratory (3,000 CAN$/month, up to 4 months). Pre-selection by the host university and our laboratory is mandatory.

Candidates from all over the world are invited to apply. Additionally, specific fellowships are available for candidates from Mexico, Brazil, China and Wallonie.

We are in the Department of Biology at Laval University, located in Quebec City, Quebec, Canada. Our laboratory is part of the Institute of Integrative and Systems Biology (IBIS). We study the underlying molecular and hormonal causes of variation in behaviour in vertebrates. We are interested in personality with an emphasis on the stress response and correlation among behaviours, as well as in reproductive tactics. We are also interested by the effects of the environment on development of behaviour, such as environmental enrichment in captive animals, maternal/paternal and social group effects, and endocrine disrupters. We therefore have a strong interest for phenotypic plasticity, along with the effects of genetic variation. We favour an integrative approach by linking data from the same individual: neuropeptides, neurotransmitters and their receptors (quantitative Real-Time PCR, microarrays, in situ hybridization, HPLC), hormones (EIA, HPLC), physiology and behaviour. Our model system is the threespine stickleback Gasterosteus aculeatus, a small fish studied in behavioural biology, which can be kept easily in the lab and whose genome is sequenced.

Laval University is one of the ten main Canadian universities. Quebec City is dynamic with all the advantages of a large city while still allowing for very easy access to wilderness and very reasonable cost of living. The chosen candidates that are successful at obtaining a fellowship will be part of the Institute of Integrative and Systems Biology. They will have access to core genomics and molecular biology facilities, lab meetings and Institute-wide group meetings, journal clubs and weekly seminars at the Institute and in the Biology Department. Several ecological genomics laboratories are part of the Institute and the Biology department, allowing for enriched interactions with members of the other laboratories working in this field. DEADLINES: Our laboratory must receive applications before July 23, 2010. We will then proceed to select candidates that will be able to apply to the University pre-selection committee with a deadline of August 9th 2010. Candidates selected by the university will then be allowed to apply to the general competition in Fall 2010, with results given in April 2011. Start date can be between May and December 2011.

Contact me directly by email for more information about the program and opportunities in our laboratory.

Nadia.Aubin-Horth@bio.ulaval.ca

Nadia Aubin-Horth

Assistant professor

Department of Biology

Institute of Integrative and Systems Biology

Pavillon Charles-Eugene-Marchand

1030, Avenue de la Medecine

Laval University

Quebec city (Quebec) G1V 0A6

Canada

http://wikiaubinhorth.ibis.ulaval.ca/Main_Page

Aubin-Horth Nadia <Nadia.Aubin-Horth@bio.ulaval.ca>

ULeeds mtDNAvariation

Faculty of Biological Sciences Institute of Integrative and Comparative Biology

Research Fellow (Internal applicants only) (Full-time, fixed term for 3 years)

Project Title: Complete mtDNA variation and the modern human settlement of Southwest Asia

An exciting opportunity has arisen for post-doctoral research in the archaeogenetics of Europe and the Near East. This project, to investigate complete mitochondrial genome variation in the Near East, focusing particularly on Anatolia, has recently been awarded to the Archaeogenetics Research Group at Leeds by the Leverhulme Trust. You will join a thriving group, several of whose members are working on related areas. You will be responsible for organising and carrying out the sequencing and analysing the data, in the context of other datasets from the region that we are generating in the lab, and others from west Eurasia that are available on the public databases. You should hold a PhD in genetics, archaeology or a related subject, and preferably have experience of DNA sequencing and with bioinformatic, phylogenetic, phylogeographic and population-genetic analysis of DNA sequences.

University Grade 7 (£29,853 - £35,646 p.a.) (It is likely that an appointment will be made at or below £30,747 due to funding limitations).

Informal enquiries to Professor Martin Richards, tel +44 (0)113 343 2984, email m.b.richards@leeds.ac.uk

To download an application form and job details please visit http://hr.leeds.ac.uk/jobs/. Alternatively these may be obtained from Faculty HR Office, tel +44 (0)113 343 2250, email fbsjobs@leeds.ac.uk

Job ref 313351 Closing date 9th July 2010

Further Details

Reports to: Professor Martin Richards

Responsible to: Director of Institute of Integrative and Comparative Biology

Background to the post

The post is part of a three-year Leverhulme Trust-funded research project, and forms part of a larger research program, funded by a number of sources, that is running in the Archaeogenetics Research Laboratory that aims to use complete mtDNA sequence variation to elucidate aspects of prehistoric dispersals and settlements, especially in Southwest Asia and Europe.

Summary of the research programme

The emerging field of archaeogenetics has become a crucial part of the project of reconstructing the human past - especially mapping out prehistoric population dispersals. It achieves this mainly by studying non-recombining genetic markers in extant human populations - in particular, the mitochondrial DNA (mtDNA), which tracks the maternal line of descent, and the Y chromosome, for the male lineage. Analysing variation in these markers allows us to reconstruct genealogical lines of descent and compare distributions of lineages from one population to another, in order to estimate the timing of migrations between them - an approach known as phylogeography. More specifically, we can use the variation accumulated exclusively within the population of a part of the world settled during prehistoric times, along with an estimate of the mutation rate or “molecular clock”, to estimate the time of settlement - a procedure we have christened “founder analysis”.

Most work on European and Near Eastern mtDNA in the past has focused on a short stretch of the mtDNA control region. The problems with this work are both a lack of genealogical resolution and very imprecise age estimates. In this project, funded by the Leverhulme Trust, we are applying the phylogeographic approach to complete mtDNA genome sequences, which provide a step-change in the level of resolution we can achieve. We will focus on the Near East, especially Anatolia, in order to study the first settlement and subsequent demographic history of human populations in that part of the world. Because of the Near East’s crucial role in west Eurasian prehistory, however, this research will allow us to illuminate the dispersal history of a much wider region.

The Near East is widely held to have been the source of European populations in both the Upper Palaeolithic - the first settlement by modern humans, ~45 kya (thousand years ago) - and, in some models, the Neolithic, from ~9 kya. Yet relatively little genetic research has been devoted to the region. There has been no concerted attempt to reconstruct the demographic history of the Near East from mtDNA sequences - in part, because of the poor resolution of the mtDNA control region referred to above. Moreover, previous work on the settlement of Europe similarly suffers from those weaknesses. In this project, we will combine the new complete mtDNA genomes from Anatolia with data we are generating from other parts of the Near East and Europe. We will first target relict lineages from throughout the region in order to address the question of first settlement and then focus on Anatolia - a crucial bridge between

— / —

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

UMinnesota PlantEvolutionaryGenomics

POST-DOCTORAL POSITION in Evolutionary Genomics and Association Mapping

As part of a multi-investigator project we are in the process of collecting whole-genome sequence data from several hundred genotypes of the model legume Medicago truncatula, as well as individuals of several related Medicago species. I am now looking for a post-doc to help in analyzing these data to investigate evolutionary forces shaping genome diversity as well as the genetic basis of phenotypic traits. We are particularly interested in identifying and characterizing the evolutionary history of genes mediating the mutualism between Medicago and symbiotic nitrogen fixing rhizobia bacteria. The position will involve some work with greenhouse experiments and the collection of phenotypic data. You would be working with several post-docs and graduate students with diverse computational and laboratory skills. There will be considerable opportunity to pursue ones own interests within the general framework of the project.

Interest and experience in statistical and population genetics, handling large data sets, and some programming skills are highly desired.

A late-summer start date is preferred but this is flexible. We offer competitive salary with full health benefits. Travel funds are also available for attending scientific meetings.

The U of M has a large urban campus on the banks of the Mississippi River with many activities and entertainment in the Twin Cities, great restaurants, biking, and outdoor activities nearby. Campus is a short bike or bus ride from both downtown Minneapolis and St. Paul.

If interested please apply by August 1st. Applicants should send a CV, a statement of research interests, and names and contact information of three references.

If you have questions please contact me (ptiffin@umn.edu). More information can be found at my website (http://www.cbs.umn.edu/tiffin/) and the project website (www.medicagohapmap.org).

Post-docs working on the project will be at SMBE and Evolution meetings and I will be attending Evolution in Portland if you would like to learn more about the project / position.

Peter Tiffin Dept. of Plant Biology University of Minnesota ptiffin@umn.edu

ptiffin@umn.edu

UMunich PlantRepetitiveDNAEvolution

Postdoctoral research position on the evolution of repetitive DNA in a group of non-photosynthetic flowering plants

I am looking for a postdoc (2 yrs, possibly 3 yrs) interested in the evolution of repetitive DNA. We are applying 454 pyrosequencing to characterize repetitive DNA in a group of non-photosynthetic flowering plants that show contrasting genome dynamics. We will test the hypothesis that this is mainly due to their repetitive DNA fractions by comparing seven species of known relationship and genome characteristics. The primary novelty of this project is the broad comparative context, which will allow assessing evolutionary trends. Three full plates of 454 data are in hand, and data analysis can begin now.

Other ongoing research topics in our group can be found at http://www.sysbot.biologie.uni-muenchen.de/en/people/renner/. The postdoc will we employed according to German BAT IIa and will be part of Munich Universitys large and active community of evolutionary biologists.

Experience with the analysis of repetitive DNA, good work ethics, and the ability to think creatively and critically are desired.

The closing date for applications is June 30, 2010, or when the position is filled. Please send your application, together with a full CV, copies of recent-most educational certificates, and the names of two referees to Susanne Renner (renner@lrz.uni-muenchen.de).

Susanne Renner Research: http://www.umsl.edu/~renners/ Susanne Renner <renner@lrz.uni-muenchen.de>

UNSW Sydney SexualConflict

The Research Group of Professor Rob Brooks in the Evolution & Ecology Research Centre (E&ERC), within the School of Biological Earth and Environmental Sciences (BEES), is seeking a postdoctoral Research Associate to work on an Australian Research Council Grant entitled "Understanding how reproduction and sexual conflict drive sex-dependent longevity and ageing".

The research group studies the evolutionary consequences of sex-dependent selection and sexual conflict. The project funding is to work on house mice, exploring the consequences sexual conflict on life-history traits, ageing and mating behaviour. Most of the work is expected to be done in the laboratory and in artificial enclosure populations. We seek somebody with skills and experience in small mammal evolutionary ecology or physiology. Expertise measuring oxidative stress or oxidative damage or working with house mouse behavioural ecology would be an asset.

The successful applicant is expected to do empirical work, analyse data and write papers. The applicant should be prepared to apply for fellowships in coming fellowship rounds, especially the ARC Discovery round in early 2011. Emphasis will be given to the quality of published research in our decision to appoint.

This is a full time position, fixed term for three years. Salary Level A A$69,853 - A$74,715 per year, plus 17% employer superannuation plus leave loading.

Applicants should systematically address the selection criteria in their application. The full information pack and selection criteria will be available from Friday at http://www.hr.unsw.edu.au/services/recruitment/employment.html Having read all the documentation you may direct any enquiries to Professor Rob Brooks on (61 2) 9385 2587 or email rob.brooks@unsw.edu.au.

Applications close 18 June 2010.

Rob Brooks www.eerc.unsw.edu.au

UOxford EvolutionaryBiology

University of Oxford The Queen's College BROWNE RESEARCH FELLOWSHIP IN BIOLOGICAL SCIENCE or BIOCHEMISTRY

The Governing Body proposes to elect to a postdoctoral Browne Research Fellowship in Biological Sciences or Biochemistry (excluding medical sciences). The successful candidate will, if possible, enter upon the Fellowship on 1 October 2010

The basic stipend of the Fellowship, which is pensionable under the Universities Superannuation Scheme, is £24,273 subject to adjustment in the light of any other emoluments enjoyed by the Fellow or in the light of any general alteration to University stipends. The Fellow will further receive an annual grant of up to £4,000 towards research expenses. The Fellowship will be tenable for three years only. The Fellow may be entitled to free rooms in College, if available (or to an allowance in lieu, currently £3,444), and to free meals in College. The Fellow may, with the leave of the Governing Body, engage in teaching up to a maximum of six hours weekly and, if teaching, would normally be expected to give priority to the College's own teaching needs.

Candidates must not have accumulated more than ten years in full-time postgraduate study or research by 1st October 2010; these ten years need not be continuous. Candidates must obtain written confirmation from the relevant Head of Department (Biochemistry, Plant Sciences, or Zoology) that laboratory space will be made available to the candidate if successful.

Further particulars are available from the College Office, The Queen's College, Oxford OX1 4AW, (telephone: 01865 279166); e-mail: particulars@queens.ox.ac.uk; or http://www.queens.ox.ac.uk/vacancies/ Applications should be submitted, preferably by e-mail to joyce.millar@queens.ox.ac.uk , the Academic Administrator, not later than 30th June 2010. Interviews will be held week beginning July 19th 2010.

John Pannell <john.pannell@plants.ox.ac.uk>

UPF Barcelona Metagenomics

A two-year postdoc position is available at the Institute of Evolutionary Biology (IBE), UPF-CSIC, Barcelona (http://www.ibe.upf-csic.es/ ; www.prbb.org), under the supervision of Francesc Calafell. The successful candidate will join a project in skin metagenomics: we are analyzing by ultrasequencing the microbial communities in human skin by themselves and in relation to the onset of psoriasis. We are looking for a Ph.D. in bioinformatics, genetics, or evolutionary biology, with a strong background in sequence analysis: assembly, alignment, tree construction, evolutionary analysis of sequences. Programming in PERL and other languages is a requirement. We seek a positive, analytical, proactive persone who feels comfortable working in a team.

Please send by July 9th a CV, a letter of intent and two references to:

Francesc Calafell, Ph D IBE, Institute of Evolutionary Biology (UPF-CSIC) CEXS-UPF-PRBB C/ Dr. Aiguader 88 08003 Barcelona, Catalonia, Spain

Tel: +34 93 3160842 Fax: +34 93 3160901 Email: francesc.calafell@upf.edu

Francesc Calafell <francesc.calafell@upf.edu>

USheffield AphidSpeciation

Postdoc - host race formation and speciation in pea aphid

University of Sheffield, Dept of Animal and Plant Sciences

We are a seeking a dynamic evolutionary genetics postdoc to work with Professor Roger Butlin and Dr Julia Ferrari (University of York) on evolutionary genetic analysis of host race formation in the pea aphid. The project focuses on chemosensory genes as candidates for key roles in host acceptance and uses a combination of gene capture, high-throughput sequencing and expression analysis. You will be responsible for the handling and analysis of large data sets and should have existing experience with the analysis of sequence and/or expression data in an evolutionary context, ideally including the development of bioinformatics pipelines and the use of model-based statistical approaches. A PhD (or equivalent experience) in evolutionary genetics is essential.

This post is fixed-term with a start date between 1st October 2010 and 1st February 2011 and is available until 30th June 2012. Salary will be in the range UKpound 28,139-31,671.

For further information contact Roger Butlin on r.k.butlin@shef.ac.uk

To apply, go to www.shef.ac.uk/jobs, post reference UOS001290

Closing date 5 July 2010

Roger K Butlin Professor of Evolutionary Biology

Animal and Plant Sciences University of Sheffield Western Bank Sheffield S10 2TN UK

Tel. +44 (0)114 2220097 FAX +44 (0)114 2220002

r.k.butlin@sheffield.ac.uk www.shef.ac.uk/aps Managing Editor, Heredity - http://www.nature.com/hdy/-index.html r.k.butlin@sheffield.ac.uk

USouthernCalifornia SpeciationGenetics

A postdoctoral position is available in the laboratory of Suzanne Edmands at the University of Southern California (Los Angeles). The postdoc would work on an NSF-funded project using the marine copepod *Tigriopus* *californicus*as a model for the genetics of speciation. The project involves 1) QTL mapping of traits involved in reproductive isolation using previously mapped SNPs and results of a large-scale breeding study and 2) development and mapping of candidate sex-linked loci.

The ideal candidate would be a recent Ph.D. with a strong background in quantitative and molecular genetics and excellent writing skills. Experience with SNPs, QTL mapping, bioinformatics and/or next-generation sequencing are highly desirable. The position is available immediately and applications will be considered until the position is filled. Initial appointment is for one year, with the possibility of a second year contingent on future funding.

Please apply via email to Suzanne Edmands (sedmands@usc.edu) and include a cover letter describing your research experience and interest in the position, your CV, your preferred start date, and contact information for three references

Suzanne Edmands Associate Professor Department of Biological Sciences 3616 Trousdale Parkway, AHF 316 University of Southern California Los Angeles, CA 90089 (213)740-5548 http://college.usc.edu/labs/-edmands/home/index.cfm edmandss@gmail.com

UStirling ResAssist BeeSpecies

I have funding for a 6-8 month post starting September 2010, based at the University of Stirling, Scotland. It has recently been discovered that the widespread bumblebee Bombus lucorum actually contains a number of cryptic species about which we know nearly nothing. Working in conjunction with partners at the Natural History Museum and Royal Holloway, this project will use mitochondrial sequencing to distinguish between species, using a large sample of bees from across the UK. Subsequent analyses will investigate niche partitioning and geographic distributions of the component species. Sequencing will be outsourced, but experience of analysing genetic data would be very useful. The post might suit a recent postdoc or experienced postgrad.

Enquiries and applications (CV + covering letter) to dave.goulson@stir.ac.uk

Professor Dave Goulson, Head of School School of Biological & Environmental Sciences, University of Stirling, Stirling FK9 4LA Tel: 01786 467759 http://www.sbes.stir.ac.uk/people/goulson/ Director, Bumblebee Conservation Trust, http://-www.bumblebeeconservation.org.uk New Book!! Dave Goulson. 2010. Bumblebees; their behaviour, ecology and conservation. OUP. http://ukcatalogue.oup.com/-product/9780199553075.do

Dave Goulson <dave.goulson@stir.ac.uk>

UToronto EvolutionOfSex TestingTheory

Post-Doctoral Position: Evolution of Sex - Testing Theory

A post-doctoral position is available in the Agrawal Lab in the Department of Ecology and Evolutionary Biology at the University of Toronto.

The evolution of sex is a classic problem that has generated much theory. However, direct experimental tests of most of these ideas are lacking. We are now using facultatively sexual rotifers to test various theories for the evolution of sex through experimental evolution and related approaches. We have had good success with our initial projects (in review) and it is clear that there is potential to do much more. I seek a postdoc interested in doing experimental work to test sex theory in any of a variety of dimensions.

I will be at this year's Evolution meetings in Portland if interested candidates wish to talk to me.

Interested candidates should contact me by email. Please include a single PDF attachment containing your c.v., a brief description of past research accomplishments and future goals, and the name and e- mail address of 2 potential references. Funding is guaranteed for 1 year, with a second year renewable depending on progress.

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.

Aneil Agrawal Ecology & Evolutionary Biology University of Toronto tel: 416-946-5563 http://-labs.eeb.utoronto.ca/agrawal/ a.agrawal@utoronto.ca

UToronto PlantAdaptation

Post-Doctoral Positions in Ecological and Evolutionary Genomics

Two post-doctoral positions are available in the Stinchcombe Laboratory, in the Department of Ecology and Evolutionary Biology at the University of Toronto. Work in my lab is focused on both the ecological causes and the genetic underpinnings of adaptation in plants.

I am interested in recruiting individuals to work on a collaborative, multi-investigator project on the genetic basis of ecologically important traits in the model plants Capsella grandiflora and Arabidopsis thaliana. Our goal is to apply association mapping, QTL mapping, and next-gen sequence / transcriptome analysis to understand the genetics of traits such as flowering time, freezing tolerance, and nitrogen-use efficiency. The project is collaborative Stephen Wrights group (http:/-/labs.eeb.utoronto.ca/wright) and there is potential for collaboration with Tom Bureau and Dan Schoen at McGill University. The position will involve greenhouse work, molecular work, and analysis of next-gen sequence and transcriptome data. A strong background in evolutionary or population genetics, experience with basic molecular techniques, and facility with data analysis and/or programming would be ideal.

I will be at this years Evolution meetings in Portland, and Stephen will be at this years SMBE meetings if interested candidates wish to talk to us.

Interested candidates should contact me by email. Please include a single PDF attachment containing your c.v., a brief description of past research accomplishments and future goals, and the name and e-mail address of 2 potential references. Funding is guaranteed for 1 year, with a second year renewable depending on progress.

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.

–

Sent from an old-fashioned desktop computer.

John Stinchcombe Department of Ecology and Evolutionary Biology University of Toronto, 25 Willcocks St. Toronto, ON Canada M5S 3B2

416-946-5986

http://labs.eeb.utoronto.ca/stinchcombe/ John Stinchcombe <john.stinchcombe@utoronto.ca>

UVirginia PlantPopulationDifferentiation

Postdoctoral Position: Plant Ecological Genetics

A post-doctoral position is available in the Galloway lab at the University of Virginia to work on an NSF-funded project to evaluate the contribution of maternal effects to population differentiation. The study will focus on phenological traits in the herbaceous autotetraploid Campanulastrum americanum. The project uses an ecological genetics approach and will include greenhouse studies and field work across a latitudinal gradient. In addition to collaborating on the project, the post-doc will have the opportunity to independently develop related research and to interact with the population biology and evolution communities at the University of Virginia. Candidates should have a background in ecological genetics and experience conducting field studies.

Start Date: as early as September Duration: potential for 3 years

To apply: Send a CV, a statement of research interests and experience, and the names and contact information for two references to lgalloway@virginia.edu . Review of applications will begin June 25. Informal inquiries are welcome.

For further information on the project and Galloway lab see: http://faculty.virginia.edu/galloway/ Or contact me directly: lgalloway@virginia.edu

– Laura F. Galloway Professor Department of Biology P.O. Box 400328 University of Virginia

http://faculty.virginia.edu/galloway/ Phone: (434) 982-5010

lgalloway@virginia.edu

UVirginia PopulationGeneticsGenomics

Postdoctoral Position

A postdoctoral position is available in the laboratory of Douglas Taylor at the University of Virginia. The postdoc would primarily involve molecular population genetics/genomics in the angiosperm species *Silene vulgaris*. The funding is not tied to a specific project, so I am looking for a colleague that would like to express their independent, creative energies to some ongoing priorities in the lab and to the future development of the system.

The ideal candidate would be a recent Ph.D. with a strong background in population and/or molecular genetics. Experience with bioinformatics, next-generation sequencing, and/or QTL mapping are desirable. We have at least two years of funding. The start date is flexible, but the position is available immediately. Applications will be considered until the position is filled.

Please apply via email to Douglas Taylor (dougtaylor@virginia.edu) and attach your CV, with a brief cover letter describing your interest in the position, your preferred start date, and contact information for three references. Please feel free to email me with questions.

The University of Virginia is an Equal Opportunity/Affirmative Action Employer.

Douglas R. Taylor Professor and Chair of Biology Department of Biology Box 400328 University of Virginia Charlottesville, VA, 22904-4328 (434) 982-5217 http://people.virginia.edu/~drt3b/index.php dougtaylor@virginia.edu

UZurich ExperimentalEvolution

Postdoctoral fellowship in experimental evolution

A postdoctoral fellowship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. The Wagner lab studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Ongoing projects involve laboratory evolution of yeast, E. coli and fruit-flies, as well as in vitro evolution of ribozymes. A sample of the laboratory's research can be found at http://www.bioc.uzh.ch/wagner/.* *Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and life's fundamental organizational principles. **

We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently on a project that he or she will develop. The labs work is concept-driven instead of system-driven, and projects are not restricted to the model organisms mentioned above. A successful candidate will have substantial research experience with molecular biological techniques, acquired in research with an evolutionary orientation. State of the art experimental technology is available through the Functional Genomics Center Zurich, which provides platforms for ultra-high throughput sequencing, transcriptomics, proteomics, and metabolomics. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further. The position offers a highly competitive salary of up to three years on annually renewable contracts.

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch: CV including publication list, a statement of research interests not exceeding three pages, including a sketch of an experimental evolution project, as well as three academic references. Please include the word "EXPEVOL10" in the subject line. The application deadline is August 1, 2010. The position is available immediately.

Andreas Wagner

Christiane Gujan Administrative Assistant of Prof. A. Caflisch and Prof. A. Wagner Zurich University Institute of Biochemistry Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Tel. 0041 (0)44 635 55 49 (secretariat Prof. Caflisch) Fax 0041 (0)44 635 68 62 (secretariat Prof. Caflisch)

Tel. 0041 (0)44 635 61 42 (secretariat Prof. Wagner) Fax 0041 (0)44 635 61 44 (secretariat Prof. Wagner)

Christiane Gujan <gujan@bioc.uzh.ch>

Vienna DrosophilaAging

Vienna, Austria: POSTDOCTORAL POSITION IN DROSOPHILA AGING

A postdoctoral research position in the genetics of Drosophila aging is available in the group of Thomas Flatt at the University of Veterinary Medicine (Department of Biomedical Research, Institute of Population Genetics), Vienna, Austria. The postdoc position is funded by a grant from the Austrian Science Foundation (FWF) and will be for three years.

This research project will focus on the identification of the molecular basis of the trade-off between reproduction and lifespan in the fruit fly, Drosophila melanogaster, a powerful genetic model system. In many organisms, from fruit flies to humans, reproduction shortens lifespan, but the underlying mechanisms remain unknown (see Flatt & Promislow 2007 in Science). Experiments in C. elegans suggest that hormonal signals from the gonad affect longevity (Hsin & Kenyon 1999 in Nature), and we have recently found that germline ablation extends lifespan and affects insulin signaling in Drosophila (Flatt et al. 2008 in

PNAS). However, the details of this systemic regulation of lifespan by the reproductive system remain unclear. In our project we are interested in dissecting the hormonal and metabolic mechanisms that modulate the reproduction-longevity trade-off. By employing mutant and transgene analysis, genetic manipulation of the gonad, epistasis experiments, metabolic measurements, and hormonal manipulations we will examine the endocrine mechanisms whereby signals from the reproductive system modulate adult longevity and physiology.

We are seeking a talented, independent, hard-working and self- motivated young biologist with good social skills. The successful candidate will have a Ph.D. and a strong background in genetics and molecular biology using the Drosophila system. Some background in the biology of aging, evolutionary biology, and/or endocrinology would be ideal, but is not required. The working language in the laboratory is English, so the candidate should be proficient in spoken and written English. German skills, although helpful, are not essential. The initial appointment will be made for one year, with a possible extension to up to three years. The annual salary is 56,110 Euro (before tax). The position is available as of now, but the starting date is negotiable.

In a 2009 world-wide survey by the William M. Mercer Institute, Vienna ranked first world-wide in terms of standards of living. Vienna is a beautiful, historical yet modern city, located in the heart of Europe, close to the Alps and to major cities like Munich, Zurich, Prague, and Budapest. Being famous for its concert sites, opera houses, theathers, museums, and coffee shops, Vienna also provides great outdoor activities, such as sailing on the Neusiedler See, ice skating, biking and hiking in the Viennese woods and the nearby Alps. Moreover, the city has a wide range of great restaurants, bars, wineries, cinemas, clubs, libraries, galleries, and art collections. The Vienna area is also an exceptional and highly international research environment. Four major life science universities and three world-class research institutes (GMI, IMBA, IMP) provide a dynamic and interactive setting. Vienna hosts an active Drosophila community, and the onsite availability of the Drosophila RNAi center (VDRC) provides a great opportunity for functional Drosophila work. In population genetics and evolutionary biology, the Vienna research area also provides excellent prospects, due to a growing number of evolutionary research groups.

To apply, please send a single pdf file including: (1) a cover letter explaining why you would like to join our group, (2) your Curriculum Vitae (including a description of your skills), (3) your publication list, (4) a statement of research interests, and (5) contact details for 2-3 references who are willing to write a reference letter on your behalf to the following e-mail address: thomas.flatt@vetmeduni.ac.at Informal inquiries are welcome and should be sent to the same e-mail address. For further information see (http://i122server.vu-wien.ac.at/pop/Flatt_website/flatt_home.html).

The deadline for submission is 15 August 2010.

Dr. Thomas Flatt Institute of Population Genetics Department of Biomedical Sciences University of Veterinary Medicine Vienna Veterinärplatz 1 A-1210 Wien Austria/Europe

VOX +43-1-25077-4334 FAX +43-1-25077-4390 E-mail: thomas.flatt@vetmeduni.ac.at

Lab Website: http://i122server.vu-wien.ac.at/pop/-Flatt_website/flatt_home.html Vienna Graduate School of Population Genetics: http://www.popgen-vienna.at flatt.thomas@gmail.com

---

Vilnius HostParasiteEvolution

I am looking for an enthusiastic and well-motivated person who would like to join my laboratory to study vector-related aspects of transmission of avian haemosporidian parasites (species of Haemosporida) in Europe for 2 years. We need her/his help in field, experimental and molecular genetics studies aiming to contribute to the better understanding of evolutionary interactions in host parasite systems involving dipteran vectors, haemosporidians parasites and passeriform birds. More specifically, he/she will be focusing on 1) determining specificity of avian haemosporidian parasites (species of Plasmodium and Haemoproteus) with respect to vectors (species of the Culicidae and Ceratopogonidae) combining molecular and microscopy tools, 2) throughput sequencing and developing of new molecular markers for avian haemosporidian parasites. This study will be done in close collaboration with other members of my group according to an ongoing long-term grant. Candidates should have 1) Ph.D. degree within the period of 5 years (maternal and childcare leave are not taken into account) and 2) a strong background in biology and molecular genetics. Experience in parasitology and studies of blood-sucking dipteran insects will be a strong merit.

For preliminary consideration, interested persons should contact Gediminas Valkiunas (Institute of Ecology, Nature Research Centre, Vilnius, Lithuania gedvalk@ekoi.lt). Please send brief curriculum vitae, brief description of research experience and interests, and the names of 2 references. If successful, an application for postdoc position should be prepared together with G. Valkiunas; it should be submitted to the Research Council of Lithuania until 10 August 2010 (see https://www.postdoc.lt/news/33/66/CALL-FOR-OUTLINE-PROPOSALS).

May I please ask you to consider this information for announcement in the Evolutionary Directory? That would be very helpful.

Thank you very much Sincerely Gediminas Valkiunas, Ph.D., D.Sc.

Member of the Lithuanian Academy of Sciences, Head of the Laboratory of Parasitology Institute of Ecology Nature Research Centre Akademijos 2, Vilnius - 21 LT - 08412 Lithuania Tel. +370 5 2729269 Fax +370 5 272 93 52 gedvalk@ekoi.lt

“gedvalk@ekoi.lt” <gedvalk@ekoi.lt>

WoodsHole MicrobialBiogeography

*****NOTE: Please apply online at http://mbl.simplehire.com. I cannot accept emailed applications. *****

Position Title: Postdoctoral Scientist, Microscale Microbial Biogeography, Bay Paul Center.

Position Summary: A postdoctoral position using advanced imaging and next-generation sequencing of leaf surface microbial communities to study microbial biogeography at small scales is available in Sheri Simmonsâs lab at the Bay Paul Center, Marine Biological Laboratory, Woods Hole MA.

Additional Information: In recent years several studies have examined whether microbial systems demonstrate the same ecological patterns documented in macro-organisms, with a particular emphasis on factors producing biogeographical patterns of microbial diversity and whether deterministic or neutral factors dominate community assembly. However, two central issues have not been addressed: (1) sampling typically occurs on length scales many orders of magnitude larger than a typical microbial cell and (2) usually only taxonomic (16s) diversity is assayed.

The successful candidate will have the opportunity to develop leaf surface microbial communities into a model system for assaying (i) how microbial community assembly operates at âmicrobialâ (micrometer to centimeter) scales and (ii) whether taxonomic, genetic, and functional measures of microbial diversity (as assayed with high-throughput next-gen sequencing) show common patterns over space and time.

The suite of tools available for this project include : a MBL-owned greenhouse for controlled growth of model plants, expertise in next-gen (454/Illumina) sequencing and microbial community imaging, a Zeiss PALM CombiSystem for laser microdissection of individual leaves, and substantial bioinformatics capacity in the Bay Paul Center.

Funding support is available for 2 years with the potential for extension. Review of applications will continue until the position is filled.

Basic Qualifications: A Ph.D. in the biological sciences; applicants with diverse backgrounds are encouraged to apply. Experience in one or more of the following areas is preferred: molecular microbial ecology techniques, ecological theory, plant biology, FISH/imaging, bioinformatics, and/or analysis of next-generation sequencing data. The candidate should be interested in interdisciplinary research and have excellent communication skills (oral and written).

Required Applicant Documents: CV, cover letter, 3 references, Research Goals

Special Instructions to Applicants: Please submit three items: (i) a cover letter describing your research goals and your specific motivation to join the lab, (ii) a CV, and (iii) contact information for three references, including your Ph.D. supervisor.

Sheri Simmons Assistant Scientist | Bay Paul Center, Marine Biological Laboratory 7 MBL St Woods Hole, MA 02543 http://jbpc.mbl.edu/cv-simmons.html

ssimmons@mbl.edu

WorkshopsCourses

AarhusU omicsTechnology Sep5-8

PhD course 5^th -8^th September 2010

Introduction to omics technology in evolutionary and conservation biology

Oraganizers: Pernille Sarup, Torsten Kristensen, Vanessa Kellermann, Department of Biological Scineces, Aarhus Universtiy, Ny Munkegade 1540, 8000 Aarhus C, Denmark.

Venue: Sandbjerg Estate, Sandbjerg 102, 6400 Sønderborg

http://www.sandbjerg.dk/eng/welcome.aspx Supported by: Nordforsk Network and Aarhus Stress Network

Exploring the use of omics technology in natural populations

5^th - 8^th September 2010

Workshop contacts: Pernille Sarup (pernille.sarup biology.au.dk), Vanessa Kellermann (vanessa.kellermann biology.au.dk)

The use of omics technology (genomics, transcriptomics, proteomics, metabolomics) in evolutionary and ecological biology is increasing. This workshop will aim to explore the different levels of omics technology in an ecological and evolutionary context with a focus on methods and analysis of different omics technology as well as exploring how these different technologies can be integrated to form a systems view of evolutionary biology.

In this Ph.D course and workshop we bring together researchers with a primary focus on the use and integration of omics techniques in evolutionary and conservation biology. We have organised attendance from leading scientists in the field that will give lectures on relevant topics. The students will receive a compendium with original research articles representing the latest research within the topic. During the course time will be set aside for group discussions on central themes based on the articles, and also there will be time to discuss your own projects. Students will be expected to actively participate in the workshop with a presentation of either a talk or poster on your design or results in order to obtain 5 ECTS.

Additional information will be available on the NordForsk website: http://www.helsinki.fi/biosci/egru/-norden/workshops.html Deadlines:

Sign up by sending an email to the workshop contacts before 30th of June. Send in your abstract before 15^th of August.

Payment:

For members of the NordForsk network participation is for free. Also you can apply for travel grants. Participants from outside Scandinavia please contact for course costs.

List of confirmed speakers

Prof Douglas Crawford, The University ofMiami,USA.

Assistant Prof Dr Margie Oleksiak, The University ofMiami,USA

ProfChristian Schlötterer,The Veterinärmedizinische Universität Wien,Austria

Anders Malmendal, The InterdisciplinaryNanoscience Center atAarhus University, DK.

Jesper Bechsgaard, Department of Biological Sciences,Aarhus University, DK.

Jesper Sørensen, National Environmental Research Institute,Aarhus Universitey, DK.

Torsten Nygård, Faculty of agricultural sciences, Aarhus Universitey, DK.

Peter Sørensen, Faculty of agricultural sciences, Aarhus Universitey, DK.

Prof Ole Nørregaard Jensen, Department of Biochemistry and Molecular Biology, University of southern-Denmark, DK.

vanessa.kellermann@biology.au.dk

Bergen Norway ContemporaryEvolution Oct4-9

Nordic Marine Academy Course held in Bergen, Norway Oct. 4-9, 2010

Contemporary Evolution: Humans as Agents of Selection Credits: 3 ECT Course website: http://www.bio.uib.no/evofish/pages/NMA2010/-NMA2010.php Deadline for application: Aug. 20th

Lecturers: 10 invited lecturers from Norway, the Netherlands, the US, and Finland

Course Description: In medicine and agriculture, managing evolution is commonplace. Breeders of domesticated animals and plants have steered evolution for millennia, whereas during past decades, attempts to avoid resistance evolution has become a major issue in both human health and agriculture. In dealing with wild populations, awakening to contemporary evolution has just started. Yet there is little doubt that humans are the greatest evolutionary force of modern times. Wherever humans are present, pristine habitats are absent or rare, and even the most remote places are influenced by climate change and pollutants. Humans transport animals and plants to novel environments. Populations that are resources to humans may have humans as their primary predator or herbivore. All these changes have evolutionary implications, and understanding them is an important task in managing and conserving the environment.

The course is an opportunity to bring together young and experienced scientists with various backgrounds in evolutionary ecology. The course aims to present theory and techniques, statistical and modeling, to measure human-induced evolution in marine, freshwater, and terrestrial environments, covering topics from the effects of environmental degradation and noise pollution through to selective removal of individuals (hunting). The course will suit both experienced postdocs and doctoral students curious in expanding their quantitative skills.

Intended audience: The course will be of interest to those working on organisms spanning both terrestrial and aquatic systems in evolutionary ecology, fisheries, behavioral ecology, life history theory (including exploitation-induced and contemporary evolution), wildlife biology, and conservation biology.

For more information, contact: Jennifer Devine jennifer.devine@bio.uib.no http://www.bio.uib.no/evofish Jennifer Devine <jennifer.devine@bio.uib.no>

ColdSpringHarbor ComparativeGenomics Nov3-9

Course announcement - Application deadline, July 15, 2010

Cold Spring Harbor COMPUTATIONAL & COMPARATIVE GENOMICS November 3 - 9, 2010 Application Deadline: July 15, 2010 INSTRUCTORS:

William Pearson, University of Virginia, Charlottesville, VA Lisa Stubbs, University of Illinois, Urbana, IL This course presents a comprehensive overview of the theory and practice of computational methods for the identification and characterization of functional elements from DNA sequence data. The course focuses on approaches for extracting the maximum amount of information from protein and DNA sequence similarity through sequence database searches, statistical analysis, and multiple sequence alignment. Additional topics include alignment and analysis of short read "Next-Gen" sequencing data, identification of conserved signals in aligned and unaligned sequences, regulatory element and motif recognition and integration of genetic and sequence information in biological databases.

The course combines lectures with hands-on exercises; students are encouraged to pose challenging sequence analysis problems using their own data. The course makes extensive use of local WWW pages to present problem sets and the computing tools to solve them. Students use Windows and Mac workstations attached to a UNIX server. Some Unix experience may be helpful, but advanced programming skills are not required. The course is designed for biologists seeking advanced training in biological sequence and genome analysis, computational biology core resource directors and staff, and for scientists in other disciplines, such as computer science, who wish to survey current research problems in biological sequence analysis.

The lecture/lab schedule for the 2009 course can be found at fasta.bioch.virginia.edu/cshl. The 2010 course will provide more emphasis on analysis of genomic DNA sequences from NextGen data.

Speakers in 2010 course will include: Aaron Mackey, U. of Virginia, Next-Gen analysis pipelines Bert Overduin, European Bioinformatics Institute, UK, ENSEMBL and BioMart William Pearson, U. of Virginia, Similarity searching, multiple alignment Saurabh Sinha, U. of Illinois, Urbana, Genomics of gene expression Lisa Stubbs, U. of Illinois, Urbana, Genome browsing, comparative genomics James Taylor, Emory, Galaxy and genome analysis pipelines Barbara Wold, California Institute of Technology, Next-Gen Biology The primary focus of the Computational and Comparative Genomics Course is the theory and practice of algorithms used in computational biology, with the goal of using current methods more effectively and developing new algorithms. Cold Spring Harbor also offers a “Programming for Biology” course, which focuses more on software development.

To apply to the course, fill out and send in the form at:

http://meetings.cshl.edu/course/-courseapp_instr.shtml wrp@virginia.edu

Germany GenomeEvolution Sep5-11

Summer School on “Genome Evolution”

5th until 11th of September 2010, Frauenchiemsee, Germany

Faculty: Claudia Acquisti (Arizona State University) William Cresko (University of Oregon) Ken Wolfe (Trinity College Dublin) Jan Korbel (EMBL Heidelberg) Kai Müller (WWU Münster) Alexandros Stamatakis (TU Munich) John Parsch (LMU Munich) Erich Bornberg-Bauer (WWU Münster) Philine Feulner (WWU Münster, summer school coordinator)

Target participants: early PhD students, advanced master students

During our summer school 18 participants will enjoy lectures, seminars and hands on practical training. Lecturers will give insights into current topics of genome evolution and demonstrate recent genomic approaches. Participants are asked to bring their laptop along for our practical sessions. In addition the participants will get the chance to present and discuss their own projects and obtain advice on their project design and analysis setup.

A tentative schedule can be found here: http://ieb.uni-muenster.de/General/Summer-School.html The costs of participation (board and lodging at Frauenchiemsee http://www.frauenwoerth.de/) will be covered by the VW foundation. The summer school is jointly organised be the WWU Münster and the LMU Munich.

To apply, send a single file (pdf) containing a short motivation letter, a cv and an abstract of your project to p.feulner(at)uni-muenster.de

Deadline for application: July 15th, 2010

p.feulner(at)uni-muenster.de

MasseyU FungalGenomics Nov22-24

International Fungal Genomics Workshop Massey University, Palmerston North, New Zealand 22-24 November 2010

* Current status of fungal genomics * Comparative and evolutionary genetics of fungi * Fungal genome sequencing and assembly * Structural and functional annotation of fungal genomes

Workshop instructors include: Murray Cox (Massey University Palmerston North, New Zealand) Natalie Fedorova (J. Craig Venter Institute, USA) Austen Ganley (Massey University Albany, New Zealand) Li-Jun Ma (Broad Institute, USA)

For further details, see http://fungal.massey.ac.nz/ More information will be posted shortly.

-Murray

Dr Murray Cox Massey University E m.p.cox@massey.ac.nz T +64-6-356 9099 ext. 2570 W http://massey.genomicus.com Murray Cox <murray.p.cox@gmail.com>

MDIslandLabs FitnessEnvironment Aug21-28

Summer Course in Environmental Genomics at the Mount Desert Island Biological Lab

A technical course to guide research into how environmental conditions affect gene responses and the fitness of organisms

Date: August 21 to August 28, 2010. Number of participants: Restricted to 20.

http://www.mdibl.org/courses/Environmental_Genomics/199/ Environmental genomics seeks to understand how gene function is influenced by environmental conditions while accounting for variation that exists within and among natural populations. Two significant advances create opportunities to finally link gene-environment interactions to the fitness of individuals and to population-level outcomes. (1) Genome and transcriptome sequences are rapidly becoming available for a growing number of species whose ecology and physiology are well understood. (2) Sophisticated tools for high-throughput biology, statistical analysis and informatics are rapidly becoming more accessible to single investigator laboratories. This course is built on the paradigm that the research field will most effectively grow by properly designing large-scale experiments enabled by drastically increased sample-throughput and lower costs. Most importantly, the challenges of manipulating and analyzing population-level genomics data must be addressed.

This course trains researchers to design studies, and to collect and analyze state-of-the-art gene expression data. Each participant will perform a new experiment using 12-plex microarrays that are designed to study the freshwater microcrustacean Daphnia. The class results will be combined for a scientific publication – coauthored by class participants – that describes the individual and shared molecular signatures of stress responses. Daphnia is used for training because of its growing use as a model system for environmental genomics and for improving environmental health protection, yet the skills learned during the course will be applicable to all study systems with mature genomics resources.

Participants will also obtain hands-on training on the latest automation protocols for higher-throughput processing of next-generation sequencing samples, and will learn computational methods to manage and analyze genomics-scale data sets.

Ultimately, participants will be better positioned to incorporate these technologies into their own research laboratories, while better understanding how functional genomics and automation can be applied to ecology, evolution and toxicology.

The faculty at MDIBL is pleased to help advance this new field of research. Support for this training course is provided by The Indiana University Center for Genomics and Bioinformatics, Beckman Coulter Inc., Roche NimbleGen Inc., and Life Technologies Inc.

Please download the poster announcement at: https://www.slashtmp.iu.edu/public/download.php?FILE=jcolbour/95321SVkA2O The Center for Genomics and Bioinformatics, Indiana University CGB - https://projects.cgb.indiana.edu/display/grp/Overview Daphnia Genomics Consortium - http://daphnia.cgb.indiana.edu/ jcolbour@cgb.indiana.edu

---

Switzerland Speciation Aug29-Sep4

We announce an ESF-funded summer school “Methods in Empirical Speciation Research”, taking place August 29 to September 4, 2010 in Switzerland. We still have travel support and accommodation for additional participants and consider applications until June 30th.

The school is part of the European Science Foundation Networking Program Frontiers in Speciation Research (FROSpects) and is open for PhD students, early stage Postdocs and exceptionally well qualified MSc students. Venue is the EAWAG Center of Ecology, Evolution & Biogeochemistry (CEEB) in Kastanienbaum on the shores of Alpine fjord Lake Lucerne.

Speciation research is currently one of the most vibrant fields in evolutionary research. Its success became possible because of advances in empirical methods, concepts and theory building in population genetics and evolutionary ecology. We are now in the early stage of yet another wave of advance, associated with the genomics era. Studying speciation is a deeply interdisciplinary endeavor that often requires good understanding of very many different concepts and methods in ecology, genetics and evolution. This makes speciation research sometimes more difficult to access for young scientists than more disciplinary research questions in ecology and evolution. In this summer school we want to introduce graduate students to the ways experienced and successful speciation researchers integrate concepts and methods from ecology, genetics, genomics and behavioural biology in an attempt to elucidate causes, mechanisms and consequences of, and constraints to speciation.

The course, taught by an international team of established speciation researchers, will provide state of the art overviews of major topics, as well as first hand insights into specific issues. In four mornings Roger Butlin (U Sheffield), Scott Hodges (UC Santa Barbara), Catherine Peichel (Fred Hutchinson Cancer Research Centre) and Glenn-Peter Saetre (CEES Oslo) will teach empirical lecture modules. Latest developments in speciation theory will be taught in a fifth lecture module by Sander van Doorn (U Bern). In the afternoons we will offer workshops and excursions to speciation study sites. These and a series of evening spotlight-on-research lectures will be taught by Elena Conti (U Zürich), Martine Maan (U Bern, Eawag), Walter Salzburger (U Basel), Ole Seehausen (U Bern, Eawag), Arjun Sivasundar (U Bern), Piet Spaak (Eawag) and Alex Widmer (ETHZ). The class size will not exceed 25 students and students will have ample opportunity to interact with teachers and staff througho ut the week. We provide students with travel grants, free on-site accommodation and meals.

For more information see http://www.eawag.ch/lehre/-phd/schools/frospects/index_EN If you are interested, email a letter of application and a CV to Nadja Pepe at nadja.pepe@eawag.ch before June 30th. Later applications can only be considered if places are available.

For questions, contact Ole Seehausen (ole.seehausen@eawag.ch), http://www.eawag.ch/-organisation/abteilungen/fishec/index_EN Ole.Seehausen@eawag.ch

---

UCaliforniaLosAngeles MathComput Genomics Fall2011

Mathematical and Computational Approaches in High Throughput Genomics, September 12-December 16, 2011.

We would greatly appreciate your help in advertising this program. Feel free to print the attached poster and hang it in your department.

At this time, we are especially interested in receiving applications to participate for the entire fall semester and would in particular welcome an application from you. To get more information and/or apply please visit

*http://www.ipam.ucla.edu/gen2011 All applicants should fill out the online application form and submit a curriculum vitae. It is important to include the desired dates of participation and possible references. Postdoctoral Scholars and Graduate Students should have two letters of recommendation sent on their behalf. Assistant Professors and Junior Faculty are advised to have one letter of recommendation sent on their behalf. Note that letters do not necessarily need to be as formal a those provided for a job application. They can be a couple of paragraphs by email, but should comment on how the person would contribute to and/or benefit from the program. IPAM is generally able to offer a housing and travel allowance to accepted participants coming from outside of the UCLA area. On the application, there is a place to indicate the support requested.

Please send any additional questions to *gen2011@ipam.ucla.edu*. We look forward to hearing from you.

Sincerely, Amber Puha

Amber Puha, Associate Director Institute for Pure and Applied Mathematics 406 Portola Plaza, Suite 1158 Box 957121 MC: 712105 Los Angeles, CA 90095-7121 1(310)206-2831 1(310)825-4756 Fax Email: apuha@ipam.ucla.edu www.ipam.ucla.edu Amber Puha <apuha@ipam.ucla.edu>

UCaliforniaLosAngeles StatGenetics Aug16-20

There will be a five-day workshop in August 16-20, 2010 on statistical genetics, and featuring the Mendel Statistical Genetics Software package. This short course will be taught by faculty from UCLA and UNC-Chapel Hill and is designed for people who will be doing statistical analysis of genetics projects.

More information is in the announcement below, and at http://genomics.unc.edu/events/statgen/-index.html Thank you,

The Statistical Genetics Short Course Instructors.

Workshop Announcement:

STATISTICAL GENETICS SHORT COURSE August 16-20, 2010 At the Rizzo Conference Center Chapel Hill, North Carolina http://genomics.unc.edu/events/-statgen/index.html We will hold a five full-day intensive workshop on state-of-the-art statistical genetics methods for detection of genetic loci for complex traits, either qualitative or quantitative.

Each day will include hands-on computer exercises using statistical genetics computer programs, especially the Mendel software package, with it's new graphical front-end.

We will cover the general theory behind the methods as well as emphasize the practical aspects needed to give the best chances of success. The Course is designed to assist people who are actively studying the genetics of complex traits. Topics will include:

* Statistical Reviews * Genetic Study Design * Quality Control and other data issues * Haplotyping * Analysis of Qualitative and Quantitative Traits including: - Parametric and Non-Parametric Linkage (NPL) analysis - Methods for Large Pedigrees - Association Testing: + Case/Control + Genome-Wide Studies (GWAS) + Family-based * Copy Number Variation (CNV) * Ethnic Admixture Analysis * Other Recent Advances

Participants in the Course need no prior experience with these methods or programs. Participants will be required to bring a laptop computer to run the analysis exercises.

The Course features instructors from the Statistical Genetics Group of the UCLA Department of Human Genetics as well as Statistical Genetics instructors from UNC-Chapel Hill:

1. Kenneth Lange 2. Rita Cantor 3. Jeanette Papp 4. Janet Sinsheimer 5. Eric Sobel

The cost of the course, which includes lunch and snacks every day and a group dinner on Thursday, is:

US $900 for students and postdocs from non-profit institutions US $1000 for staff and faculty from non-profit institutions US $1200 for individuals from for-profit institutions

Transportation and lodging are not included

Deadline for application is 1 July 2010. The course will be held 16-20 August 2010 in Chapel Hill, North Carolina. Lectures will be at the Rizzo Conference Center. Accommodations are available at the Rizzo Center or other nearby hotels.

For more information, including the simple application process, please visit http://genomics.unc.edu/events/-statgen/index.html Thank you!

Janet@mednet.ucla.edu

UHawaii WaterAndEvolution Jan3-17

Title: Astrobiology Winter School for Graduates

The University of Hawaii branch of the NASA Astrobiology Institute will host a winter school on the theme of water and the evolution of life in the cosmos, from Monday January 3rd to Monday January 17th 2011. This school will provide approximately 40 post-graduate participants with a broad but high-level introduction into astrobiology, emphasizing the origin and role of water in the emergence of life on our planet, and in the search for life elsewhere. It will be truly multidisciplinary, bringing together students and researchers from the diverse scientific backgrounds that contribute to our understanding here. Hawaii offers ideal resources for this training opportunity, from world-leading astronomical observing facilities through state of the art cosmochemistry simulation equipment to unique geologic environments in which extremophile life exists. Applications are invited from all graduate and post-doctoral students whose research interests intersect with astrobiology.

For evoldir readers, the primary draw of this winter school may be its emphasis on communicating the non-biological context for the origin of life (i.e. the chemistry, geology and astronomy of relevance to astrobiology)

Successful applicants will be funded for travel, accommodation and all relevant costs (although we are still figuring out some new legislature which may require us to charge a small paperwork processing fee and tax for participants who are not U.S. citizens - if you are interested in the opportunity, then we encourage you to apply, and we can talk through these details at the time of making an offer!) Further details and application form are available at : http:/-/www.ifa.hawaii.edu/UHNAI/2011winterschool/ Stephen Freeland <freeland@ifa.hawaii.edu>

UManchester Morphometrics Nov8-Dec17

Dear colleagues

I am pleased to announce this year's morphometrics course from the University of Manchester. This year's course will run in the six weeks from 8 November to 17 December 2010.

The course information can be found on the following we site: http://www.flywings.org.uk/MorphoCourse Course content: * Data acquisition: the kinds of data and the equipment used to collect them. * Definitions of size and shape * Geometric methods to characterise shape from a configuration of landmark points (Procrustes superimposition) * Statistics of variation, scatter plots, basic multivariate statistics * Principal component analysis * Measurement error and outliers * Shape transformations and 'warping' – the thin plate spline * Analysis of outline shapes * Distinguishing between groups (taxonomy, clinical diagnosis, etc.) * Allometry and size correction * Influence of external factors on shape (ecomorphology, dose- response studies) * Symmetric forms and measurement of asymmetry. * Morphometric inferences on developmental processes, morphological integration, modularity * Genetics of shape: analyses of resemblance between relatives, QTL analyses. * Phylogeny: reconstructing the evolution of shape

Practice examples: As far as possible, practical exercises are provided to accompany the course content. These practice exercises consist of data sets and explanations on how to run the respective analyses using the MorphoJ software (http://www.flywings.org.uk/MorphoJ_page.htm). Participants who already have their own data are encouraged to use those and to discuss them as part of the course. I hope there will be a bit of a 'workshop' feel to the course unit.

Group work: Participants will work in small groups to prepare web presentations of possible morphometric studies (wikis prepared by the groups). This activity stimulates discussion and provides a broad overview of the broad range of questions that can be addressed with morphometric methods.

The fee for the course is GBP 250.00 (I'm afraid it's gone up again from last year – this is out of my control).

All prospective participants need to pre-register for the course. The deadline for this is the *10 September 2010*.

For further details, see the course web page: http://www.flywings.org.uk/MorphoCourse Best wishes, Chris

–

Christian Peter Klingenberg Faculty of Life Sciences The University of Manchester Michael Smith Building Oxford Road Manchester M13 9PT United Kingdom

Telephone: +44 161 275 3899 Fax: +44 161 275 5082 E-mail: cpk@manchester.ac.uk Web: http://www.flywings.org.uk Skype: chris_klingenberg

cpk@manchester.ac.uk

Yunnan China TropicalConservation Nov20-Dec18

Field Course in Tropical Biology and Conservation

This course is an introduction to tropical forests dynamics and conservation designed for advanced undergraduate and beginning graduate students.

Format: Course activities will be split between lecture and field exercises. Students will participate in on-going experiments to establish long term monitoring efforts. Students will design independent projects. The course concludes with a symposium, where students present results of course activities and compete for the AFEC best research award.

Where: The course convenes in Kunming (capital city of Yunnan Province, China) after which we move to Xishuangbanna Tropical Botanical Garden near the Lao ?C Burma borders. The field work will take place in Mengsong near the Burma border, an area with a variety of rice fields, tea plantations, secondary forests and magnificent primary forest.

Topics: Tropical Ecology, Eco-Physiology, Taxonomy, Evolutionary Ecology, Plant and Animal Interactions, Biodiversity, Conservation Biology, Invasive Species and more!

Instructors: The various topics will be taught by professors from several institutes including The Chinese Academy of Sciences, Leiden University, Texas Tech University, Netherlands Center for Biodiversity, Kunming Institute of Zoology.

For more information and registration visit http://www.pfs-tropasia.org/ Ferry Slik Professor Ecological Evolution Group Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences Menglun, Mengla, Yunnan 666303, China Tel. +86-15969470367

Website http://www.phylodiversity.net/fslik/ Plants of Southeast Asia http://www.asianplant.net Trees of Sungai Wain http://www.nationaalherbarium.nl/Sungaiwain/ Asian plant species synonym website http://www.phylodiversity.net/fslik/synonym_lookup.htm Macaranga and Mallotus of Borneo http://www.nationaalherbarium.nl/MacMalBorneo/index.htm Ferry Slik <ferryslik@hotmail.com>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly 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.

Afterword

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.