EvolDir

June 1, 2018

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.

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Conferences

AGA Hawaii Origins Jul22-25 Deadline

Registration for the 2018 American Genetic Association Symposium, “Origins of Adaptive Radiation” ends June 1st!

The meeting, to be held July 22-25 in Waimea, Hawaii, will explore processes at the early stages of adaptive diversification.

The Kohala region where the meeting will take place is far from the volcanic activity. Here is a link to the hazard zones on the island: volcanoes.usgs.gov/vhp/hazard_zones.html Hawaii Preparatory Academy is in Zone 8, a low-risk area.

Register at https://www.theaga.org - $225 fee includes opening reception, closing luau, lunches and coffee breaks, and a 3-YEAR AGA membership plus Journal of Heredity subscription.

All details are available on the website. If you have additional logistical questions, please contact Anjanette Baker. For any questions regarding the content of the symposium, please contact Rosemary Gillespie.

Best wishes,

Rosemary Gillespie, AGA President gillespie@berkeley.edu

Anjanette Baker, AGA Manager theaga@theaga.org

theaga@theaga.org

AGA Hawaii Origins Jul22-25 Update

Yes, the AGA:Hawaii symposium is still on!

The Kohala region where the meeting will take place is far from the volcanic activity. Here is a link to the hazard zones on the island: volcanoes.usgs.gov/vhp/hazard_zones.html Hawaii Preparatory Academy is in Zone 8, a low-risk area.

The 2018 American Genetic Association Symposium, "Origins of Adaptive Radiation" will be held July 22-25 in Waimea, Hawaii. The meeting will explore processes at the early stages of adaptive diversification.

Invited speakers will explore concepts of admixture, hybridization, fragmentation, plasticity, and priority using diverse systems. The goal is to look for commonalities, while also exploring the many local Hawaiian radiations.

Register at https://www.theaga.org - $225 fee includes opening reception, closing luau, lunches and coffee breaks, and a 3-YEAR AGA membership plus Journal of Heredity subscription.

If you have any logistical questions, please contact Anjanette Baker. For any questions regarding the content of the symposium, please contact Rosemary Gillespie.

Best wishes,

Rosemary Gillespie, AGA President gillespie@berkeley.edu

Anjanette Baker, AGA Manager theaga@theaga.org

Anjanette Baker <theaga@theaga.org>

Barcelona Hennig2018 Sep16-20

Dear Colleagues

The early bird registration and abstract submission to the XXXVII Annual Meeting of the Willi Hennig Society, has been extended to June 1st, 2018.

The meeting will be held in Barcelona, from September 16th to 20th, 2018. Please, save the dates.

Travel and childcare awards are available to assist the congress, deadline submission July 1st

For any further information and updates, check the congress website at http://www.hennig2018bcn.org Confirmed plenary speakers include:

Christophe Dessimoz, University of Lausanne, Switzerland Greg Edgecombe, The Natural History Museum, London, UK Gonzalo Giribet, Harvard University, USA Dan Rabosky, University of Michigan, USA Isabel Sanmartín, Real Jardín Botánico de Madrid, Spain

We look forward to seeing you in September!

The organizing committee XXXVII Annual Meeting of the Willi Hennig Society

Miquel Arnedo <marnedo@gmail.com>

Bordeaux Morphometrics Jun18-20 DeadlineMay15

Dear colleagues,

We are pleased to announce that the deadline for registration to the SMEF10 has been extended to May, 15th.

The 10th SMEF "Symposium de Morphométrie et Ãvolution des Formes" which will be held in Bordeaux (France), June 18th to 20th, 2018

The SMEF meetings aim to foster exchanges among users of morphometric approaches in different fields of research, such as evolutionary biology, developmental biology, systematics, paleontology, bioarchaeology and ecology. This approach is traditionally targeted at researchers interested in the morphological quantification of biological form. This year, the symposium will also include a special focus on the material culture in archeology.

More information, registration, and abstract submission are available on the SMEF10 website:

https://smef-2018.sciencesconf.org/ This year we are very glad to welcome Dr. Philipp Mitteröcker (University of Vienna) as keynote speaker.

For anyone interested in visiting the historical center of Bordeaux, a mid-congress guided visit will be organized.

We look forward to seeing you in Bordeaux!

The organizing committee of the 10ˆth SMEF

Nicolas Navarro <nicolas.navarro@u-bourgogne.fr>

Curacao InvertGenomics Oct19-21

Travel Support Award to attend 3rd Bi-annual Global Invertebrate Genomics Alliance Conference and Workshop (GIGAIII)

We would like to announce a funding opportunity to support graduate and postdoctoral student attendance to the 3rd bi-annual Global Invertebrate Genomics Alliance Conference and Workshop (GIGAIII) to be held in Curaçao this Fall, October 19-21st, 2018. The funding is available through a recent NSF conference grant awarded to GIGA researchers at Florida International University. The overarching goal of GIGA is to form a collaborative network of diverse scientists that wish to advance the state of invertebrate (non-insect/non-nematode) genomic research for the international scientific community. The 3-day conference will include a series of training and breakout sessions in addition to more formal presentations and posters. GIGAIII will provide opportunities for training at multiple career levels and the purpose of this travel support is to encourage advanced graduate student and postdoctoral attendance to actively engage with experts in their field. More information on GIGAIII can be found on the conference website (https://gigaiii.weebly.com/). A limited number of fellowships are being made available to advanced-standing graduate students and postdoctoral researchers and will facilitate international travel to Curaçao and lodging at the conference hotel (Hilton Hotel Curaçao). Applicants must be registered for the conference and currently enrolled/ employed at a US-based institution to be eligible for this funding. Applications by members of underrepresented groups are especially encouraged. To apply, applicants must submit *1)* a curriculum vitae *2)* a 2-page statement that includes a) how attendance at this conference will advance their future career goals and b) an explanation for the financial need. Applicants must also include *3)* a budget with a cost breakdown for the proposed travel, including total costs and any possibility of co-funding. *If applicants are willing to share hotel lodging (max. 2 person/room), this should be indicated in the budget justification and will increase the number of awards we can provide. *Successful applicants will receive support towards airfare expenses and/or lodging at the Hilton Curaçao < https://secure3.hilton.com/en_US/hi/reservation/book.htm?execution=e2s1 > during GIGAIII. Applications must be submitted to hbracken@fiu.edu as a *single PDF* by June 1, 2018.

Contact information about award:

Heather Bracken-Grissom, PhD

Dept. of Biological Sciences Florida International University-Biscayne Bay Campus

North Miami, Florida 33181, USA

Email: hbracken@fiu.edu

CRUSTOMICS LAB: *http://www.brackengrissomlab.com/ – Heather Bracken-Grissom, PhD Assistant Professor Dept. of Biological Sciences Florida International University-Biscayne Bay Campus 3000 NE 151 Street, MSB-353 North Miami, Florida 33181, USA 305 919-4190 (Phone) 305 919-4030 (Fax)

CRUSTOMICS: Crustacean Genomics and Systematics Lab *http://www.brackengrissomlab.com/ heather.brackengrissom@fiu.edu <Valerie.Hall@fiu.edu> www.fiu.edu/~marine Heather Bracken-Grissom <heather.bracken@gmail.com>

Entebbe Uganda SpeciationInAncientLakes8 Jul29-Aug3

Dear colleagues, this is a reminder for the International Symposium “Speciation in Ancient Lakes 8” (SIAL 8) that will take place from 29 July-3 August, 2018 in Entebbe, Uganda. This will be the first time for SIAL to be held in Africa and we are looking forward to celebrate the 25th anniversary of SIAL at the shores of famous Lake Victoria.

Deadline for registration and abstract submission is 31 May. Please, check the website for further details: sial-online.org/conferences/sial8

Contact Christian.Albrecht@allzool.bio.uni-giessen.de for general information

Contact Bjoern.Stelbrink@allzool.bio.uni-giessen.de for registration and abstracts

Björn Stelbrink <Bjoern.Stelbrink@allzool.bio.uni-giessen.de>

Finland MolEcolEvol Oct10-12

Dear colleagues,

Please save the date for the 3rd Finnish Symposium for Molecular Ecology and Evolution. We are excited to announce that this year it will take place at the University of Jyvaskyla, in Central Finland. This symposium aims to bring together people working in different areas of Molecular Ecology, both in Finland and overseas, to present their latest research achievements and discuss them in a friendly atmosphere.

For more information, please visit our website: http://www.jyu.fi/3mee . Sincerely,

Venera Tyukmaeva

On behalf of organizing committee

Dr. Venera Tyukmaeva Dept. Biological & Environmental Science University of Jyvaskyla Ambiotica, YAC424.1 Survontie 9, P.O.Box-35 Jyvaskyla, FI-40014, Finland e-mail: vtyukmaeva@gmail.com or venera.v.tyukmaeva@jyu.fi

Venera Tyukmaeva <vtyukmaeva@gmail.com>

Marseilles EvolBiol Sep25-28 AcceptedAbstracts

Dear all the list of the first accepted abstracts(22nd evolutionary biology meeting at Marseilles) is available

see aeeb.fr and follow the evolutionary biology meeting link.

Date of the meeting : September 25-28

Deadline June30

best regards

Pierre

Pierre Pontarotti DR CNRS

1 Aix Marseille Univ, IRD, APHM, MEPHI, IHU Méditerranée Infection,Marseille France Evolutionary Biology team. 2 CNRS

PONTAROTTI Pierre <pierre.pontarotti@univ-amu.fr>

Marseilles EvolutionaryBiology Sep25-28

Dear all , the dead line for the next evolutionary biology meeting at Marseilles is June 30 The meeting Will take place on September 25-28 2018 in Marseilles (South of France) more info : aeeb.fr (follow the evolutionary biology meeting link)

The following subjects will be discussed: Evolutionary biology concepts and modeling; Biodiversity and Systematics; Comparative genomics ans post-genomics (at all taxomic levels); Functional phylogeny; Environment and biological evolution; Origin of life and exobiology; Non-adaptative versus adaptative evolution; The ≪ minor ≫ phyla: their usefulness in evolutionary biology knowledge; Convergent evolution Evolution of complex traits (Evo-Devo) education

contact : Marie-Hélène Rome marie-helene-rome@univ-amu.fr

Pierre Pontarotti DR CNRS

1 Aix Marseille Univ, IRD, APHM, MEPHI, IHU Méditerranée Infection,Marseille France Evolutionary Biology team. 2 CNRS tel 33 (0) 4 13 7 32425 http://aeeb.fr/?page_id=1013 we are organizing the 22nd evolutionary biology meeting at Marseilles September 25-28 2018 aeeb.fr

PONTAROTTI Pierre <pierre.pontarotti@univ-amu.fr>

MLBS Virginia SEPEEG EvolutionaryGenetics Oct5-7

Please join us for the 44th annual SEPEEG conference at Mountain Lake Biological Station (MLBS). The conference will be held Oct. 5th-7th, 2018. The scientific fields represented at the meeting are diverse, and span evolution, ecology, genetics, and behavior. SEPEEG is a single-session meeting that provides a comfortable, engaging environment for formal and informal interactions between attendees. The meeting generally attracts at least 120 participants, who are at all career stages and from diverse institutions throughout the southeastern United States.

Please visit http://mlbs.virginia.edu/SEPEEG-2018 for more information.

Registration Cost: Registration cost covers room, food, and conference expenses. General Registration Rate: $135 Student Members of the American Society of Naturalists: $90 Conference Attendees staying off site: $105 (food is included in this cost)

Joshua Puzey <jrpuzey@gmail.com>

Montpellier OriginAgriculture Sep11-14 Registration

Dear colleagues,

We are pleased to announce that registration is now open for the Third Jack R. Harlan International Symposium, dedicated to the Origins of Agriculture and the Domestication, Evolution, and Utilization of Genetic Resources (10-14 Septembre 2018, Montpellier, France) - www.harlan3symposium.org

In addition, the deadline for abstracts submissions is extended to Tuesday, 5th June 2018.

Note also that the conference organizing committee will be able to contribute to the cost of attendance of a limited number of delegates, depending on the funds available.

Please refer to our website for all practical and scientific details : www.harlan3symposium.org Thank you for sharing this information with your colleagues and scientific network,

Sincerely,

The organization team.

contact@harlan3symposium.org

www.harlan3symposium.org

34394 Montpellier Cedex 5

Anne-Céline THUILLET <anne-celine.thuillet@ird.fr>

Montreal DiversityInGenomics Jun15-17

The Gairdner Foundation and McGill University present

CLOSING THE GENOMICS RESEARCH GAP

An international symposium about inequalities in genomics research and health (And what to do about them)

www.genomicsgap.com Montreal, Canada, June 15-17, 2018

Confirmed speakers: Laura Arbour (UBC), Kathleen Barnes (U. Colorado), Carrie Bourassa (CIHR), P.aul Brennan (IARC), Zenming Chen (U. Oxford), Simon Easteal (ANU), Nanibaa' A. Garrison (U. Washington), Brenna Henn (UC Davis), Ryan Hernandez (UCSF), Adrian Hill (U. Oxford), Bartha Knoppers (McGill), Kwadwo Koram (U. Ghana), Joanna Mountain (23andMe), Dan Roden (Vanderbilt U.), Lluis Quintana-Murci (Institut Pasteur), Charles Rotimi (NIH), Anavaj Sakuntabhai (Institut Pasteur), Swee Lay Thein (NIH), Noah Zaitlen (UCSF)

Simon Gravel <simon.gravel@gmail.com>

Sherbrooke Quebec RECOMB-CG2018 Oct9-12 CallPapers

RECOMB-CG 2018, THIRD CALL FOR PAPERS

16th RECOMB Satellite Conference on Comparative Genomics, RECOMB-CG 2018

Magog-Orford (Sherbrooke), Quebec, Canada - October 9-12, 2018

https://recombcg2018.usherbrooke.ca SCOPE

The annual RECOMB Comparative Genomics Satellite Conference (RECOMB-CG) brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and the analysis of novel experimental results. The program will include keynote talks, contributed talks, and a poster session.

The 16th RECOMB-CG conference will be held at the Manoir des Sables, in beautiful Magog-Orford, near Sherbrooke, Québec, Canada on October 9-12 2018. With this Call for Papers we invite high-quality original full papers on topics related to the conference theme. The conference will also have a poster session. A detailed call for posters will be published later on the conference web page.

TOPICS

Papers are solicited on, but not limited to, the following topics:

- genome evolution
- population genomics
- genome rearrangements

- genome variation, diversity and dynamics
- phylogenomics
- comparative tools for genome assembly
- comparison of functional networks
- gene identification and/or annotation
- cancer evolutionary genomics
- comparative epigenomics
- paleogenomics
- epidemiology

IMPORTANT DATES

- Paper Submission Deadline: June 18, 2018
- Author Notification: July 20, 2018
- Final Version Due: August 3, 2018
- Conference: October 9-12, 2018

DETAILS ON SUBMITTING MANUSCRIPTS

Submitted papers must have not been published or be currently under consideration for publication in any other journal or conference with formal proceedings. Each accepted paper has to be presented by one of the authors at the conference.

Accepted papers will be published in the conference proceedings, a volume in the Lecture Notes in Bioinformatics (LNBI) series. In addition, authors of selected papers will be invited, but not required, to submit a significantly extended version of their papers to Algorithms for Molecular Biology. Extended papers submitted will be handled by the Program Committee co-chairs. Authors who choose to publish their extended manuscripts will have to pay the journal's publication fees.

Authors are encouraged to submit their manuscripts in PDF format according to the LNBI series guidelines:

http://www.springer.com/us/computer-science/lncs/conference-proceedings -guidelines

Submitted papers must be within 15 pages (in the LNBI format), with optionally a clearly marked appendix containing supplementary material made available to the reviewers.

All submissions must be made online, through the EasyChair submission system, at the following address:

https://easychair.org/conferences/?conf=recombcg2018

Authors need to register on that web site before submitting. A standard PDF file must be received by midnight on June 18, 2018 (any time zone) in order for a submission to be considered. Re-submission of already submitted papers will be possible until midnight June 18, 2018 (any time zone).

CONFIRMED KEYNOTE SPEAKERS

Belinda Chang (Department of Ecology and Evolutionary Biology, University of Toronto, Canada)

Dannie Durand (Department of Biological Sciences, Carnegie Mellon University, USA)

Daniel Durocher (The Lunenfeld-Tanenbaum Research Institute, Mount Sinai Hospital, University of Toronto, Canada)

Christian Landry (Institute for Integrative Systems Biology, Laval University, Canada)

Gwenaël Piganeau (Banyuls Oceanographic Observatory and National Centre for Scientific Research, France)

Xavier Roucou (Department of Biochemistry, University of Sherbrooke, Canada)

PROGRAM COMMITTEE

Max Alekseyev (George Washington University)

Lars Arvestad (Stockholm University)

Sèverine Bérard (U. Montpellier)

Mathieu Blanchette (McGill University), co-chair

Anne Bergeron (U. du Québec à Montréal)

Marília Braga (Bielefeld University)

Alessandra Carbone (CNRS, Université Pierre et Marie Curie)

Cedric Chauve (Simon Fraser University)

Leonid Chindelevitch (Simon Fraser University)

Miklós CsÅ±rös (University of Montreal)

Daniel Doerr (Bielefeld University)

Ingo Ebersberger (Goethe University Frankfurt)

Nadia El-Mabrouk (University of Montréal)

Oliver Eulenstein (Iowa State University)

Guillaume Fertin (University of Nantes)

Pawel Gorecki (University of Warsaw)

Michael Hallett (Concordia University)

Katharina Jahn (ETH Zurich)

Asif Javed (Genome Institute of Singapore)

Manuel Lafond (University of Ottawa)

Jens Lagergren (Stockholm University)

Kevin Liu (Michigan State University)

Joao Meidanis (UNICAMP)

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Spain EMPSEB24 Sep9-15

24 European Meeting of Students in Evolutionary Biology - we open the abstract submission on 4th of May! This year, EMPSEB24 will be held in Bubión, a beautiful village in Granada, Spain. We invite all students to present their research, discuss other projects and to take part in plenary talks with our guests! The deadline for abstract submission is on 13th of May. For more details, check our webpage (https://congresos.ugr.es/empseb24/) and Twitter (@EMPSEB24) for more information. If you have any question, feel free to e-mail us: contact.empseb24@gmail.com

This Ph.D. meeting is organized by and dedicated to Ph.D. students studying Evolutionary Biology from across Europe although participants from other countries are also welcome. Thus, it provides a platform for students to present their work and meet their peers from different countries. Along with the participants, are 10 key speakers who are working on influential Evolutionary Biology topics. They are invited to give plenary talks, run discussion groups, and to provide guidance about starting your scientific career. The meeting provides the unique opportunity for students to hear the latest research being conducted in Europe, meet future international collaborators, and to present their own work to peers.

empseb24 <empseb24@gmail.com>

Spain EMPSEB24 Sep9-15 CallExtended

We would like to inform all of you that the deadline for abstract submission for the upcoming EMPSEB24 in Bubión-Granada-Spain has now been extended. Grab your chance! Please submit your abstract by *18th MAY 2018!*

You may submit your proposal at the following link: https://congresos.ugr.es/empseb24/abstract-submission/ Stay in touch, follow us on twitter @EMPSEB24 < https://twitter.com/empseb24?lang=3Des >!

empseb24@gmail.com

Toronto Barrettfest Aug10-11

The draft program is now posted for a 2-day symposium entitled 'Evolution of Plant Reproductive Systems: From Muddy Boots to Genomics' at the University of Toronto, August 10-11. For details, registration and banquet tickets, please visit http://bit.ly/2ExKsh3 .This symposium will mark Professor Spencer Barrett's 70th birthday and 40th year at the University of Toronto, and will be an opportunity to explore the latest cutting edge research in this field. The list of confirmed speakers includes: Aneil Agrawal (U Toronto), Tia-Lynn Ashman (U Pittsburgh), Andrea Case (Kent State), Deborah Charlesworth (U Edinburgh), Joana Costa (U Lisbon), Lynda Delph (Indiana U), Chris Eckert (Queens U), David Field (U Vienna), Jannice Friedman (U Syracuse), Sean Graham (UBC), Lawrence Harder (U Calgary), Kay Hodgins (Monash University), Brian Husband (U Guelph), Michael Lenhard (U Potsdam), John Pannell (U Lausanne), Daniel Schoen (U McGill), James Thomson (U Toronto), Stephen Wright (U Toronto). Many thanks to the University of Toronto's EEB department, the Faculty of Arts & Science, and the New Phytologist Trust for co-sponsoring the event. For details, registration and banquet tickets, please visit http://bit.ly/2ExKsh3 .

Stephen I. Wright Professor and Canada Research Chair in Population Genomics Department of Ecology and Evolutionary Biology University of Toronto 25 WIllcocks St. Toronto ON M5S 3B2 Office: (416) 946-8508 http://labs.eeb.utoronto.ca/wright/Stephen_I._Wright/ Stephen Wright <stephen.wright@utoronto.ca>

Toulouse EconomicsEvolution May24-25 DeadlineMay11

Dear colleagues,

Registrations for the 6th Toulouse Economics and Biology Workshop - Evolution, Cognition and Rationality, May 24-25 are now open. Please register HERE before 11th May 2018.

Click HERE to see the program of the conference.

The speakers are:

Immanuel Bomze, University of Vienna - Operations Research

Joanna J. Bryson, University of Bath & Princeton University - Computer Science

Noam Brown, Carnegie Mellon University - Computer Science

Iain Couzin, Max Planck Institute for Ornithology & University of Konstanz - Biology

Audrey Dussutour, CNRS University Toulouse III - Biology

Yuval Heller, Bar-Ilan University - Economics

Cecilia Heyes, University of Oxford - Biology & Psychology

Peter Gardenfors, Lund University - Cognitive Science

Alex Kacelnik, University of Oxford - Biology

Marc Mezard, ENS Paris Sud University - Physics

Erik Mohlin, Lund University - Economics

Arthur Robson, Simon Fraser University - Economics

Ariel Rubinstein, Tel Aviv University - Economics

Aldo Rustichini, University of Minnesota - Economics

Besides the plenary sessions, there will be a poster session to which post-docs and Ph.D. students are most welcome to submit applications (abstract + CV + cover letter) to econbio_poster@iast.fr no later than March 30, 2018. A limited number of travel grants will be available. To apply, please join a cover letter explaining why you are applying for a grant and why you are interested in attending the workshop.

For any further information please contact us directly at econbio@iast.fr or visit our website https://www.iast.fr/-conferences/2018-6th-toulouse-economics-and-biology - workshop

We look forward to seeing you in May!

Organizers: Ingela Alger and Jorgen Weibull,

Co-organizers: Lauriane Rat-Fischer and Slimane Dridi

Administrative assistants: Cynthia Diaz and Aline Couratier

The Toulouse Economics and Biology Workshop <econbio@iast.fr>

UEdinburgh RobinThompson Jun29

Dear colleagues,

It is our pleasure to invite you to a symposium in honour of Professor Robin Thompson that will take place on the 29thof June (9h - 17h) at The Roslin Institute on the Easter Bush Campus of University of Edinburgh: https://www.ed.ac.uk/roslin/about/contact-us/-how-to-get-here Most will know Robin and his scientific contributions, which are briefly summarised in the biography below.

At the event a series of speakers will highlight some of the Robin's direct and indirect contributions to statistics, quantitative genetics, animal and plant breeding, and human genetics as well as their current research. The list of speakers and their talks is provided at the end of this e-mail.

Attending the event is open to all and free, but requires prior registration by e-mail to: kjerstine.severinsen@roslin.ed.ac.uk

The Organising Committee

Gregor Gorjanc and John Hickey

Biography

Robin Thompson is a pioneering leader in the fields of statistics, quantitative genetics and animal and plant breeding. He started his career in Edinburgh in the late 1960's in the then Agricultural Research Council Unit of Statistics, later moving to the Animal Breeding Research Organisation, which ultimately became part of the Roslin Institute. He remained there until the mid 1990's when he moved to the Institute of Arable Crops Research at Rothamsted as the head of the prestigious department of statistics, established by R.A. Fisher, that laid the foundation for much of modern statistics.

In the 1970's, while based at the University of Edinburgh, Robin and Desmond Patterson proposed and developed a new statistical method which came to be called REML. It now dominates in several fields including statistics, genetics, breeding, and field trial analysis. Data collected in many real-life settings are inherently unbalanced and REML provides optimized statistical methodology for such data. The foundation paper from 1971, “Recovery of inter-block information when block sizes are unequal” is a citation classic with more than 3,700 citations to date. These days, REML is implemented in most widely used statistical analysis packages.

In addition to inventing REML, Robin has made significant contributions to the development of computationally efficient algorithms to facilitate the application of REML to large datasets. Of these, the most important is the Average Information algorithm, developed in the 1990s. Robin, together with Arthur Gilmour, developed a *versatile and efficient*software package called ASReml that is the most widely used in animal and plant breeding across the globe today.

Robin has made a broad range of contributions to the development of rigorous science underpinning UK and global animal and plant breeding programmes. His collaborations with the various Edinburgh groups had, and continue to have, particular impact in UK dairy, beef and sheep breeding.

Finally, Robin has made a major input to post-graduate education in Edinburgh. For many years, he taught components of the MSc in Animal Breeding and Quantitative Genetics. He was a formal supervisor of more than twenty research students and an informal mentor of many more. Robin has been incredibly generous with his ideas to both students and established researchers. Several of his former students now have high international reputations.

Speakers

Session 1 - Animal Breeding

§Geoff Simm - Chair

Global Academy of Agriculture and Food Security, University of Edinburgh

§Brian McGuirk - MOET

Independent animal breeding consultant

§Mike Coffey - Genetic evaluations in UK

Animal Breeding & Genomics, Scotland's Rural College

§Raphael Mrode - Genomic evaluations in small holder systems

Animal Breeding & Genomics, Scotland's Rural College & International Livestock Research Institute

§John Woolliams - Optimal contributions

The Roslin Institute, University of Edinburgh

Session 2 - Statistics in breeding

§Esa Mäntysaari - Chair

Animal Genetics, Natural Resources Institute Finland

§Arthur Gilmour - ASREML: A Story about REML

Consultant Biometrician Research Scientist at Cargo Vale Olives

§Ismo Stranden - How REML learned to stop apologising and love Monte Carlo

Animal Genetics, Natural Resources Institute Finland

§Roel Veerkamp - Covariance functions and Random regression

Animal Breeding & Genomics, Wageningen University & Research

§Augustin Blasco - Elliptic selection

Institute for Animal Science and Technology, Polytechnic University of Valencia

Session 3 - Plant breeding

§Brian Cullis - Chair

Centre for Bioinformatics and Biometrics, University of Wollongong

§Alison Smith - Robin Thompson's contribution to the Australian grains industry

Centre for Bioinformatics and Biometrics, University of Wollongong

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UMiami SEEC Oct5-7 CallForAbstracts

This is a Call for Abstracts. We only have a few weeks left for 2018 SEEC abstract deadline.

The University of Miami is excited to host the 2018 Southeastern Ecology and Evolution Conference (SEEC) from October 5 -7, 2018 in Miami, Florida. The SEEC is a regional, student-run meeting that provides undergraduates, graduate students, and post-docs an opportunity to present research in ecology and evolution. This conference is open to anyone with an interest in ecology and evolution research in the southeastern region of the United States.

The conference will feature outstanding plenary speaker: Dr. Daniel Simberloff, University of Tennessee. Some of his research interests include biogeography, invasive species, and statistical ecology.

As part of the conference, individuals are invited to attend workshops on Biological Invasions and Modern Applications.

Abstracts are due by June 1st 2018. Early registration will start on July 1st, for $45, after you hear back from our conference committee about the acceptance of the submitted abstract. There will be cash prizes awarded to the best talks and posters. Further details about the conference, abstract submission instructions, and registration information can be found at https://seecconference2018.wordpress.com/ Questions or inquires can be directed to SEEC 2018 (email: SEEC.Host@gmail.com) *SEEC Planning Committee* University of Miami website / https://seecconference2018.wordpress.com/ email / seec.host@gmail.com FB / SoutheasternEcologyEvolution < https://www.facebook.com/SoutheasternEcologyEvolution >

seec.host@gmail.com

UMinnesota MidwestPopGen Aug24-25

Midwest Population Genetics Meeting 2018 Aug 24th-25th at the University of Minnesota *tl/dr Register here:* https://docs.google.com/forms/d/1aRmrzw3cjykAVWrQyATUPXxbQZyPo7PVZZNmRaakMD8/< http://goo.gl/NFp7RK%5Dbut > *info here *https://mwpg2018.wordpress.com/

The field of population genetics has a remarkable tradition of being a tight-knit and nurturing community. In order to continue to foster that sense of community for popgen groups in the Midwest, we are organizing the fifth annual Midwest PopGen conference. https://mwpg2018.wordpress.com/ The location and date this year will be The University of Minnesota - St Paul Campus on August 24th-25th. The meeting will begin Friday at noon and continue to Saturday evening with a BBQ on Friday evening, and an opportunity to check out the state fair on saturday night!

We will select talks from submitted abstracts to balance the topics, career stage etc of the presenters. There will be a poster session (anyone can give a poster, no abstract needed). The meeting will be trainee-oriented, so students and postdocs are especially encouraged to present their work. There will be prizes awarded for best poster and best talk by a student and postdoc.

If you would like to give an oral presentation, submit your abstracts by June 22nd. Submitters will be notified if their abstract is chosen for a talk by July 1st.

Registration is free, [link https://docs.google.com/forms/d/1aRmrzw3cjykAVWrQyATUPXxbQZyPo7PVZZNmRaakMD8/please RSVP by Aug 3rd (June 22nd for talk submissions) by adding your name and information to the registration list (https://docs.google.com/forms/d/1aRmrzw3cjykAVWrQyATUPXxbQZyPo7PVZZNmRaakMD8/).

Additional notes *- The meeting overlaps with the state fair.* This should be very fun (and was part of the reason that we chose this date) but adds a degree of difficulty to meeting logistics. Look for a place to stay soon (we are soliciting twin cities folks interested to put people up), and plan on taking public transport. *- The meeting follows a FREE symposium on machine learning* on august 23rd (in the same location) with speakers including Casey Greene, Katie Pollard, and Dan Schrider. Come early for the fun! We also have one open speaker slot for that meeting so contact Yaniv if you would like to present at that meeting. We hope to pair people up with a place to stay, so locals should let us know how many people they can host, and out-of-towners should let us know if they are looking for a place.

Additional info / details / schedule etc will be made available on https://mwpg2018.wordpress.com/ ybrandvain@gmail.com

UPotsdam BioMove Sep26-28

Dear everyone,

we cordially invite you to join us at the 1st international BioMove Symposium from 26th to 28th September 2018 in Potsdam / Germany. You can now submit your talk or poster contributions at https://biomove2018.org We are looking forward to your applications for talks and posters.

With regards, BioMove Group

Important dates: End Abstract submission: 01.06.2018 Registration for presenters: 15.06.2018 'V 30.06.2018 Registration for everyone: 30.06.2018 'V 10.08.2018

Please stay tuned for updates on the scientific program and social events:

Homepage: https://biomove.org/biomove-symposium-2018/ Twitter: @bio_move If you have any further questions, feel free to contact us:

Email: biomove2018@uni-potsdam.de

University of Potsdam Karl-Liebknecht-Str. 24-25, D-14476 Potsdam Germany biomove2018@uni-potsdam.de

biomove2018 <biomove2018@uni-potsdam.de>

GradStudentPositions

Auckland PlantPathogenEvolution

PhD position in Plant Pathogen Evolution Massey University Auckland, New Zealand

A PhD scholarship is available to pursue a doctoral degree on the evolution of a bacterial plant pathogen. The project is based at the New Zealand Institute for Advanced Studies, Massey University (Albany campus, NZ).

The student will participate in a Marsden funded project 'Population Genomics of an Emergent Plant Infectious Disease'. Disease emergence is a growing threat to agricultural productivity and food security worldwide, identifying the source and evolutionary processes involved in the emergence of crop disease is therefore of fundamental importance. We use recurring outbreaks of Pseudomonas syringae pv. actinidiae on kiwifruit as a model system for investigating how agricultural pathogens emerge from the wild, how coevolutionary dynamics shape pathogen virulence and host immunity in natural and cultivated populations, and the genetic basis of host specificity and pathogen transitions to agroecosystems. The PhD student will acquire computational, laboratory and field experience in pathogen evolution, population genomics and plant-microbe interactions.

Suitable candidates will have completed a Masters or equivalent degree in microbiology, plant pathology, evolutionary biology, ecology, genetics, plant biology, genomics or computer science. Candidates who have demonstrated excellence in their Bachelors degree may also be considered. Previous research experience or training in microbiology is preferred.

How to apply: Send the following materials to Dr. Honour McCann (h.mccann@massey.ac.nz) by May 31st, 2018 1. One page cover letter describing your interest and suitability for the position 2. A CV including contact details for 2 referees and list of publications (if applicable) 3. Academic transcript 4. TOEFL or IELTS score (if applicable)

honour.mccann@gmail.com

EastTennesseeStateU DaphniaLifeHistory

A funded PhD position is available immediately with the Biomedical Sciences Graduate Program at East Tennessee State University to study biology of life-history and aging in Daphnia. Start date Fall 2018 or Spring 2019. A possibility of a collaborative project with Dr. Marc Kirschner's lab at Harvard exists. Discuss details with Lev Yampolsky (yampolsk@etsu.edu). Applications: https://www.etsu.edu/gradstud/applynow.php . "Yampolsky, Lev" <YAMPOLSK@mail.etsu.edu>

MaxPlanck Jena DefenceToPredators

We have a PhD position available, funded by the Max Planck International Research School in Chemical Ecology, in Jena, Germany. I would be grateful if you shared this advert on evoldir . The deadline for applications is May 16th.

Link to application page http://imprs.ice.mpg.de/ext/-index.php?id=917 Predators that eat toxic food

Supervisors: Hannah Rowland, Christian Paetz, MPI for Chemical Ecology

Background: The evolution of warning colour patterns in prey that have chemical defences is an important area of research in evolutionary biology (1). Variability in the colour patterns and chemical profiles of prey is frequently documented (2, 3). In comparison to variability in prey signals, variability in the predators that respond to these signals has less often been considered and, where it has, not directly quantified (4, 5). The evolutionary dynamics of warning colour patterns will depend on the extent of (genetic) variation both in prey and in their predators (6-8). Where predators are capable of circumventing the chemical defences of prey, this often involves the evolution of elaborate mechanisms for avoiding(9), tolerating (10), or resistance to the toxic effects of the defence (11).

Project Description: This aim of this project is to understand the molecular and physiological mechanisms that underpin avian predator's ability to feed on chemically defended prey. You will conduct feeding studies to determine the effect of chemical defences (positive or negative) on predator behaviour and physiology. You will use transcription profiling to detect up-regulated genes associated with defence consumption, and also investigate the fate of chemical defences after ingestion in order to identify potential detoxification mechanisms and to detect possible metabolites. There is the potential to move toward In vitro enzyme/receptor assays.

Candidate profile: We are searching for a highly motivated student with a scientific, and curiosity-driven attitude and a strong interest in interdisciplinary research combining molecular biology, chemistry, and ecology. Excellent communication skills and proficiency in written and spoken English is required. A background in biochemistry and/or molecular biology is preferable. Experience with one of more method of transcriptomics/cell culture/ HPLC or liquid chromatography coupled with mass spectrometry (LCMS-MS) would be desirable, but not absolutely necessary (training will be given).

References 1. J. Mappes, N. Marples, J. A. Endler, The complex business of survival by aposematism. Trends Ecol. Evol. 20, 598-603 (2005). 2. M. P. Speed, G. D. Ruxton, J. Mappes, T. N. Sherratt, Why are defensive toxins so variable? An evolutionary perspective. Biological Reviews 87, 874-884 (2012). 3. K. Summers, M. P. Speed, J. D. Blount, A. M. M. Stuckert, Are

aposematic signals honest? A review. Journal of Evolutionary Biology, n/a-n/a (2015). 4. O. Nokelainen, J. Valkonen, C. Lindstedt, J. Mappes, Changes in predator community structure shifts the efficacy of two warning signals in Arctiid moths. J. Anim. Ecol. 83, 598-605 (2014). 5. J. K. Valkonen et al., Variation in predator species abundance can cause variable selection pressure on warning signaling prey. Ecology and Evolution 2, 1971-1976 (2012). 6. J. A. Endler, J. Mappes, Predator mixes and the conspicuousness of aposematic signals. American Naturalist 163, 532-547 (2004). 7. H. M. Rowland, A. J. T. Fulford, G. D. Ruxton, Predator learning differences affect the survival of chemically defended prey. Animal Behaviour 124, 65-74 (2017). 8. C. G. Halpin, J. Skelhorn, C. Rowe, The Relationship between Sympatric Defended Species Depends upon Predators' Discriminatory Behaviour. PLoS ONE 7, e44895 (2012). 9. L. S. Fink, L. P. Brower, Birds Can Overcome the Cardenolide Defense of Monarch Butterflies in Mexico. Nature 291, 67-70 (1981). 10. N. M. Marples, P. M. Brakefield, R. J. Cowie, Differences between the 7-spot and 2-spot ladybird beetles (Coccinellidae) in their toxic effects on a bird predator. Ecological Entomology 14, 79 (1989). 11. S. Mohammadi, A. H. Savitzky, J. Lohr, S. Dobler, Toad toxin-resistant snake (Thamnophis elegans) expresses high levels of mutant Na+/K+-ATPase mRNA in cardiac muscle. Gene 614, 21-25 (2017).

Hannah Rowland <hrowland@ice.mpg.de>

Montpellier France EvolutionaryGenomicsOfAsexuality

Interested by the evolution of (a)sex, theory and genomics? A graduate position is available to work with Christoph Haag and me in CEFE < https://www.cefe.cnrs.fr/fr/ > in Montpellier.

Send application before June 25th 2018. Details here: https://bit.ly/2IJyVMD Montpellier is a beautiful city with a very strong research community in evolutionary biology

Thomas Lenormand

CEFE < http://www.cefe.cnrs.fr/index.php/fr/ >, campus CNRS 1919 route de Mende 34293 Montpellier

tel +33 (0)4 67 61 32 91 web page < http://www.cefe.cnrs.fr/index.php/fr/recherche/accueil-dpt-ecologie-evolutive/genetique-et-ecologie-evolutive/800-gge/gge-chercheurs/193-thomas-lenormand >

LENORMAND Thomas <Thomas.LENORMAND@cefe.cnrs.fr>

MurrayStateU Kentucky EvolutionCommunication

Graduate position (M.S.): Evolution of animal communication at Murray State University (KY)

Note: Funding opportunities have recently become available (see below). To be considered for a TAship and/or the biodiversity stipend, application should be submitted to me by 5/24/18.

The Beckers' Lab at Murray State University accepts a Masters student who is interested in the evolution of animal communication starting in the fall of 2018.Our lab uses Orthopterans (i.e., katydids, and crickets) as model organisms to address questions pertaining the evolution of animal behavior. More specifically, we study the effects of the environment (i.e., phenotypic plasticity) on mating songs. In our main study species, Neoconephalus triops, day length induces two substantially different mating songs. These differences in the songs are comparable to species differences within the genus. In a collaboration with two other labs (Missouri and West Virginia), we study the genetic underpinnings of this behavioral plasticity and how the involved genes related to speciation within the genus.

A second line of research focuses on the evolutionary arms race between katydid hosts and their eavesdropping parasites in the local population of N. triops.The flies use the katydid mating songs to find their hosts and deposit deadly larvae on them. Thus, sexual selection and natural selection act in opposing directions on male singing behavior. The evolutionary ramifications of this deadly parasitism on male singing and mate acquisition behavior are the focus of future studies.

I seek driven, enthusiastic, and focused students to join my lab at Murray State University. Successful applicants have a B.S. in biology, ecology, or related discipline and are interested in studying animal behavior and evolution. If you are interested in this opportunity and/or have any questions, please email Dr. Beckers at obeckers@murraystate.edu. For your application, make sure to address in an attached document your research interests, how they relate to the Beckers' lab research, and your GPA.

Funding for tuition and a summer stipend are available for the N. triopsplasticity project through a grant. In addition, a TAship ($10,000/year) and a biodiversity stipend ($10,000 per year + research supplies and meeting expenses) are available. Review of applications starts immediately. Once you indicated interest in the position, an interview will be set up shortly after.

Please find more information on Dr. Beckers' research here:

https://www.murraystate.edu/-academics/CollegesDepartments/-CollegeOfScie nceEngineeringandTechnology/CollegeOfSciencePrograms/biologyDept/facult y/oliver-beckers/index.aspx

Information on the Department of Biological Sciences at MSU:

https://www.murraystate.edu/-academics/CollegesDepartments/-CollegeOfScie nceEngineeringandTechnology/CollegeOfSciencePrograms/biologyDept/facult y/

Oliver Beckers <obeckers@murraystate.edu>

NewZealand FishDiseaseGenomics

PhD Scholarship: Disease genomics of two New Zealand finfish species We are seeking a highly motivated PhD student to be part of a group to investigate the disease genomics of the New Zealand snapper (Chrysophrys auratus) and trevally (Pseudocaranx georgianus).

Supervisors Associate Professor Maren Wellenreuther, Auckland University and Plant and Food Research (PFR), Nelson, New Zealand. https://unidirectory.auckland.ac.nz/people/profile/m-wellenreuther Dr. Steve Bird, Waikato University, New Zealand. http://sci.waikato.ac.nz/about-us/-people/sbird Aquaculture is the fastest growing food-production sector and New Zealand has the potential to develop a range of locally grown finfish species to meet this increasing demand. New genomics-based selective breeding programs are needed to help develop recently domesticated fish species into premium products. Plant and Food Research (http://www.plantandfood.co.nz) is known worldwide for its innovative breeding and genomics research, and it is leading the development of New Zealand seafood genomics.

This PhD project will involve working alongside a group of experienced researchers to study the genomes of the New Zealand snapper and trevally to identify and characterize immune genes, screen for genome-wide disease markers using a pedigree from domesticated populations, evaluate the bacterial disease metacommunities and conduct gene expression analyses using transcriptomics and qPCR. This will involve using high-throughput sequencing approaches, coupled with automated and error-reduced phenotyping. The overall goal is to characterize the immune systems of both fish species to better understand disease resistance in domesticated populations, facilitating a rapid and efficient selective breeding programme.

PhD Project Aims 1. Use whole genome assemblies and transcriptomes to identify immune genes and pathways, 2. Use genomic information to improve detection of novel disease QTLs, 3. Assess stress and disease resistance of hatchery individuals, and understand their bacterial disease communities.

This PhD project will provide an excellent opportunity to learn the latest interdisciplinary technologies and apply them to fish genomics. The PhD student will gain experience working in academic, government and private sector institutions. They will be a member of a highly active and collaborative group of researchers, and help develop new technological approaches and applied-genomic tools.

The successful candidate will be a highly motivated researcher with a strong background in computational approaches in biology or computer science. Data analysis of next generation sequencing data will be the main workload of the project. Therefore, knowledge and experience of a scripting language (Python/Perl) is needed. A proven ability and motivation to write research papers is a plus.

Students will be enrolled at the University of Auckland but primarily based in Nelson (http://-www.nelsonnz.com). We will provide a three-year scholarship that provides a stipend and university (domestic-level) fees. This project is supported by the MBIE grant 'Enhancing production of New Zealand's seafood sector using accelerated breeding techniques'.

Applicants should send a CV, a statement of their research interests and a cover letter to Maren Wellenreuther (Maren.Wellenreuther@plantandfood.co.nz).

Maren Wellenreuther Senior Scientist, Plant and Food Research, Nelson Associate Professor, University of Auckland, Auckland

< http://www.plantandfood.co.nz/ >

T: +64 3 989 7658 M: +64 22 357 5802 F: +64 3 546 7049 E: maren.wellenreuther@plantandfood.co.nz www.plantandfood.co.nz The New Zealand Institute for Plant & Food Research Limited

Postal Address: Plant & Food Research Nelson PO Box 5114, Port Nelson, Nelson, 7043, New Zealand Physical Address: Plant & Food Research Nelson 293 Akersten St, Port Nelson, Nelson, 7010, New Zealand

Maren.Wellenreuther@plantandfood.co.nz

NordU PlanktonPopGenomics

PhD fellowship (3 years) in population genomics of Calanus hyperboreus

Deadline june 1st

Online application:

https://www.jobbnorge.no/en/available-jobs/job/151069/phd-fellowship-3-years-in-population-genomics-of-calanus-hyperboreus About the PhD fellowship

A three-year PhD position for studies on population genomics of Calanus hyperboreus is available at the Faculty of Biosciences and Aquaculture, Nord University (Bodø, Norway) from September 1, 2018.

FBA invites applications from outstanding candidates for a three-year PhD fellowship within the project “population genomics of Calanus hyperboreus”.

Copepods of the genus Calanus are predominant in the zooplankton biomass, playing a key ecological role. The goal of the project is to address the evolutionary relationships between species and populations of copepods of the genus Calanus in the North Atlantic/Arctic Oceans. The project will investigate their population genetic structure and phylogeography. The approach will rely on Next Generation Sequencing Technologies to study genetic variation at the genome level using both genome wide SNPs genotyping and mitogenome sequencing.

Qualifications and requirements

* We are looking for highly motivated, creative and ambitious applicants with an excellent academic record and the ability to collaborate with other members of a multidisciplinary team, whilst developing their own research project. The grades at the qualifying MSc examination needs to be C or better (ECTS scale from A-E) to be admitted to the program. However, the Faculty seeks highly qualified candidates with top grades.

* At the time of taking up the appointment, the candidate should have an MSc degree in molecular biology, ecological genomics, population genetics or related disciplines.

* Practical experience in molecular biology and population genetics is required. Knowledge and experience in zooplankton and/or bioinformatics is desirable. Practical experience with Next Generation Sequencing is also desirable.

* Proficiency in oral and written English is essential and must be documented either by the Norwegian Higher Education Entrance Qualification or internationally recognised certificates, such as TOEFL, IELTS, APIEL or similar. Skills in Scandinavian language is an advantage for the position.

The successful candidate will join the PhD programme in Aquatic Biosciences at Nord University and is expected to complete a doctorate within the three-year project period. The candidate should fulfill the admission requirements of this PhD programme at the Faculty of Biosciences and Aquaculture and participate in the training components stipulated in regulations of the PhD program. Application for admission to the programme must be submitted within three months after taking up the position.

Salary and Working Conditions

The annual salary for PhD candidates is set at wage level 50 (approximately 436 900,-) in the Norwegian State Salary Scale.

As an employee at the Nord University, the Fellow will become a member of the Norwegian Public Service Pension Fund and will get access to other social benefits. A statutory amount to the Norwegian Public Service Pension Fund will automatically be deducted from the salary. The successful person must abide by the laws, agreements and directives that apply to the position at any time

According to the employment policy of the institution, our staff should reflect the population in general. The University practices follow gender quotas in accordance with the Basic Agreement for the Civil Service, and women are encouraged to apply for the position.

Contact Information

Professor Galice Hoarau (Galice.g.hoarau@nord.no) Office manager Irene Stork e-mail: irene.stork@nord.no).

Application

Applicants for this position are requested to include the following information:

* Cover letter outlining the candidate’s suitability for

this position (one page), and a project outline based on the theme "Population genomics of Calanus hyperboreus" (maximum 2 pages) must be submitted. The non-submission of these documents will lead to the rejection of an otherwise qualified candidate.

* Curriculum vitae, including a list of publications (maximum 3 pages)

* Certified copies of academic degree transcripts and any other relevant qualifications

* Contact details for at least two referees

* Signed consent form

Applicants should not attach unsolicited documents, such as co-authored publications, high school transcripts, documents not relevant for the position, etc.

All documents must be uploaded as attachments to the electronic application form. It is the applicant's responsibility to submit the

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SouthernConnStateU HumanModifiedEvolution

M.S. position: Evolution & conservation in human-modified environmentâ€ Start date: August 2018

A research assistantship to support a M.S. student is available for the 2018-19 academic year in the Brady Lab at Southern Connecticut State University (New Haven, CT, USA). Candidates with interest or expertise in evolution, conservation, aquatic ecology, genomics, and/or epigenetics are particularly encouraged to apply.

Responsibilities for this position may include: -Coordinating and executing field (especially aquatic) and laboratory experiments -DNA/RNA extractions; Western blot assays -Image analysis; microscope work with preserved amphibian specimens -Data analysis / synthesis and database management -Dissemination (writing manuscripts, presenting at meetings) -Lab management and maintenance -Maintenance of lab website and social media

Independent thesis research will be encouraged and the awardee will be expected to apply for internal and external grants to support their research.

ABOUT THE FELLOWSHIP: The awardee will complete 20-hours of work per week and must be enrolled full time in the graduate program. The award will be made initially for the fall 2018 semester and, contingent upon performance, can be renewed for the spring 2019 semester. The position includes a stipend of $6,000 per semester and a waiver of University fees (as described by the Graduate Catalogue http://catalog.southernct.edu/graduate/general-information/financial-aid.html).

Additional details about the fellowship can be found here (under "Graduate Student Graduate Assistantship"): http://www.southernct.edu/academics/graduate/research/student-research/graduatefellowships.html TO APPLY: Email CV, unofficial undergraduate transcript, and a cover letter to brady.steven@gmail.com. Pre-application inquiries are welcome.

Applications will be considered as they are received. All applications received by May 21, 2018 will be given full consideration. The selected candidate will then be required to successfully apply and matriculate in the Graduate School. Graduate School Admission details can be found here: https://www.southernct.edu/gradadmissions/index.html Steven P. Brady Assistant Professor | Southern Connecticut State University Lab: Jennings 214 | Office: Jennings 215A Web: stevenpbrady.weebly.com | Phone: 203-392-7206

"Brady, Steven P." <bradys4@southernct.edu> "Brady, Steven P." <bradys4@southernct.edu>

TexasStateU ConservationGenomics

Applications are being sought from energetic and capable students who wish to pursue a Masters degree in Population and Conservation Biology and are interested in the application of next-generation DNA sequencing tools to problems in conservation. The research focus is on plethodontid salamander population genetics. Applicants with experience in population genetics and computational biology are preferred. During the fall and spring semesters, we can offer an Instructional Assistant (teaching labs) for the length of your degree. Funding has been secured for research costs and 3 months of summer pay for the first summer. See http://nicelab.wp.txstate.edu for details about our lab, papers and our research interests.

The Department of Biology offers a strong environment for training students in conservation and evolutionary ecology. The Masters program in Population and Conservation Biology would be the best fit for such an applicant. For program information see http://www.bio.txstate.edu/Graduate-Programs/-M.S.PopulationConservationBiology.html .

Interested students should send an email with a statement of interest that includes any additional topics you might be interested in working on in our lab and your long term goals/interests. Please include a copy of your CV, relevant coursework, GRE, and any other relevant experience to Chris Nice by email (ccnice at txstate.edu). Reference letters for top candidates will be solicited at a later date. Applications will be reviewed as they come in. Applications to our Masters program are evaluated on a rolling basis so it is possible to start Fall 2018.

– Chris C Nice Department of Biology Texas State University 601 University Drive San Marcos, TX 78666 Email: ccnice@txstate.edu Tel: 512-245-3358

Chris Nice <txbugnut@gmail.com>

TexasTechU BighornSheepMicrobiomes

The Phillips Laboratory (Department of Biological Sciences, Texas Tech University) is accepting applications from highly motivated individuals interested in pursuing a graduate degree in Biology, with a research project focusing on the dynamics of microbiomes in wild populations of bighorn sheep. The successful applicant will be an individual that is excited about the opportunity to integrate bioinformatics, biostatistics, ecology, and evolutionary biology to understand and publish results about complex biological systems. No prior experience in scripting (mainly bash and R) is required, but only applicants that are serious about the opportunity to develop advanced scripting capabilities and strong foundations in biostatistics and ecological principles need apply. This position is available at the master's or PhD level, but only individuals currently holding a master's degree or with experience in microbiome research will be considered to enter at the PhD level. The position will be supported by a Research Assistantship funded by the Texas Bighorn Society and the Wild Sheep Foundation. The position also provides teaching experience in the form of Teaching Assistantships. Collaboration with researchers in Tech's Department of Natural Resource Management will be a part of this position, and research findings may inform disease risk across portions of bighorn sheep range in Texas. This position will provide career development through a diverse and technical training experience.

Applicants should send their CV and a Statement of Interest to Caleb Phillips (caleb.phillips@ttu.edu, subject line = bighorn microbiome).

Caleb D. Phillips, Ph.D. Curator of Genetic Resources, Natural Science Research Laboratory Assistant Professor, Biological Sciences Texas Tech University, Lubbock Texas Office: 806-834-8181 caleb.phillips@ttu.edu

"Phillips, Caleb" <Caleb.Phillips@ttu.edu>

UAberdeen EvolutionArchaea

Funded PhD studentship in microbial evolution at the University of Aberdeen (Scotland, UK): 'Experimental evolution of Thaumarchaeota' The fundamental aim of this project is to determine the process of adaptive diversification and associated trade-offs in fitness, by studying microbial evolution experimentally.

A 4-year PhD studentship in microbial evolution, starting in October 2018, is now open for application at the University of Aberdeen, Scotland, UK. The deadline for applications is June 5th 2018 and this studentship is available to students of any nationality (providing funding for tuition fees and stipend). The PhD project is funded by the Royal Society and will target key evolutionary questions with a special focus on Thaumarchaeota to align with the research thematic of the University of Aberdeen Nitrification Group.

Using microbes to test theory in evolutionary biology has led to major scientific advances. In particular, microbial experimental evolution has allowed analysis of both microbial adaptation (genomic and phenotypic changes) and diversification (phenotypic evolution and lineage-splitting) using controlled environments, through increased understanding of the nature and frequency of genomic substitutions, their effects on microbial fitness and the mechanisms by which diversity is created and maintained in microbial populations. These concepts were established from studies of bacteria, fungi, viruses and phage, focussing mainly on a few bacterial model organisms (1, 2). However, an entire domain of life, the Archaea (3), has largely been ignored by evolutionary biologists, despite their widespread distribution in natural environments, high abundance and essential contribution to global ecosystem functioning that sustains the planet. A priori, no clear reasons for different evolutionary processes between archaea and bacteria can be advanced, but their ancient evolutionary divergence (despite the existence of lateral gene transfer between domains) suggests that the relevance of established microbial models of adaptation and diversification should be tested on these organisms if they are to be considered universal. Indeed, despite the global importance and diversity of archaea, our understanding of the ecological and evolutionary processes generating their high diversity is scarce compared to that of eukaryotes and, to a lesser extent, bacteria.

This project will focus on members of a key microbial phylum, the Thaumarchaeota (4, 5), which are abundant and ubiquitous and perform a critical ecosystem function, ammonia oxidation. The distribution of natural microbial communities is influenced by environmental characteristics, and pH is the major abiotic factor influencing extant thaumarchaeotal niche specialisation (4), and has also influenced their diversification and patterns of lineage formation through deep evolutionary time (5).

This project will involve re-isolation of a thaumarchaeotal strain (6) followed by the study the evolution of these microbes experimentally. Experimental evolution will be performed in automated mini-bioreactors by imposing environmental changes under controlled conditions and the evolutionary mechanisms of adaptation and diversification as well as the existence of trade-offs will be determined using genomic and fitness changes over time.

The PhD student will join a dynamic team of researchers led by Dr Cécile Gubry-Rangin (https://www.abdn.ac.uk/ibes/people/profiles/c.rangin) and will benefit from the presence of strong groups in the department working on related topics as well as being embedded in a strong network of international collaborations. The University of Aberdeen provides an excellent scientific environment, state-of-the-art technological support facilities and diverse training opportunities for all aspects of research and for transferable academic and generic skills.

Candidate should have (or expected to achieve) a minimum of 2:1 Honours degree, ideally (but not required) an MSc in evolution, ecology or related, strong theoretical skills and enthusiasm for learning and developing microbial experimental evolution.

Application Process: Formal application should be made as described on https://www.findaphd.com/search/ProjectDetails.aspx?PJID-539 . References: 1. Barrick JE, Yu DS, Yoon SH, Jeong H, Oh TK, Schneider D, Lenski RE, Kim JF. (2009) Genome evolution and adaptation in a long-term experiment with Escherichia coli. Nature 461(7268):1243-7 2. Rainey PB, Travisano M. (1998) Adaptive radiation in a heterogeneous environment. Nature 394:69. 394(6688):69-72. 3. Spang A, Caceres EF, Ettema TJG. (2017) Genomic exploration of the diversity, ecology, and evolution of the archaeal domain of life. Science 357(6351). pii: eaaf3883.

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UBielefeld RaptorMalariaGenomics

Short-term and long-term consequences of avian malaria-like infection

A PhD position in behavioural ecology is available at the Faculty of Biology at Bielefeld University, in the Department of Animal Behaviour (with Dr. Nayden Chakarov, see http://www.uni-bielefeld.de/biologie/animalbehaviour/nchakarov/jobs). The position runs for three years from 2018 to 2021 and is funded by the German Research Foundation (DFG). The PhD student will be part of the buzzard research team (together with the group of Prof. Dr. Oliver Krüger) and of a large PhD cohort, which is supported by a DFG-funded collaborative research centre NC3 (full details at www.uni-bielefeld.de/biologie/crc212).

The PhD project will combine field work, lab work and genomics.

We'll explore physiological causes and consequences of a very common blood parasite infection in a common buzzard population (Leucocytozoon in Buteo buteo). The student will conduct experiments in the field, produce transcriptomic data and analyse it in combination with health and fitness correlates. The long-term fitness consequences for buzzards will be monitored using lifelong wing-tags, and survival and recruitment data will be collected. So far, over 2500 individual buzzards have already been fitted with lifelong wing tags and the resulting data set will be used. The goal is to understand the extent and mechanisms of resistance and tolerance to the parasite in these hosts.

Main responsibilities

- Research tasks (90%) - Conducting field work on a buzzard population, including chick-ringing and treatment from late March to early July each year; RNA extraction and library preparation; Transcriptomic and statistical analyses; Writing scientific publications - Organisational tasks in the research group and collaborative efforts (10%)

Applicant's profile

We seek a bright and highly motivated student with a university degree in a relevant discipline with specialization in either behavioural ecology, ornithology, population ecology and/or bioinformatics, and a strong eagerness to delve into the others; interest to develop scientific capabilities and questions; experience with field work, preferably in birds of prey; experience with molecular lab work; interest in behavioural and life history, immunological and parasitological questions; coding experience, preferably with Unix command-line, omics-techniques, and/or R; ability to work both independently and as part of a team; excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage: papers in peer-reviewed international journals; experience in tree-climbing with rope techniques; experience with large-scale research projects.

Remuneration

Salary will be paid according to Remuneration level 13 (65%) of the Wage Agreement for Public Service in the Federal States (TV-L). Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling, and prevention programmes. Bielefeld University places great importance on a work-family balance for all its employees.

Application procedure

To apply, please provide: (i) a letter of motivation including a statement of your research interests and skills and experience relevant to the position; (ii) a brief but specific research plan, considering hypotheses and ideas related to the project outline and study system; (iii) a CV including publication list; (iv) names and contact details of two referees willing to write confidential letters of recommendation.

All materials should be emailed as a single PDF file to: nayden.chakarov@uni-bielefeld.de. The application deadline is July 31st 2018 and interviews will take place shortly thereafter. After the decision, the position should start on September 1st. For further information on the project and the department, please contact

Nayden Chakarov nayden.chakarov@uni-bielefeld.de with any informal inquiries.

Bielefeld is a city of 325,000 inhabitants with all expected amenities and easy access to the Teutoburger Wald for hiking and other outdoor pursuits. It offers a high standard of living and is well connected to most major European cities. Bielefeld University has received a number of awards for its achievements in the provision of equal opportunity and has been recognized as a family friendly university. The University welcomes applications from women. This is particularly true with regard both to academic and technical posts as well as positions in Information Technology and Trades and Craft. Applications are handled according to the provisions of the state equal opportunity statutes. Applications from suitably qualified handicapped and severely handicapped persons

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UBritishColumbia PopGenomics

I am looking for two graduate students (one MSc, one PhD) to join my research team at The University of British Columbia (Okanagan Campus) investigating the genetic basis of life history evolution in sockeye salmon, with direct applications to fisheries management in multiple systems. I am hoping to find highly motivated individuals to join the group in January 2019 (but a Sept. 2018 start is also possible). The projects offer opportunities for both laboratory and field-based research, and direct collaboration with researchers and managers from government and participating universities. Individuals with a population genetics background, bioinformatics experience and strong analytical skills are especially encouraged to apply.

Visit the Ecological and Conservation Genomics laboratory website (http://people.ok.ubc.ca/mirussel/) for more information on our current research directions, including recent publications involving sockeye salmon population genomics, life history evolution and fisheries management. Additional information about our Biology graduate program at UBCO can be found at the following website: http://biol.ok.ubc.ca/graduate/biology.html . To apply, send via e-mail (michael.russello@ubc.ca) a CV, unofficial transcripts, and contact information for at least two references.

Dr. Michael Russello Professor The University of British Columbia Okanagan Campus Department of Biology 3247 University Way, FIP346 Kelowna, BC Canada V1V 1V7 michael.russello@ubc.ca

michael.russello@ubc.ca

UCalgary VertebrateEvolutionaryBiol

The Rolian lab at the University of Calgary is seeking highly motivated graduate students (MSc or PhD) with an interest in skeletal evolution in mammals, to start as soon as possible. The core of the Rolian Lab's research program is an artificial selection experiment targeting increases in limb bone length in mice. This unique resource, known as Longshanks, was developed to study skeletal evolution in 'real time', from genomics to development to phenotypic coevolution and whole organism performance. Students will be able to develop specific projects in accordance with their own interests, and with the long-term goals of the Rolian lab. Individuals with a background and interest in vertebrate evolutionary biology, developmental biology and/or biomechanics are particularly encouraged to apply.

The University of Calgary is one of Canada's leading research-intensive universities, with diverse faculty working on evolutionary, developmental and skeletal biology. Funding is available through the lab and through teaching assistantships, although it is expected that students will also apply for competitive external and internal grants (e.g. NSERC). Calgary is a world?\class city near the Canadian Rockies, with excellent amenities and year?\round opportunities for recreation and culture.

More information on the Rolian lab can be obtained at: http://www.rolianlab.com, where links to our most recent projects on Longshanks can also be found under Publications. Information on admission requirements to pursue graduate studies at the U of C can be obtained at: http://www.ucalgary.ca/future-students/graduate/apply Interested candidates should email Dr. Campbell Rolian (cprolian@ucalgary.ca) by May 20^th 2018, with a brief description of their research interests, background preparation and current studies/work. Please note that the deadline for admissions varies by program, with the earliest possible start date of Fall 2018.

Campbell Rolian <cprolian@ucalgary.ca>

UComplutense Madrid ResAssist AvianGenomics

We are seeking an enthusiastic and self-motivated individual to join our research group (http://www.ucm.es/-bcveng/vetebrate-biology-and-conservation). This is one-year Research Assistant position to work within the project entitled 'Genomic study in the hoopoe: temporal patterns of gene expression in the uropigial gland and functional and evolutionary implications of its peculiar chromosomal organization', funded by the Talent Attraction Program of the Community of Madrid (Spain).

We would be interested in a person who intends to do the doctoral thesis in the near future, since we offer the possibility to participate in public calls for PhD-student positions to do the doctoral thesis within this project. The selected person will join the Department of Biodiversity, Ecology and Evolution, in the Faculty of Biological Sciences of the Complutense University of Madrid.

The study at the genomic level of adaptations that organisms have to environment is a fundamental topic in evolutionary biology. Thanks to the great advance of techniques and genomic tools in recent years, this type of approaches is progressing rapidly and have opened the possibility of addressing new questions about how genetic changes result in adaptive changes in the phenotypes. These same technological advances have made possible the inclusion in this field study of wild species, that are ecologically well characterized and/or possess relevant characteristics.

The project aims the development and use of genomic tools in the European hoopoe (Upupa epops). In this species of bird has been described a defensive symbiosis with bacteria living in its uropigial gland. In addition, the study of the genome of this bird species has an added interest, since it has a peculiar karyotype within birds, with a significantly higher number of chromosomes compared to the rest of avian species.

-Candidate requisites: The interested person should have a Bachelor or University Degree in Life Sciences, Statistics or related fields. We are looking for a person with the capacity to work as a team, responsible, proactive and oriented to results.

- Tasks to be carried out: - Fine tuning of the sampling technique. - Participation in the sampling in the field. - Preparation of samples for sequencing. - Bioinformatic analysis of the data from the sequencing of the samples. (Illumina, PacBios). In this first phase, the data will be mainly gene expression (possibly RNA-seq).

- Merits to be considered - Possess or be studying a Master in Bioinformatics or related. - Good academic record to have real possibilities of getting a PhD-student position. - Experience in Unix/Linux environment and in the Bash shell. - Knowledge of programming languages such as R, Python or Perl. - Knowledge of genome analysis pipelines (eg, FastQC, BWA, Bowtie, GATK, SAMtools, TopHat2, STAR, etc) would be an advantage. - Experience in the basic techniques used in the molecular ecology laboratory (extraction of DNA / RNA, electrophoresis, PCR, etc 'Â') would be an advantage. - Experience in field work with wild animals would be a plus. - Good level of English.

- Selection process It is expected that the official call of the contract will be published in mid June on the portal of the Complutense University of Madrid (https://www.ucm.es/personal-de-apoyo-a-la-investigacion-pai-ucm) and in the employment portal of the Community of Madrid (http://-www.madrimasd.org/empleo). The expected start date is early September. Due to the tightness of the anticipated deadlines once the call is open, interested persons are invited to contact the researcher responsible for the project before the publication of the call, by email (dmartingalvez@ucm.es), to send the CV and a motivation letter (in English or Spahish), as well as to ask any questions.

David MartÂÂn-GÂ'lvez Departamento de Biodiversidad, EcologÂÂa y EvoluciÂÂn Facultad de BiologÂÂa - Universidad Complutense de Madrid José Antonio NovaÂÂs,12 28040 - Madrid dmartingalvez@ucm.es

David MartÂÂn GÂ'lvez <damargal@gmail.com>

ULaRochelle BirdEvolutionaryBiology

Dear colleagues,

Funding is available for a PhD student in our labs (LIENSS and CEBC, CNRS / University of La Rochelle, France) to work on the phylogenetics & phylogeography of petrels. The full advertisement is here, with instructions on how to apply: https://epante.wordpress.com/-opportunities/ Best regards, Eric Pante & Vincent

Bretagnolle

Eric Pante <pante.eric@gmail.com>

ULausanne EvolutionaryBiology

Available:

The University of Lausanne (UNIL) is a higher teaching and research institution composed of seven faculties where approximately 15,000 students and nearly 5,000 collaborators, professors, and researchers work and study. Ideally situated along the lake of Geneva, near Lausanne's city center, its campus brings together over 120 nationalities. The Department of Ecology and Evolution of the UNIL invites applications for the position of

Graduate assistant at 80%

Expected start date : Autumn 2018 (e.g. October 1st, 2018)

The initial contract is for 1 year, renewable twice for two years, up to a maximum of 5 years in total.

Our group studies the selective forces that act on freshwater fish, i.e. the effects of human activities in interaction with natural and sexual selection. The position is in the context of a larger project that focuses on induced evolution in salmonid fish (whitefish, brown trout, grayling, and char) and combines fieldwork, experimental work in the laboratory, molecular genetics and bioinformatics, and population modelling. We are collaborating with several cantons and with other research groups at UNIL and elsewhere. Our website: https://www.unil.ch/dee/wedekind-group Graduate assistants in our department assist in teaching and supervise master students (up to 25% of the activity). At least 50% of their working time is devoted to personal thesis research. During the first year of employment, the monthly gross salary, 80%, is CHF 4'333.-.

We are seeking candidates with a Master in Biology and with a strong interest in one or several of the following fields: fish biology, population genetics, population management, life history, bioinformatics, evolutionary ecology. The working language in the group and in the department is English. Knowledge in French and/or German would be a plus.

We offer a nice working place in a multicultural, diversified, and dynamic academic environment, with possibilities of continuous training and other types of activities and benefits. Contact for further information: Prof. Claus Wedekind (claus.wedekind@unil.ch)

Please use on the UNIL recruitment platform at https://bit.ly/2KJSyWq to upload your full application containing a Curriculum vitae, a short description of your research interests and research experience, and contact details of two references. Review of applications will begin May 31st 2018, but applications will be accepted until the position is filled. UNIL is committed to promoting gender equality and strongly encourages applications from female candidates.

– Claus Wedekind Department of Ecology and Evolution, Biophore, University of Lausanne, 1015 Lausanne, Switzerland. Tel. +41 21 692 42 50, Fax +41 21 692 42 65 http://www.unil.ch/dee/home/menuinst/people/group-leaders/prof-claus-wedekind.html

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ULethbridge EvolutionaryNeurobiology

The Iwaniuk lab at the University of Lethbridge is currently seeking applications from students interested in pursuing a MSc or PhD on testing the social brain hypothesis in ground squirrel species. Graduate students will have the opportunity to work with several ground squirrel species in Alberta, BC, Manitoba and Montana. Dedicated lab facilities include microtomes, cryostat, fluorescent microscope, a high-resolution digital slide scanner (Olympus VS-120), and the latest in stereology and neuron tracing software (StereoInvestigator and Neurolucida). Confocal and electron microscopy are also available within the Canadian Centre for Behavioural Neuroscience at the University of Lethbridge. Field research is supported by a brand new 4x4 field vehicle and a specialized mobile lab trailer for preparing samples. In addition to our fieldwork in the Rocky Mountains, foothills and prairie regions of western Canada, opportunities are available for students to travel to and collaborate with researchers at other institutions in Canada, USA, Chile and Australia and attend national and international conferences.

The University of Lethbridge offers competitive scholarship funding, including tuition waivers, for applicants based on grades and research experience. Potential students must have a background in biology, psychology or neuroscience, some research experience (of any kind) and a valid driver's license. No fieldwork experience is required, but applicants should be prepared to conduct fieldwork in rural and remote locations. For application deadlines see: https://www.uleth.ca/graduate-studies/ Start dates are flexible, but the deadlines for graduate school applications are May 1st and October 1st.

To apply, send: 1) a c.v.; 2) unofficial copies of academic transcripts; and 3) a brief description of your research interests to: andrew.iwaniuk@uleth.ca. More information about our lab can be found at: http://scholar.ulethbridge.ca/iwaniuk/home Andrew N. Iwaniuk Associate Professor Canada Research Chair in Comparative Neuroanatomy Canadian Centre for Behavioural Neuroscience University of Lethbridge Lethbridge AB T1K 3M4 Canada ph. +1 403 332 5288 fax +1 403 329 2775 http://scholar.ulethbridge.ca/iwaniuk/ "andrew.iwaniuk@uleth.ca" <andrew.iwaniuk@uleth.ca>

ULincoln PopulationGenetics

MSc project on wolf population genetics

An exciting opportunity has arisen for a funded MSc by Research studentship in population genetics for a UK/EU student. We are looking for a qualified and motivated student to work on genetic analysis of historical wolf populations in comparison with modern wolf populations from Europe. The project will run at the University of Lincoln (UK) under supervision of Dr Malgorzata Pilot, in collaboration with Prof. Annik Schnitzler (University of Lorraine, France). The successful candidate will enrol on the MSc by Research programme in the School of Life Sciences. The student will be responsible for carrying out laboratory experiments and data analysis, under the supervision of Malgorzata Pilot. The student will join a multicultural and interdisciplinary research-oriented environment at the School of Life Sciences, University of Lincoln. This position is an excellent opportunity to gain research experience before enrolling on a PhD programme.

Qualifications/Experience: We welcome applications from candidates with background in Evolutionary Biology, Genetics, Zoology, or related fields. Priority will be given to applicants who have experience in molecular genetics labwork and knowledge of population genetics. Good spoken and written English is an essential requirement for this position. Knowledge of French will be considered as an advantage.

Funding: In the case of UK or EU candidates, tuition fees will be covered by the project funder. Non-EU candidates will receive a partial fee waiver equivalent to home/EU student fees. The student will have to cover their living expenses. The costs of project consumables will be covered by the funder.

Terms of Appointment: Start date should be ideally in July 2018. The project has to be completed with the thesis submission within one year from the date of enrolment. The student is expected to live in/near Lincoln for the duration of the project.

Application Deadline: 15 June 2018. Successful candidates will be invited for interview by w/c 18th June and interviews (via Skype) are anticipated to take place in the same week.

How to apply: In order to apply please email a short cover letter (1 A4 page maximum) explaining previous experience, interests and suitability for the position along with a CV (2 A4 pages maximum) and contact details of two referees to Dr Malgorzata Pilot (mpilot@lincoln.ac.uk). Referees should be former supervisors/ tutors and should be able to provide a reference when contacted. For informal enquiries please contact Dr Malgorzata Pilot. Applicants who are invited to interview will subsequently need to complete online application form to enrol for MSc by Research.

[TEF Gold] < http://www.lincoln.ac.uk/opendays >

The University of Lincoln, located in the heart of the city of Lincoln, has established an international reputation based on high student satisfaction, excellent graduate employment and world-class research.

Malgorzata Pilot <MPilot@lincoln.ac.uk>

UmeaU EcologyEvolution

4-year PhD position in Ecology (alternatively Computational Science) with focus on speciation dynamics

The Department of Ecology and Environmental Science, UmeÃ¥ university, opens a PhD student position for studies on ecological speciation and species boundary dynamics in plants. The position will start in September or according to agreement. The last day for application is June 25, 2018.

The project investigates the genomics of ecological selection and adaptation, and how genetic factors interact with ecology to facilitate speciation. The project is broadly defined and represents an opportunity to work at the intersection of theoretical ecology and population genetics, both conceptually and empirically. The project is financed by the Swedish Research Council and UmeÃ¥ University.

https://www.umu.se/en/work-with-us/open-positions/phd-position-in-ecology-or-computational-science_210254/ Contact Xiao-Ru Wang Dept. of Ecology and Environmental Science UmeÃ¥ Univeristy SE-901 87 UmeÃ¥, Sweden

Xiao-ru.wang@umu.se

Xiao-Ru Wang <xiao-ru.wang@umu.se>

UMemphis ComparativeGenomics

PhD position in Evolutionary Genomics

The Puckett Lab at the University of Memphis will hire a PhD student to being Fall 2018. The student will work on genome assembly and annotation, then use the generated genomes to answer questions in bear and/or carnivore comparative genomics.

Candidates should have academic interests in evolution, genetics, and/or bioinformatics. Prior experience working within Unix/Linux or a programming language (R, perl, python, etc) is not a pre-requisite, although it is a preferred qualification. Candidates without such experience should be exceptionally motivated to learn these skills. Wet lab skills are similarly preferred but can be taught. Candidates should be organized, persistent, a team-player, and have strong writing skills.

Students will receive five years of stipend support via TA-ships and tuition waivers. To learn more about the graduate program and intellectual community within the department, visit: http://www.memphis.edu/biology/ Please email Emily Puckett (emily.e.puckett@gmail.com) with either informal inquiries, or an application (CV, cover letter highlighting relevant experience and motivation for the position, and contact information for two references) as a single pdf. Review of applications will begin Friday May 25, 2018 and close Friday June 15, 2018.

Emily Puckett

Assistant Professor

Department of Biological Sciences- University of Memphis

https://puckettresearch.org/ emilyepuckett@gmail.com

UMontreal EvolutionSexDetermination

PhD POSITION : EVOLUTIONARY BIOLOGY/BIOINFORMATICS

The position :

The Breton lab (University of Montreal) is looking for an ambitious and highly motivated PhD student interested in understanding the genetic and epigenetic mechanisms of sex determination in the marine mussel Mytilus edulis.

PROJECT : The blue mussel Mytilus edulis is the most important cultured mollusc and therefore a major economic driver in the Gulf of St. Lawrence (Fisheries and Oceans Canada), and one of the most important in the world. Once successful in southern North Carolina, M. edulis has undergone a worrying decline in recent years in the Atlantic Provinces and the United States. Different hypotheses have been proposed to explain the reasons for this decline: overexploitation, ocean acidification, pollution, diseases, increased predators and global warming. Notably, global warming has been used as a hypothesis in several other studies to explain the decline of blue mussel populations, a result that could be attributable, among other things, to a drastic change in the sex ratio (i.e. the ratio of males and females), which could jeopardize the viability of certain populations. Indeed, marine mussels and oysters are known to have a sex ratio regulated by the environment (temperature and/or food). However, unlike oysters, very few studies have focused on sex determination mechanisms in marine mussels. A major reason for studying sexual determinism in mussels relates to their economic and nutritional importance. It is widely accepted that the success of livestock operations is largely related to the characteristics of the breeding populations (natural or captive), and in particular the need to control sex ratios, reproduction periods, fecundity and fertility.

This FRQNT-funded project aims to better understand the genetic and epigenetic mechanisms of sex determination in Mytilus edulis. Therefore, the successful applicant should have experience or a strong interest in bioinformatics, evolutionary biology and molecular biology.

Funding (15K/yr) is available to support the successful candidate for three years in addition to a limited travel budget. Expected start date is September 2018 or January 2019. The Universite de Montreal is a French language institution where graduate work may be undertaken in English or French.

Interested students should contact s.breton@umontreal.ca and attach a CV, academic transcript, contact details of two academic referees, and a brief description of their research interests.

The position will remain open until a suitable candidate is found.

Please note that only those selected for an interview (Skype or telephone) will be contacted. Preference will be given to Canadian citizens and permanent residents.

sophie breton <breton.sophie@gmail.com>

UPadua Italy GuppySexualSelection

PhD scholarship for a project on sexual selection in guppies (Poecilia reticulata)

Supervisor Andrea Pilastro, University of Padova, Italy

Proposed project

Aim of this project is to explore how social environment shapes the evolutionary dynamics associated with pre- and post-copulatory sexual selection in the guppy (Poecilia reticulata). The project will be part of a collaboration with J. Evans (University of Western Australia), A. Wilson (University of Exeter, UK) and and F. Garcia-Gonzalez (Doñana Biological Station, Spain). The candidate will have to possibility to spend part of the three-years project at one, or more of these institutions. Potential candidates are encouraged to contact me (andrea.pilastro@unipd.it).

Application deadline: 26th June 2018, Starting: Oct 1st, 2018

For more information: University of Padova http://www.unipd.it/en/ Department of Biology https://www.biologia.unipd.it/en/ PhD School in Biosciences https://dottorato.biologia.unipd.it/ –

Andrea Pilastro Dept. of Biology, University of Padua via Ugo Bassi 58/B - 35131 Padova, Italy T. +39 049 827 6224 F. +39 049 827 6209 E. andrea.pilastro@unipd.it W. https://scholar.google.it/citations?user=tB5pGx4AAAAJ&hl=en&oi=ao Andrea Pilastro <andrea.pilastro@unipd.it>

UPadua MicrobialBiodiversity

PhD Position available at the Department of Comparative Biomedicine and Food Science (University of Padua, Italy)

Call opens at the end of May 2018

Ecology and food safety in shellfish production.

Climate change and anthropogenic pressures may have dramatic effects on marine ecosystems with strong negative impacts on fisheries and aquaculture as the spread of emerging pathogens and the modification in distribution and balance among bacterial species. Vibrio spp. represent the majority of the marine and estuarine biomass. Several studies demonstrated the spread of Vibrio cholerae in many regions, including Italy, where cholera outbreaks have never been reported. Changes in environmental bacterial communities may affect host-microbiota interactions and mutualistic symbiotic relationships, causing potential adverse effects on the physiological state of animals, growth performance and product safety and quality. This research topic aims to explore biodiversity in microbial ecosystems, focusing on Vibrio populations, in order to elucidate the complex dynamic interactions between molluscs and their microbiota. Culture-dependent and culture-independent methods will be applied on two different shellfish species, Crassostrea cigas and Ruditapes philippinarum, to evaluate the composition of bacterial community focusing on Vibrio populations. In addition different methods of shellfish depuration will be also assessed. All these data will be integrated with environmental and animal health parameters in order to develop dynamic models providing useful forecasts to farmers and authorities involved in food safety controls.

http://www.dottorato.veterinaria.unipd.it/node/2151 (Further details available from the end of May 2018)

Official contact: barbara.cardazzo@unipd.it

– Font Face *Maria Elena Martino, Ph.D.* Department of Comparative Biomedicine and Food Science (BCA) University of Padua Viale dell'Università, 16 Legnaro (PD) Italy

Maria Elena Martino <mariaelena.martino@unipd.it>

UppsalaU ComputationalGenetics

PhD Student position available: Computational Genetics, Uppsala University

The Department of Medical Biochemistry and Microbiology at Uppsala University seeks a PhD student candidate in Computational Genetics in the research group of Ãrjan Carlborg.

The selected candidate will be offered a full time four year employment at Uppsala University. The position comes with salary and full benefits of being a Swedish University employee. Up to 20% teaching can be requested annually, in which case the position will be prolonged to five years. The PhD program includes a total of 30 credits (20 weeks) of courses, a few obligatory and most optional, the rest of the program is own research. More information on the PhD program can be found at http://www.imbim.uu.se/Education/Postgraduate+education/information-and-documents/ .The starting date is flexible, but the initial plan is for admission during the fall semester of 2018. Review of applications will start immediately and will continue until a suitable candidate has been found.

The research group focus on studying the genetics of complex traits with a particular emphasis on non-additive genetic inheritance in polygenic genetic architectures. An interdisciplinary, interspecies approach is used, where new genetic models, statistical methods, and bioinformatics approaches are developed to explore experimental data from a range of species - from yeast to plants and domestic animals. We always attempt to make use of the most powerful experimental data available and therefore obtain it from a variety of sources including public repositories, collaborators or by generating it ourselves. This PhD-student project is an important part in this effort and will be performed in this strong, inter-disciplinary research environment. You can find more information about our group at http://katalog.uu.se/organisation/?orgId=X38:50 . During the studies, the PhD candidate will have full access to state of art computing resources and training programs provided by SciLife & Uppsala University. Limited travel funding for attending conference and summer schools are available within the program.

The first half (2 years) of this PhD project is to work with the Virginia lines - a chicken population developed during a long-term (60 year) bi-directional, single-trait selection experiment. This is an excellent model to study the genetic basis of long-term selection response on an adaptive trait that is highly polygenic. Earlier work has shown that selection has acted on a complex genetic architecture including loci with either tightly linked adaptive variants, multiple segregating haplotypes and/or interactions between loci. The PhD student will be involved in efforts to map and model the genetic architectures of the adaptive trait in and its contributions to the long-term selection responses. A valuable resource to the project is a new dataset including approximately 4000 phenotyped, pedigreed and individually low-coverage sequenced individuals from a 19 generation deep advanced intercross line between the divergently selected lines. The later half (2 years) of the project will be decided depending on the interest and competence of the admitted PhD student, and could therefore involve, for example, detailed explorations of specific genetic mechanisms via analyses of data from other species or data simulations, or more focus on development of new models and methods for trait mapping or modeling of genotype-to-phenotype mappings.

Qualifications MSc in Bioinformatics, Statistics, Computational biology, Quantitative/Population/Evolutionary genetics or similar qualifications is a requirement. If the degree is not complete at the deadline of applications, it should be indicated when it is estimated to be obtained.

Given the analytical content of the project, it is a merit to have good knowledge and experience of both genetics and informatics. This can be shown through earlier research experience in the field. Programming is an important tool in the project and therefore you should have experience in programming in e.g. R, C++, Fortran, Perl, Python or Java. You should have excellent English abilities, both orally and in writing. If you are a mathematician/statistician/computer scientist, complementary knowledge in genetics or genomics is meriting. Knowledge in mathematics/statistics/computer science is in the same way meriting if your exam is in biology.

The letter of interest, including a description of your formal qualifications together with any questions about the PhD project, should be directed to Prof. Ãrjan Carlborg, Department of Medical Biochemistry and Microbiology, Uppsala University; orjan.carlborg@imbim.uu.se.

Selected references of relevance to the project are:

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

UppsalaU PopGenomicsAncientDNA

PhD student position in Population Genomics and ancient DNA at Uppsala University

The PhD position will be financed by a VetenskapsrÃ¥det starting grant and the research will be conducted within the Human Evolution Program at the Department of Organismal Biology (Evolutionary Biology Center, Uppsala University). The Günther group is specifically studying the prehistory of humans in Europe and the genomic history of animal domestication while developing and improving population genomic and bioinformatic methods to analyze palaeogenomic data. The Human Evolution Program, in which the Günther group is situated, has a broad interest in population genetics and human evolution. There are ample opportunities to work closely with postdocs and other PhD students who focus on related projects. The research environment is international with English being the working language. See Dr. Günther's web-page for more information on research and recent publications (https://tgnthr.wordpress.com) and the Human Evolution Program web-page for more information on the program (http://www.iob.uu.se/research/human-evolution/).

*Project description: *Obtaining ancient DNA from prehistoric remains has opened up the time dimension for genetic research by allowing us to study populations across time and space. The student will analyze such data to study the evolutionary history of prehistoric domesticated animal (e.g. sheep) and human populations. While genomic studies on prehistoric human populations can complement results from other disciplines (e.g. archaeology, linguistics), animal domestication is a great model for evolutionary changes in a relatively short time frame and under strong selection pressures. Particular focus of the project will be on the development of population structure over time and how selection shaped the genomes of these populations. In addition to the analysis of published and newly generated datasets, the student will test and extend computational methods for working with such data.

*Requirements: *A Masters degree (or equivalent) in a relevant field is required. The ideal candidate is highly motivated with thorough education and strong interest in evolutionary genetics/genomics, population genetics and bioinformatics. Previous experience with large-scale genetic data analysis, ancient DNA, and scripting/programming is advantageous. Mathematical, computational and statistical training is also advantageous. Candidates must be fluent in English.

In filling this position, the university aims to recruit the person who, in the combined evaluation of competence, skills and documented qualifications, is judged most suitable to carry out and develop the work-in-hand and to contribute to a positive development of the department.

The PhD-student position is a 4-year appointment, and the candidate will primarily devote the time to—his/her own research studies. Other departmental work, such as teaching or administration can be part of the position (maximum 20 %). Salary placement is in accordance with local guidelines at Uppsala University. The applicant must be eligible for PhD studies at Uppsala University. Information about research education can be found at the web site of the Faculty of Science and Technology, http://www.teknat.uu.se/Doktorand/ . *Application: *The application should include a letter of intent describing yourself and your research interests. The application should also include a CV, copy of master degree diploma and course grades, master thesis,—contact information for references and other relevant documents. Application deadline is *17 June 2018*

*Apply here: *http://uu.se/en/about-uu/join-us/-details/?positionId=208508 ****

Pay: According to local agreement for Phd students and teaching assistants.

Starting:—2018-09-01, temporary positions ending 2022-08-31.

Torsten Günther Evolutionary Biology Centre Uppsala University Norbyvägen 18C 752 36 Uppsala, Sweden https://-tgnthr.wordpress.com/ "torsten.gunther@ebc.uu.se" <torsten.gunther@ebc.uu.se>

URennes EvolutionOnIslands

Dear all

Sorry for possible cross posting. Please distribute as appropriate.

This is to inform you about a PhD project on "Microevolution on macroevolution islands: Does phylogenetic isolation of trees from neighbors trigger rapid phenotypic responses in phytophages?". The project is one out of 5 for in our research unit competing for 3 fundings.

The PROJECT: Evolution may operate very rapidly, in particular on oceanic islands were colonizers are released from natural enemies and competitors and face genetic drift. However, islands are only a small part of the earth's surface. Individual plants, in particular mature trees, are distinct host patches for phytophages. Plants of different species often grow in close spatial proximity but may nevertheless belong to lineages separated by many million years of macroevolutionary history. Just like oceanic islands, such "macroevolutionary island trees" might hence be characterized by fast trait evolution of their insect phytophages. M*a*croevolutionary islandness of host trees might trigger m*i*croevolutionary responses in phytophages. In short, in this we try to understand whether a small event in tree macroevolution - a tree converges and coexists with distantly related neighbors - changes the phenotypes of its insect colonizers, including their capacity to respond to climate change.

The host lab here is the UNITE MIXTE DE RECHERCHE (UMR) ECOBIO - ECOSYSTEMES, BIODIVERSITE, EVOLUTION, co-funded by University of Rennes 1 and Centre National de la Recherche Scientifique, with particular expertise in mechanisms of speciation, life history evolution, and adaptation, expertise at the interface between macroevolution and macroecology, expertise in ecophysiology, landscape ecology and behavioral ecology, environmental genomics (very strong), community assembly and plant/herbivore interactions. It is a large institution with several dozen CNRS-researchers, docents and professors, plus (some) technical staff. See http://ecobio.univ-rennes1.fr/ . It was ranked A in the national evaluation of research institutions. Several further research institutions in ecology and evolutionary biology exist at Rennes.

RENNES has approximately 200 000 inhabitants and is the capitol of the Bretagne region with exceptional coastal and mainland landscapes, and a french-celtic heritage (http://www.bretagne.fr/internet/jcms/-TF071112_5061/tourisme). It is situated some 1.5 hours by train from Paris. English is spoken everywhere in Academia, but not necessarily outside, and French should be learned. Like in any French city, child care is excellent (almost for free, no waiting list, nearby). Several bilingual French-English schools are available at all levels of education, as well as one French-German grammar school.

Formal deadline is June/3 at https://theses.u-bretagneloire.fr/egaal/theses-2018 . **If interested, please directly contact me directly at least a week before **

Best regards

Andreas Prinzing

Andreas Prinzing, Prof.

Ecology of Diversification

Research Unit "Ecobio: Ecosystems - Biodiversity - Evolution";

Team "Evolution, Structure and Dynamics of Diversity"

Universite de Rennes 1 / Centre National de la Recherche Scientifique

Campus de Beaulieu, Batiment 14 A ; 35042 Rennes, France

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E-mail andreas.prinzing@univ-rennes1.f

https://ecobio.univ-rennes1.fr/Fiches_perso/-Fiche.asp?pseudo=APrinzing https:/-/scholar.google.com/citations?user=-w5Ogsc0AAAAJ&hl=en Andreas Prinzing <andreas.prinzing@univ-rennes1.fr>

UStrasbourg EvolutionaryPysiology

3-year PhD position in Animal Physiology and Behavioural Ecology on

* Exploring the impact and adaptation to social and environmental stress in the king penguin *

supervised by Dr Jean-Patrice Robin and Dr Pierre Bize at the University of Strasbourg, France

King penguins are unique by their biology: they reproduce in an aggressive social environment and extreme environmental conditions, and parents alternate long fasting periods on land with intense foraging periods at sea. Furthermore, both sexes display conspicuous ornaments used in sexual and social contexts. We have previously demonstrated that king penguins are sensitive to their neighbours: breeders get stressed when reproducing in socially dense environments and they rely on the size of their auricular patch to establish social dominance. In this project, we aim to explore further inter-individual physiological and behavioural variation in responses to social stress, and in particular to test whether some individuals are better adapted to cope with social stress, what make them better adapted to stress and whether individuals can signal their social competences. Research will be carried on the Sub-Antarctic Island Crozet, and the applicant should have a keen interest in doing experimental work in free living birds and to embrace an integrative approach, addressing changes in states ranging from the cell to the whole organism level. This project will rely both on newly data collected by the candidate in the field over up to 2 expeditions in sub-Antarctica and on archived data, thereby allowing the candidate to start the PhD project without delay and guarantying results on the project.

For this PhD project we are seeking somebody who is independent, mobile, creative, highly motivated, and has interest in animal physiology and behavioural and evolutionary ecology. Our ideal candidate has previous experience working in the field (preferentially with birds), likes working in a team, has excellent written and oral communication skills in English, and is not afraid of statistics and lab work. Experience with programing in R (or other languages such as SQML or Matlab) and with lab work is not essential but is a welcome addition; the willingness to learn such techniques is, however, crucial.

The successful applicant will be mainly based in the Department of Ecology, Physiology & Ethology (DEPE) at the University of Strasbourg, France, under the joined supervision of Dr Jean-Patrice Robin (Strasbourg) and Dr Pierre Bize (University of Aberdeen, UK). The DEPE is a lively Department where the student will benefit from interaction with a thriving community of postgraduate students, postdocs and researchers in animal physiology, marine biology and behavioural ecology. Furthermore, the student will integrate an international team working on the French Polar Program ÂÂECOENERGYÂÂ, and will thus benefit from the interaction and support of research partners, namely Vincent Viblanc and Yves Handrich (Strasbourg, France), Quentin Schull (MARBEC, France), Antoine Stier (Turku Univ., Finland), Steve Dobson (Auburn Univ, U.S.A.) and Rudy Boonstra (Toronto Univ., Canada). The student will be encouraged to visit the partners to conduct specific analysis. The student will participate in the PhD program of the Doctoral School ED414 of the University of Strasbourg (http://ed.vie-sante.unistra.fr/) providing additional learning of transferable skills.

Strasbourg is one of EuropeÂÂs most attractive cities. It has a rich historical and architectural heritage, with Strasbourg's historical city centre being listed as a World Heritage Site by UNESCO. Its human size, its pedestrian city centre and 500 km of cycling paths make it a very pleasant city to wander around. Vibrant and affordable, Strasbourg is a true student city providing a great learning and living environment (Check out the New York Time's video: https://www.nytimes.com/video/travel/100000003269152/36-hours-in-strasbourg.html).

Applications must include 1) a cover letter outlining why you want to work on this project, 2) a detailed curriculum vitae, 3) the contact details of two academic referees, 4) a 1Â©\page summary of your MSc project or undergraduate work.

Please send the above as a single pdf file to both jean-patrice.robin@iphc.cnrs.fr AND pierre.bize@abdn.ac.uk

Application deadline is 17/06/2018 23:00 - Europe/Brussels; interviews will take on July 13th; starting date is Sept 17th.

The PhD project is fully funded for 3 years by the IDEX program from the University of Strasbourg; monthly salary of 1769 euro.

Eligibility criteria: Holding a Master degree or equivalent from a University outside France

For more information, feel free to contact Jean-Patrice Robin or Pierre

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USunshineCoast HumanGenomics

Human Genomics PhD Scholarship at the University of the Sunshine Coast, Australia

Humans migrated out-of-Africa over 60,000 years ago and spread to different parts of the globe. In this process human population was subsampled serially along the routes of the migration. This project will investigate the footprints of migrations manifested in the frequencies and patterns of genetic variations in human populations. The main research foci of our group include the effects of genetic drift in modulating mutation and selection, quantifying mutational load, investigating the rates and patterns of mutations, estimating divergence times between species and populations and ancient genomics. We work on a number of species including humans and other mammals, birds and oysters.

The current project focuses on a) investigating genetic relationships and gene flow between global human populations. b) estimating the mutational load in humans c) understanding the unique patterns of genetic variations in different human populations. All the above objectives will need to be examined in the context of human migrations out of Africa.

This project involves collecting samples for whole genome sequencing and performing a series of bioinformatic analyses to process raw sequence data. The processed data will need to be analysed using a range of methods in population genomics and evolutionary biology to answer the questions related to objectives mentioned above.

The project provides an opportunity to work and acquire knowledge in inter-disciplinary sciences such as molecular biology, genetics, computer science and statistics.

SELECTION CRITERIA: Academic qualifications - An honours or master's degree in biological, physical or computational sciences is highly preferred; however, persons with a non-biology degree should have some basic understanding of genetics, evolution and molecular biology Record of research publications Professional research experience Additional desirable selection criteria: Scripting (Perl/Python) Familiarity with Unix/Linux systems Experience in using High Performing Clusters Knowledge about software and tools used in next generation sequence data analyses Previous research experience in Bioinformatics Number of scholarships: 3 Stipend: $27,082. If the successful recipient is an International student, tuition fees and Overseas Student Health Cover (single cover) will be included in the scholarship.

Standard duration of the program: 3 years For more information contact Dr Sankar Subramanian: ssankara@usc.edu https://www.usc.edu.au/learn/what-will-i-pay/scholarships/research-scho larships/human-genomics-phd-scholarship

Sankar Subramanian <ssankara@usc.edu.au>

UToronto PhenologyAmphibiansReptiles

The Fortin group and the Rollinson group at the University of Toronto St. George are seeking a highly-motivated MSc student to study spatial and temporal patterns in the phenological timing of amphibians and reptiles. In collaboration with Ontario Nature, the candidate will leverage hundreds of thousands of citizen science observations made during the last century to inform a spatially-explicit model that maps annual variation in temperature to variation in activity patterns of amphibians and reptiles throughout Ontario.

The goal is to understand how variation in climate patterns maps directly onto activity patterns in ectotherms, which will broaden our understanding of how climate change is influencing the realized length of the activity season across Ontario. The ideal candidate would have an interest in spatial ecology, evolutionary ecology, quantitative methods, and conservation, coupled with an enthusiasm to collaborate with NGOs. Candidates that have a demonstrated ability to learn quickly and an interest in modelling are also encouraged to apply.

The position begins in September 2018 or January 2018. The position is funded, however the candidate will be expected to apply for NSERC funding. The position will remain open until it is filled.

Please apply by emailing your (unofficial) transcripts, a writing sample, and your CV to njal.rollinson@utoronto.ca and fortinmj@gmail.com

https://fortin.eeb.utoronto.ca/ www.njalrollinson.com https://ontarionature.org/ Njal Rollinson Assistant Professor Ecology & Evolutionary Biology / School of the Environment Earth Science Building Office ES3051 University of Toronto Phone: 416-978-3665 Research Homepage: www.njalrollinson.com

Njal Rollinson <njal.rollinson@gmail.com>

UVienna ChemicalEcology Evolution

The Division of Tropical Ecology and Animal Biodiversity at the University of Vienna, Austria is seeking a highly-motivated MSc student to study the detoxification strategy of the cabbage stem weevil Ceutorhynchus pallidactylus to overcome the chemical defenses in its crucifer (Brassicaceae) host plants.

Background Weevils of the genus Ceutorhynchus feed exclusively on crucifers (Brassicaceae), although these plants evolved a strong phytochemical defense system to prevent being eaten by herbivores. Upon feeding damage, glucosinolates are hydrolyzed by B-thioglucosidase enzymes (myrosinases) to form isothiocyanates well known for their toxicity for herbivorous insects. Few groups of insects successful adapted to this so-called 'mustard oil bomb' and are specialized to feed on crucifers. Cabbage-white butterflies (Pieridae) use nitrile-specifier proteins to produce less toxic nitriles instead of isothiocyanates upon glucosinolate hydrolysis. The association of Pierinae butterflies with their host plants is a key example of Ehrlich and Raven's 'escape and radiate' model of insect-plant coevolution. With over 400 species, the genus Ceutorhynchus represents by far the largest insect radiation on Brassicaceae. It can therefore be expected that Ceutorhynchus considerably contributed to the 'arms-race' between insects and crucifers. Their species richness further implies that these beetles evolved an efficient strategy to overcome the chemical defense in crucifers.

Goals To infer the adaptation of Ceutorhynchus species to their crucifer hosts, feeding bioassays will be performed with Ceutorhynchus pallidactylus and Arabidopsis thaliana, a plant containing 4-methylsulfinylbutyl glucosinolate. After ingestion of A. thaliana leaves, weevil bodies and feces will be extracted in methanol and the extracts analyzed by liquid chromatography-tandem mass spectrometry (LC-MS/MS). The lab work will be conducted in the Max Planck Institute for Chemical Ecology (MPI-CE) in Jena, in collaboration with Dr. Franziska Beran (Research Group Sequestration and Detoxification in Insects).

Schedule Work may begin May 2018 or soon thereafter and is scheduled for one year. Publication of results is intended. The project is ideally suited as MSc thesis work in the curricula Zoology or Ecology & Ecosystems at the University of Vienna.

Contact Dr. Harald Letsch Department of Botany and Biodiversity Research Division of Tropical Ecology and Animal Biodiversity Rennweg 14 A-1030 Vienna Email: harald.letsch@univie.ac.at Phone: +43 1 4277 57403

Harald Letsch <harald.letsch@univie.ac.at>

Vairao Portugal ConservationGenetics

Dear Colleagues,

I would like to inform you about the call for applications for a research fellowship (MSc) in Conservation Genetics, at the Research Center in Biodiversity and Genetics Resources (CIBIO-InBIO), Vairao, Portugal, which will be open until May 18th, 2018.

If possible, I would greatly appreciate to be able to count on your collaboration in the dissemination of this opportunity amongst potential candidates.

Thank you so much!

All the best,

CIBIO-InBIO's Science Communication and Outreach Office

CIBIO - Centro de Investigaçao em Biodiversidade e Recursos Genéticos/ InBIO Laboratório Associado, Universidade do Porto

Campus Agrário de Vairao

Rua Padre Armando Quintas

4485-661 Vairao

Portugal

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Research Fellowship MSc

Reference: ICETA-2018-22

Link to the call - http://www.eracareers.pt/-opportunities/index.aspx?task=global&jobId395
Main research field: Biological sciences

A Research Fellowship MSc (BI) (Reference ICETA 2018-22) is now available in the area of conservation genetics, framed within the project PTDC/AAG-REC/6480/2014/ "ECOLIVES ' Fostering sustainable management in Mediterranean olive farms: pest control services provided by wild species as incentives for biodiversity conservation" at ICETA-Instituto de Ciências e Tecnologias Agrárias e Agro-Alimentares, financed by national funds by FCT / MCTES and co-financed by Fundo Europeu de Desenvolvimento Regional (FEDER) throughout COMPETE ' Programa Operacional Factores de Competitividade (POFC).

Admission requirements:

Candidates should hold a MSc degree in Biology or related fields and should have a solid experience in molecular biology and invertebrates' taxonomy. The candidates should demonstrate experience in:

(i) Invertebrate sampling with special focus on insects, samples preservation and preparation for DNA analysis;

(ii) molecular biology techniques, including DNA extraction and DNA sequencing;

(iii) curation and analysis of DNA sequences: barcoding, phylogenies and species delimitation methods;

(iv) management of databases and biological collections. High motivation, communication and team work skills, as well as fluency in English (spoken and written) will be highly valued.

Work plan:

The work plan is included in a project which investigates the value of natural biological control of the Olive fruit fly (Bactrocera oleae) and the Olive fruit moth (Prays oleae), the two major pests in olive farms worldwide, in farms following distinct pest management strategies. The project will particularly focus on the invertebrate communities that are present in olive tree tops and will be carried out throughout the region of Alentejo, one of the main olive production region in Europe. The candidate will be involved in several tasks:

(i) sample preparation for DNA analysis;

(ii) DNA extraction, amplification and sequencing of several molecular markers using both Sanger sequencing and Next Generation Sequencing techniques;

(iii) barcoding of parasitoids and other organism of small size;

(iv) screening of larvae for the presence of parasitoids

(v) management of databases and biological collections.

The successful candidate is expected to collaborate in writing technical reports and scientific publications.

Legislation and regulations:

A fellowship contract will be celebrated according to the regulations defined by FCT "Regulations for Advanced Training and Qualification of Human Resources", in accordance with Law 40/2004, of 18 August, as amended and republished by Decree-Law No. 202/2012 of 27 August, and as amended by Decree-Law No. 233/2012 of 29 October and by Law No. 12/2013, of 29 January, and Decree-Law No. 89/2013 of 9 July, to Fellowships Regulation of FCT, and to Fellowships Regulation of ICETA approved by FCT.

Salary: Monthly stipend is euro 980 according to the stipends established by FCT, I.P. in Portugal (http://alfa.fct.mctes.pt/apoios/bolsas/valores). Payment will be made by bank transfer on a monthly basis.

Workplace:

The work will be carried out at CIBIO - Research Centre for Biodiversity and Genetic Resources, Vairao, Portugal, under the scientific supervision of Doutor Pedro Beja.

Grant duration:

The fellowship is expected to start in the 1st of June 2018 and have the duration of one year.

Selection methods:

The ranking of candidates will be performed by a global evaluation based on the CV (40%), previous experience of the applicant relevant to the project and work-plan (40%) and motivation letter (20%). If necessary, an interview with a shortlist of candidates may be performed. The jury may not award the fellowship if the expected quality and requirements of candidates are not fulfilled.

Composition of the Selection Panel:

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WesternSydneyU AdaptiveCapacityClimateChange

"Saving Our Species: Adaptive Capacity to Climate Change"

We are looking for a highly motivated and qualified candidate for a 3- year PhD program of research at the Hawkesbury Institute for the Environment, Western Sydney University, commencing in 2018. This studentship is part of an exciting new research programme established under the Office of Environment and Heritage "Saving Our Species" initiative, investigating the adaptive capacity of threatened species and ecological communities to climate change. This project aims to quantify the physiological tolerance of woody plants to heat waves and droughts. It will test the assumptions and predictions of species distribution models within a comparative framework with species from a range of climatic distributions, dispersal modes, and life-history traits. This work will provide empirical information to inform policy decisions and management practices for threatened plants through improved predictions of species' climate thresholds and ability to persist under climate change.

The Hawkesbury Institute for the Environment is situated in a semi agricultural landscape at the base of the Blue Mountains national park. Offering excellent outdoor recreational activities. There is easy access to Sydney with a direct 1h 20min train, providing a range of cultural activities.

Applicants should discuss their eligibility and interests with Dr Paul Rymer (mailto:p.rymer@westernsydney.edu.au) or Professor David Tissue (mailto:d.tissue@westernsydney.edu.au) or Dr Brendan Choat (mailto:b.choat@westernsydney.edu.au). Please submit an application form (PDF, 278.77 KB), CV, names and contact information of two referees, and a one-page document stating how your research interests and experience align with the project's aims.

https://www.westernsydney.edu.au/graduate_research_school/grs/scholarships/current_scholarships/current_scholarships/hie_saving_our_species_adaptive_capacity_to_climate_change Shortlink: http://bit.ly/2L1OAYs Paul Rymer Lecturer in Plant Ecological Genetics Hawkesbury Institute for the Environment Western Sydney University https://www.westernsydney.edu.au/hie p.rymer@westernsydney.edu.au office 0245701094 mobile 0415963139

"P.Rymer@westernsydney.edu.au" <P.Rymer@westernsydney.edu.au>

Jobs

Bayer Biostatistics

Biostatistics Scientist - Bayer - West Sacramento, CA Please apply at: https://www.career.bayer.us/en/job/Biostatistics-Scientist-I–SF17334.html YOUR TASKS AND RESPONSIBILITIES

We are seeking a highly motivated scientist to join the Biologics R&D team as a Biostatistics Scientist I at our West Sacramento, California site. This is a highly interdisciplinary role that requires collaboration with internal and external collaborators in statistics, plant pathology, entomology, fermentation, chemistry and bioinformatics. The candidate will integrate data, make recommendations, produce statistical pipelines, and improve the overall quality and value of our data collection.

The primary responsibilities of this role, Biostatistics Scientist I, are to:

. Develop and improve statistical tools for discovery and characterization of microbial compounds in vitro, in planta, and/or in field; . Support bench scientist teams in the analysis of large data sets by integrating different data types into statistical frameworks; . Train research staff on experimental design, basic statistical concepts, and the use of relevant statistical tools; . Keep abreast of new statistical techniques, including technological developments in machine learning; . Provide guidance to external collaborators regarding experimental design and/or statistical analysis; . Be able to work with Data Engineers to translate statistical analyses and experimental designs into standardized pipelines; . Be able to communicate effectively through listening, documentation, and presentation, especially using compelling visualization tools to share analysis and the interpretation of data.

WHO YOU ARE

Your success will be driven by your demonstration of our LIFE values. More specifically related to this position, Bayer seeks an incumbent who possesses the following:

Required Qualifications: . Ph.D. in Biology, Statistics or a related field or Master's degree and two (2) years of experience; . Expertise in the statistical analysis software R.

Preferred Qualifications: . Prior experience in plant breeding, plant pathology, plant biology, entomology, ecology, or evolutionary biology; . Prior experience in agriculture and/or an R&D environment; . Knowledge of other programming languages (UNIX, Python, SQL).

*Position may offer domestic relocation assistance.

Freundliche Grüße / Best regards,

Matt Armstrong Recruiter

Bayer U.S. LLC 100 Bayer Road Pittsburgh, PA 15205 United States Tel: 412-778-6688 E-mail: matthew.armstrong@bayer.com Web: www.career.bayer.us

Matthew Armstrong <matthew.armstrong@bayer.com>

ClemsonU 2 MolecularGenetics StatGenetics

A position is available for a molecular geneticist in the newly established Center for Human Genetics at Clemson University. The Clemson Center for Human Genetics is located on the Greenwood campus adjacent to the Greenwood Genetic Center. This is a non-tenure track high level Research Scientist position, which requires a Ph.D. degree with a record of productivity. The ideal candidate will have expertise in preparation of libraries and performing next generation sequencing (DNA, RNA, ChIP, ATAC) and CRISPR gene editing. The successful candidate will conduct experiments with a great deal of independence, is expected to publish, and will provide advice and support to faculty members, postdocs and students in the Center for Human Genetics. The position requires excellent interpersonal and communication skills. Application and inquiries should be addressed to Dr. Trudy F. C. Mackay, Self Family Endowed Professor and Director of the Center for Human Genetics, Clemson University, Self Regional Hall, 114 Gregor Mendel Circle, Greenwood, SC 29646. Email: tmackay@clemson.edu.

Applications must include a cover letter explaining the qualifications for this position, a curriculum vitae with list of publications, and the names of three references. The position is available as early as July 1, 2018, or until the position is filled. Salary is competitive and commensurate with experience. Clemson University is an equal opportunity employer.

Applications should be submitted electronically via the link:

https://cujobs.clemson.edu/psc/ps/JOBS/EXT/c/HRS_HRAM.HRS_APP_SCHJOB.GBL?Page=HRS_APP_JBPST&Action=U&FOCUS=Applicant&SiteId=1&JobOpeningId=102928&PostingSeq=1 —

A position is available for a statistical geneticist/bioinformatician in the newly established Center for Human Genetics at Clemson University. The Clemson Center for Human Genetics is located on the Greenwood campus adjacent to the Greenwood Genetic Center. This is a non-tenure track high level Research Scientist position, which requires a Ph.D. degree with a record of productivity. The ideal candidate will have expertise in statistical genetic and quantitative genetic data analysis, computational biology and bioinformatics analyses of next generation sequencing data (DNA, RNA, ChIP), and analysis of metabolic and proteomic data. The successful candidate will conduct collaborative research and is expected to publish, and provide advice and support to faculty members, postdocs and students in the Center for Human Genetics. The position requires excellent interpersonal and communication skills. Application and enquiries should be addressed to Dr. Trudy F. C. Mackay, Self Family Endowed Professor and Director of the Center for Human Genetics, Clemson University, Self Regional Hall, 114 Gregor Mendel Circle, Greenwood, SC 29646 (tmackay@clemson.edu).

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https://cujobs.clemson.edu/psc/ps/JOBS/EXT/-c/HRS_HRAM.HRS_APP_SCHJOB.GBL?Page=-HRS_APP_JBPST&Action=U&FOCUS=-Applicant&SiteId=1&JobOpeningId=-102946&PostingSeq=1 –

Trudy F. C. Mackay, PhD, FRS Distinguished University Professor and Goodnight Innovation Distinguished Chair Director, Program in Genetics Associate Director, Comparative Medicine Institute Department of Biological Sciences North Carolina State University Campus Box 7614 Raleigh, NC 27695-7614 Tel: 919-515-5810 Fax: 919-515-3355 Email: trudy_mackay@ncsu.edu

Trudy Mackay <trudy_mackay@ncsu.edu>

EarlhamInst UK ResAssist CropPathogens

Applications are invited for a Research Assistant to join the Population and Evolution Group at the Earlham Institute, to work on genome sequencing in crop pathogen evolution.

The role:

This exciting opportunity would suit an early career scientist or those with experience of field biology with an eye for detail and an interest in host-pathogen coevolution. The post is immediately available, and ideally the post-holder will be able to join us by June.

Based at the Earlham Institute in Norwich the project involves collection of wheat fungal root samples and culturing for DNA extraction at the Rothamsted Research site in Hertfordshire. The role is diverse and will allow the successful candidate to work between collection of plants and their pathogens in the wild and working in the lab to maintain cultures of fungal pathogens.

Working on a number of plant pathogen systems, the RA will be responsible for day to day care of plants. They will also work with the Genomics Pipeline Group to prepare libraries in preparation for genome re-sequencing. This unique position will allow the candidate to gain experience working in both world leading agricultural and genome sequencing institutes.

The ideal candidate:

Candidates are required to have a degree in a relevant scientific subject as well as a good knowledge of molecular biology for applications in genome biology. Candidates must be willing to travel between UK sites and some work outside normal working hours may be required during the growing season.

Additional information:

Salary on appointment will be within the range 24,300 to 29,750 per annum depending on qualifications and experience. This is a full-time post for a contract of 24 months.

For further information and details of how to apply, please visit our web site http://jobs.earlham.ac.uk/ or contact the Human Resources team on 01603 450462 or nbi.recruitment@nbi.ac.uk quoting reference 1003470. Informal enquiries regarding the role can be made to Dr Mark McMullan at mark.mcmullan@earlham.ac.uk

Please note, this post does not meet the requirements to provide tier 2 visa sponsorship.

As a Disability Confident employer, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy.

The closing date for applications will be 24th May 2018. Interviews are expected to take place on Tuesday 5th June.

"Eve Edwards (NBI)" <Eve.Edwards@nbi.ac.uk>

FieldMuseum Chicago CollectionsManager

Collection Manager, Mycology & Lichenology

Chicago, IL

The Field Museum of Natural History has an immediate opening for a Mycology/Lichenology Collections Manager. This full-time, permanent position reports to the Head of Botanical Collections in the Gantz Family Collections Center. The incumbent must have experience in Mycology/Lichenology with strong management skills, preferably with convincing taxonomic expertise. The Collection Manager is charged with overseeing the direct care, organization, and the management of approximately 250,000 specimens, based on best practices. The incumbent will be evaluated on their ability to build, care for, and ensure accessibility to the great wealth of specimens in the collection. The Museum particularly encourages applicants with a proven dedication to collections management. EMu is the Museum's shared web accessible database platform. Candidates should either have experience with this database or another fully relational database system.

This is a collection position. While there will be the opportunity to conduct research, this will be constrained by the management priorities of the collection. The Collections Manager will be expected to raise awareness of the collection among the general public and promote its use (either digital or actual) by the scientific community. In addition, depending on strategic priorities, the Collections Manager maybe expected to organize efforts to make new collections accessible for molecular research and develop a DNA barcode library of fungi and lichens.

Duties and Responsibilities

Curation of physical specimens, including specimen preparation, organization, care, housing of specimens, and potentially DNA barcoding of new collections.

Conduct and coordinate the appropriate processing of new collections or existing collections including physical preparation, labeling, cataloguing, accessioning and loans.

Establishing priorities for collection care and management in coordination with curatorial and research staff.

Development and implementation of collections management policies that are aligned with best herbarium practices.

Provide collection access to the research community, including assisting researchers and students with the use of the collections.

Digitization and continuing documentation of collections including databasing, capturing digital images of scientific labels and specimens, correspondence, archives, publications and loan records using the Emu collection management software.

Maintain electronic and digital records, including updating taxonomic and auxiliary information.

Provide support in terms of service to the Museum community, e.g., serving on committees.

Training and supervision of staff and volunteers in their collection related duties.

Develop grant proposals for collections improvements and other collection-based initiatives.

Collaboration including but not limited to other collections areas, research scientists, conservationists, exhibits and education, including funding opportunities.

Collaboration and liaison with external partners, e.g., Symbiota, iDigBio, GBIF.

Provide support for promotional and institutional advancement activities, including opportunities to engage with donors and participate in behind-the-scene tours.

Apply taxonomic expertise in identification of collections.

Qualifications

PhD (with an emphasis in Mycology and/or Lichenology) with collections experience is desirable, or, equivalent combination of education and experience, e.g., Masters in Biology (with an emphasis in Mycology and/or Lichenology) with at least 3 year's collection experience.

A strong background in Mycology and Lichenology is required, including familiarity with other Mycology/Lichenology collections, researchers, and molecular lab work.

Knowledge of taxonomic principles and collection management.

Strong organizational skills necessary to keep collection accessible.

Supervisory skills necessary for directing collection personnel, including volunteers, students and interns.

Databasing and imaging skills highly desirable.

Deadline for applications is July 31, 2018.

For more information contact Dr. Matt von Konrat, Head of Botanical Collections mvonkonrat@fieldmuseum.org

https://www.fieldmuseum.org/about/-careers?hireology_job_id=201870 – Matthew P. Nelsen The Field Museum Integrative Research Center (Insects & Botany) 1400 S. Lake Shore Drive Chicago, Illinois 60605, USA

mpnelsen@gmail.com https://www.fieldmuseum.org/-about/staff/profile/2556 https://sites.google.com/site/-mpnelsen/ Matthew Nelsen <mpnelsen@gmail.com>

HarvardU Bioinformatician

The Harvard FAS Informatics Group is looking for a PhD-level bioinformatician, computational biologist, or population geneticist for a staff scientist position. This individual will collaborate with faculty, post-docs and students to help them arrive at the best analysis procedure for their data, and contribute to the independent research happening in our group. This is a flexible job that provides opportunities for teaching, research, and extensive collaboration, in the context of a stable position in a strong intellectual environment with good work-life balance.

The Bioinformatics group lies at the intersection of scientific research and large scale computational analysis and works with many research groups. We are thus looking for someone who has a keen ability for picking up new knowledge and enjoys working on a wide variety of projects across a range of methods, although we are particularly interested in candidates with population genetics experience. Our primary research interests are in comparative genomics and population genetics, and generally focus on using large-scale comparative data to understand the genomics of adaptation.

We are committed to diversity and especially encourage members of underrepresented communities to apply.

Key Responsibilities: -Lead ongoing efforts in the Bioinformatics group to develop methods and resources for non-model and comparative population genomics, and to use these resources to address novel questions in population genomics. -Work closely with Harvard faculty, postdocs, and graduate students to advise on analysis of sequencing data and other biological 'big data', with a focus on population and ecological genomics. -Teach bioinformatics workshops to the Harvard community on topics of interest. -Collaborate with scientists generating sequencing data at Harvard, including participating in the writing and execution of grant proposals with faculty members.

About You: -PhD in evolutionary biology, population genetics, bioinformatics, genomics, or a related field, or a Masters degree with at least 5 years experience with bioinformatics methods. -Strong background in population genetics, with experience in non-model systems preferred. -Expertise in programming languages commonly used in bioinformatics (such as Python or R). -Fluency with Linux shell scripting and high performance computing.

To apply, please submit an application at http://bit.ly/-2FJXIxT. Review of applications will begin immediately, but the position will remain open until filled. The anticipated start date is flexible but no earlier than August 2018.

Questions? Contact Tim Sackton (tsackton@g.harvard.edu), Director of Bioinformatics

– Tim Sackton, PhD Director of Bioinformatics Informatics Group Faculty of Arts and Sciences Harvard University

"Sackton, Timothy" <tsackton@g.harvard.edu>

LiverpoolJohnMooresU BehaviouralEvolution

Lecturer or Senior Lecturer in Behavioural Ecology

The School of Natural Sciences and Psychology at Liverpool John Moores University seeks to appoint a Lecturer or Senior Lecturer in Behavioural Ecology to contribute to our successful undergraduate programmes in Animal Behaviour, Biology, Wildlife Conservation and Zoology. We would particularly welcome applications from persons whose research has an applied focus in aspects such as companion/ domestic animal behaviour, animal welfare, and/or conservation.

We have a strong profile in evolutionary and behavioural biology: https://www.ljmu.ac.uk/research/centres-and-institutes/evolutionary-and-behavioural-biology-research-group The deadline for applications is 20th June and full details can be found here: https://jobs.ljmu.ac.uk/vacancy/lecturer-or-senior-lecturer-in-behavioural-ecology-351035.html Salary: 39,993 - 49,149 Contract Type: Permanent Hours: Full

Time Vacancy Type: Academic / Research Closing Date: 20/06/2018 Ref No: 2287

W.T.Swaney@ljmu.ac.uk

MaxPlanck Cologne BioinformaticsTech

Bioinformatics Position

The Department of Comparative Development and Genetics at the Max Planck Institute for Plant Breeding Research (MPIPZ) in Cologne is seeking a Bioinformatician to contribute to high throughput sequence data analyses for the purpose of understanding trait development and diversification of plants. The candidate will work in the group of the Director Prof. Dr. Miltos Tsiantis and will also enjoy opportunities for collaborating with the bioinformatics group of Dr. Xiangchao Gan and the newly established population genetics group of Dr. Stefan Laurent. Tasks will involve analysis and interpretation of high throughput sequencing data including RNA-seq, ChIP-seq and DNA-seq. Both Illumina short-read and long-read platforms are in use. Outstanding teamwork and communication skills as well as willingness and ability to work collaboratively towards common goals are essential. Recent work by the group can be seen in: Vuolo et al. (2016) Coupled enhancer and coding sequence evolution of a homeobox gene shaped leaf diversity Genes and Development 30:2370-75; Gan et al. (2016) The Cardamine hirsuta genome offers insight into the evolution of morphological diversity Nat Plants 2:16167; Rast-Somssich et al. (2015) Alternate wiring of a KNOXI genetic network underlies differences in leaf development of A. thaliana and C. hirsuta Genes and Development 30:132; Cartolano et al. (2015) Heterochrony underpins natural variation in Cardamine hirsuta leaf form PNAS 112, 10539-10544; Vlad et al. (2014) Leaf shape evolution through duplication, regulatory diversification, and loss of a homeobox gene Science 343, 780-3. The position will suit creative, highly motivated individuals who can interact productively with biologists and are interested in the genetic basis for natural variation and evolutionary change.

Your profile

The basic qualifications for the outlined position are: PhD/masters degree in bioinformatics or equivalent background - expertise in next-generation sequencing data analysis - excellent skills in statistics - proficiency in programming in at least one script language: Perl/Python/Ruby/R - proficiency in Unix (Linux), scripting and bioinformatics tools and databases - strong interest in and understanding of molecular biology and evolution of gene function - excellent communication skills in English (spoken and written) - high quality publications that provide evidence for the skill set outlined above.

Any of the following additional qualifications would be an advantage: - expertise in population genetics - expertise in phylogenetic and evolutionary analyses - knowledge of C++

The position will be for one year at first with very good possibilities of extension.

The Max Planck Institute for Plant Breeding Research (MPIPZ) is one of the world's premier sites committed to research into fundamental processes and training in plant biology. There are three science departments plus independent research groups and specialist support. The Max Planck Society is committed to increasing the number of individuals with disabilities in its workforce and therefore encourages applications from such qualified individuals. Furthermore, the Max Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply.

Applications in English can be sent to Dr. Ismene Karakasilioti (applications.tsiantis@mpipz.mpg.de) as a single PDF file and should include a short letter of motivation, explaining how the applicant's profile and aspirations fit with the group, a list of publications and names and contact details of two academic referees. The search will continue until a suitable candidate is identified and the first evaluation of applications will take place end of July 2018. Only shortlisted candidates will be contacted.

Friedhelm Schnitzler <post@f-schnitzler.com>

MCZ HarvardU CuratorialAssociateEntomology

Business Title: Curatorial Associate, Entomology

Duties & Responsibilities: Harvard University's Museum of Comparative Zoology (MCZ) is hiring a Curatorial Associate in Entomology. With input from the Director, the Faculty-Curators in Entomology, and the Director of Collections Operations, the Curatorial

Associate (CA) determines short- and long-term collection priorities. Assists with development of policies and processes that conform to best-practice standards for long-term preservation and conservation of specimen collections in accordance with and as defined by natural history museum associations (e.g., Society for the Preservation of Natural History Collections, American Alliance of Museums). Supervises daily activities of the regular curatorial staff assigned to the entomology collection, temporary staff and students. Oversees activities of academic and non-academic visitors, researchers and students using the collections. Management responsibilities include building and developing a diverse and effective team; planning and delegating work effectively; communicating and monitoring performance expectations; motivating and developing direct reports; and ensuring compliance with Harvard-wide, FAS and MCZ policies and procedures, as well as local, state and federal laws and regulations. Expected to attend selected national and international meetings of professional associations related to management, research, and teaching activities in entomological collections. Responsible for managing the curation of existing and new collections. Oversees and processes all incoming/outgoing specimen loans, including proper documentation for import/export permits. Facilitates new acquisitions through fieldwork, donations, etc. Oversees the proper accessioning with required documents, including capture in MCZbase and maintenance of departmental accession files. Responsible for the accurate input, enhancement and updating of departmental collections data in MCZbase. Prepares and monitors departmental budgets, and orders needed collection-related supplies. Consults with Collections Operations on the development of work/research areas and collection space for specimens. May assist in preparation of grant proposals for collection or facilities improvement. Participates in museum-wide initiatives and collaborative projects, including with other MCZ curatorial departments. Assists professional and student researchers, and the public, with questions.

Basic Qualifications: Master's degree required in a biological field with an emphasis in entomology and/or natural history museum studies. At least 7+ years hands on curatorial experience in an entomology collection equivalent. Minimum 3 years of supervisory experience. Experience in handling entomological specimens required.

Additional Qualifications: Knowledge of insect taxonomy required. Knowledge of federal and state permitting requirements, importing/exporting regulations, and shipping regulations required. Experience in acquisition of collection and loaning materials to other institutions highly desired. Demonstrated writing, public speaking, and organizational skills; excellent computer skills, including database management. Excellent interpersonal and communication skills required, as well as the ability to work both independently and in a busy team environment. Must be able to stand for extended periods, walk, climb or balance, stoop, reach, kneel and/or crouch, often on uneven terrain or wet surfaces. Must be able to lift and/or move objects weighing 50 pounds. Must be able to maintain a valid Massachusetts driver's license.

Additional Information: All formal written offers will be made by FAS HR. We are unable to provide visa sponsorship for this position. With rich collections comprised of more than 21 million extant and fossil invertebrate and vertebrate specimens, the Museum of Comparative Zoology (MCZ) at Harvard University has been a center for research and education focused on advancing evolutionary biology and biodiversity science since its founding in 1859.

EEO Statement: We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability status, protected veteran status, gender identity, sexual orientation, pregnancy and pregnancy-related conditions, or any other characteristic protected by law.

To be considered for this position: Apply through the Harvard Employment website: www.employment.harvard.edu. Search requisition#: 45571BR.

Best, Megan

Megan McHugh Human Resources Coordinator Dept. of Organismic and Evolutionary Biology 26 Oxford Street, Cambridge, MA 02138 Phone: (617) 495-0813 Fax: (617) 496-8308 Email: meganmchugh@fas.harvard.edu Office Hours: Monday - Thursday, 8:45am - 6:00pm

"McHugh, Megan" <meganmchugh@fas.harvard.edu>

NCState ResearchTechnicianInsectEvolution

A Research Specialist position is now open in Bonnie Blaimer's lab in the Department of Entomology and Plant Pathology at North Carolina State University. The successful candidate will assist in conducting molecular genomics laboratory work and data analyses, as well as support field sampling and collection-based research for several ongoing projects on the diversity and evolution of ants and other Hymenoptera.

Candidates must have a B.S. in Biology, Entomology or related discipline (MSc. preferred). Prior work/research experience in a molecular laboratory, knowledge in insect identification (or a strong interest to learn) and basic experience with linux/mac command line and the R environment are further required. Preference will be given to candidates with bioinformatics skills, such as experience with Python or a different programming language, and advanced knowledge of collection-based research techniques in Entomology, such as specimen identification, preparation, imaging and databasing. We seek an individual with good organizational, interpersonal and verbal communication skills, as well as good physical fitness and willingness to perform field work under variable conditions.

For more details and information on how to apply please see this link: https://blaimerlab.weebly.com/uploads/1/1/6/9/116966090/ncstateresearchtechnician.pdf
"bblaime@ncsu.edu" <bblaime@ncsu.edu>

RiceU HuxleyFellowship

HUXLEY FELLOW IN ECOLOGY & EVOLUTION http://biosciences.rice.edu/ http://rice.edu/ BioSciences at Rice University seeks to fill a position in the prestigious Huxley Fellow Program in Ecology and Evolutionary Biology < http://biosciences.rice.edu/Content.aspx?id=2147484167 > starting in January, 2019. Huxley Fellows are outstanding early-career scientists who pursue their own independent research programs in ecology and/or evolution while teaching at the graduate and undergraduate levels. Huxley Fellows appointments are for two years with a third year extension possible. We seek candidates with a Ph.D. and outstanding potential, who can contribute through their research and teaching to the inclusive excellence of the Rice academic community. We particularly welcome applications from women and members of historically underrepresented groups who bring diverse cultural experiences and who are especially qualified to mentor and advise members of our diverse student population. Huxley Fellows receive non-tenure track faculty status, benefits, salary commensurate with experience, and modest research funds.

To apply, please submit the following materials: (1) cover letter, (2) curriculum vitae, (3) research statement, and (4) statement of teaching philosophy at the link: http://jobs.rice.edu/postings/14197. In addition, candidates will be asked to provide the names and contact information for 3 references, who will automatically be emailed for letters of recommendation at the time of application. Application review will begin August 15, 2018. For informal inquiries, contact Dr. Scott P. Egan <mailto:spe1@rice.edu>, Huxley Fellow Search Committee Chair. Rice is a private university, located in Houston, Texas, with a strong commitment to the highest standards of research and undergraduate and graduate education.

Rice University is an Equal Opportunity Employer with commitment to diversity at all levels, and considers for employment qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national or ethnic origin, genetic information, disability, or protected veteran status.

Scott Egan <spe1@rice.edu>

RoyalMuseumCentralAfrica ResAssistant

The Royal Museum for Central Africa hires a research assistant (m/f) In the framework of an initiative of the Belgian Science Policy (BelSPo), the Royal Museum for Central Africa (RMCA) and the Royal Belgian Institute of Natural Sciences (RBINS) launched in 2007 a common research center of excellence the "Joint Experimental Molecular Unit (JEMU). The unit provides support to the scientific research carried on in the two Institutions. It also promotes and facilitates the use of the large museum collections of both Institutions. During the last few years, the JEMU has been mainly active in the fields of molecular taxonomy, phylogenomics and population genomics (see http://jemu.myspecies.info/). The RMCA recruits a young scientist (m/f, MSc level) for a short-term collaboration with possibility of extension. Tasks: - analysing High Throughput Sequencing (HTS) data (including SNP calling, data quality filtering and phylogenomic/population genomic analyses) - drafting scientific papers in collaboration with colleagues of the JEMU and other scientists of RMCA-RBINS - contributing to DNA library preparation for HTS (whole genome sequencing, reduced- representation of genomes including RAD- seq)as well as to data collection via Sanger sequencing. Profile - MSc in Biology, Bioinformatics or related disciplines - Being able to write scrips in order to process HTS data (Python, Perl, R etc.) -

Minimum experience in a wet DNA lab (DNA extraction and quantification, PCR and sequencing)

General skills: scientific curiosity, team player, good knowledge of English We offer - a fixed-term, full-time contract until 30/11/2018 (extension possible) - salary according the standard scale for an assistant (minimum gross annual income: 35.191,79 EUR, indexed).

- interesting holiday regulation

- free public transport;

- a dynamic and interesting working environment

How to apply? E-mail motivation letter and CV before 25/05/2018 to HR-RH@africamuseum.be with subject: ≪ JEMU application ≫ Interview: 31/05 - 01/06/2018 info: - Tasks: marc.de.meyer@africamuseum.be@africamuseum.be, massimiliano.virgilio@africamuseum.be - Contract: Anic Flahou, anic.flahou@africamuseum.be

- RMCA : http://www.africamuseum.be Massimiliano Virgilio, PhD

Royal Museum for Central Africa Joint Experimental Molecular Unit (JEMU) Leuvensesteenweg 13, B-3080 Tervuren, Belgium, +32 (0) 27695854

massimiliano.virgilio@africamuseum.be http://www.africamuseum.be/home/contact/staff/VIRGILIO_Massimiliano/ http://jemu.myspecies.info Virgilio Massimiliano <massimiliano.virgilio@africamuseum.be>

SouthAfrica ResearchManager StripedMouse

Please poste the following for me on evoldir. Many thanks, Carsten

Position as research manager (September 2018-November 2019)

at the striped mouse project in South Africa,

We are looking for an extremely motivated and independent biology student with a master's degree to join the striped mouse project in August or September 2018 at least until November 2019 and for a maximum of 3 years as research manager. This position is suitable for somebody who would like to gain experience in field work and scientific management. Managers get free accommodation at the station and a compensation to cover their daily costs. Travel costs can be refunded by up to an additional R 12 000 / year. As such, the position compensates for all arising costs but does not represent a real employment.

As research manager you will work closely together with the station manager and both managers will share responsibilities. However, each will have specific main duties, but should also be able to deal with all other duties (for example when the other manager is on leave, or when a new manager has to be trained). Our current research manager will leave the project in October 2018. The new research manager will be instructed by the present research manager.

Skills needed: Good experience in field work and good knowledge of behavioural ecology or a similar field of research. Experiences in working with small mammals, radio-tracking, blood sampling, living at a remote location are of advantage.

You must be hard-working, highly motivated, able to work independently, good in communicating with people, able to supervise others, and not afraid of snakes. You must have a drivers licence and you must love to live at a remote place in nature, without regular internet and cell-phone reception. Most importantly, you are fascinated by nature and science!

Great opportunity: This is a great opportunity to spend 1.5-3 years in Africa, acquiring important skills in field biology and project management, while improving your CV. These skills will become valuable whether you later continue with a PhD or other jobs. It will be very hard and demanding, but also a once in a life time experience!

Job description: Five working days a week (Mo, Tue, Thu, Fr, Sat), with Wednesday being used for a shopping trip to town (not counted as working day) and Sundays being free. Included are four weeks of holiday for 12 months, which has to be taken outside the main breeding season (August to November) during periods when other students are present at the research station.

Primary duties research manager / secondary duties station manager

. Data:

o Weekly data entry

o Weekly data check

o Monthly data backup

o Monthly data report

o Training and supervision of field assistants

o Training of students and postdocs

o Support for students and postdocs

o Management of transmitters

o Management of field and laboratory supplies

Primary duties station manager / secondary duties research manager

. Technical support research station:

o Water system incl. sewage system

o Solar system

o Gas bottles replacement

o House and furniture

o Running of the respirometry laboratory

o Management of the captive colony

o Management of the research station car

o Management of bank account and cash box

o Management of research station supplies

Compensation:

. Free accommodation.

* A monthly compensation of R 4 700, which is sufficient to pay all costs of living. * For travel costs, R12 000 per year can be refunded, but proof (receipts) must be presented for this. This refund is only payable after October 2019 and will not be paid if the person leaves earlier than agreed. * You will become an honorary researcher at the University of the Witwatersrand in the group of Prof. N. Pillay. * Scientific co-authorship will be possible if the manager contributes to the success of projects by not only collecting the majority of data, but also by data analysis and writing of the manuscript.

Responsibilities:

. The manager has to cover the costs to get to the station, including travel costs and visa fees. For this, a refund can be paid (see above).

* The manager needs to arrange for a health insurance covering him / her during the stay. A copy must be sent to C. Schradin before travelling to the stations.

Place and project: Succulent Karoo Research Station (SKRS) in the Goegap Nature Reserve near Springbok in the Northern Cape of South Africa. The research projects are on the socio-ecology of small mammals, studying ecological and physiological reasons of social behaviour, behavioural flexibility, cognition, and physiological adaptation.

Period: The new manager is expected to start in August or September 2018 and to stay at least until the end of November 2019, the end of the breeding season 2019. The agreement might be extended for a total period of up to 3 years.

— / —

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StockholmU ExperimentalEvolutionaryBiology

Experimental and Evolutionary Biology Tenure Track Position

as Assistant Professor **

*at the Department of Zoology < http://www.zoologi.su.se/en/index.php >**. Closing date:—28—June—2018.*

The Department of Zoology has a long history of basic and applied research on animals ranging from insects to large mammals, at five divisions: Animal Ecology, Ethology, Population Genetics, Functional Animal Morphology and Systematic and Evolutionary Zoology. The Department has a staff of around 100 employees, of which about 40 are PhD students. In addition, the Department keeps a research station (Tovetorp) south of Stockholm with facilities for various field and laboratory experiments. The advertised position will be affiliated to the Division of Functional animal morphology, which has a long tradition of research in neuroscience, endocrinology, reproductive biology, and more recently insect sensory physiology and behaviour, as well as genomics and the evolution of life history traits of insects. At present the organisms under study are insects, particularly Drosophila, Bactrocera, bumblebees and butterflies, and the water flea Daphnia, for all of which rearing facilities are available. Access to state-of-the-art imaging equipment, as well as genomics and bioinformatics resources are provided by affiliated core facilities.

*Subject** *Functional animal morphology

*Subject—description** *Experimental biology with a focus upon the physiology or functional morphology of animals

Main responsibilities Research and in addition some teaching and supervision.

*Qualification requirements** *In order to qualify for the position of assistant professor, the applicant must have completed a doctoral degree in Sweden or an equivalent degree from another country. In the first instance, an applicant should be considered who has received such a degree no more than five years before the deadline for applications. However, an applicant who has received such a degree earlier may be considered under special circumstances.

All teaching positions at Stockholm University require the ability to collaborate and the general ability and suitability to perform one's duties.

*Assessment criteria** *In the appointment process, special attention will be given to research skills. Teaching skills will also be considered. The assessment of research skills will focus primarily on merits within the subject area of the position.

*Terms of employment** *For this position the assistant professor is employed until further notice, but no longer than six years. The contract may be extended to a maximum of eight years under special circumstances, such as due to sick leave or parental leave.

An assistant professor may, on application, be promoted to a permanent position as associate professor. Specific criteria for promotion from assistant professor to associate professor have been established by the Faculty of Science < http://www.science.su.se/english/ >.

An application for promotion to associate professor should be submitted to the faculty at least nine months before the appointment as assistant professor expires. At the time of promotion, the candidate is expected to be able to carry out teaching and administrative duties that require proficiency in Swedish.

*Additional information** *This position, in Swedish "biträdande lektor", is a tenure track position and the qualification requirements and terms of employment are regulated by the Higher Education Ordinance (SFS 2017:844).

Since most lecturers at the department are men, applications from women are particularly welcome. Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Contact Further information about the position can be obtained from the Head of the Department, Professor Linda Laikre, telephone: +46 8 164283, linda.laikre@popgen.su.se.

For questions regarding the application process, please contact administrator Katarina Gustafsson, telephone: +46 8 16 22 92, katarina.gustafsson@su.se.

Application https://www.su.se/english/about/working-at-su/jobs?rmpage=job&rmjob=5426&rmlang=UK** /Stockholm University - our education and research produce results./

– Linda Laikre Professor, Head of Department Head of Division of Population Genetics Director of Studies in Population Genetics Department of Zoology Stockholm University SE-106 91 Stockholm, Sweden phone: +46 8 164283, +46 705 254574 email: linda.laikre@popgen.su.se www.zoologi.su.se twitter.com/zoology_su

Linda Laikre <linda.laikre@popgen.su.se>

UCalgary TeachingBioinformatics

The Department of Biochemistry & Molecular Biology, Cumming School of Medicine, University of Calgary invites applications for a full-time tenure-track position at the Instructor level in the area of bioinformatics, as part of the Bachelor in Health Sciences (BHSc) undergraduate honours degree program (cumming.ucalgary.ca/bhsc). The department and BHSc program are seeking candidates with a passion for teaching and teaching innovation, as well as an interest in curriculum development, student mentorship and the ability to participate collaboratively within an interdisciplinary group. http://careers.ucalgary.ca/jobs/2744065/ The closing date for applications is June 8, 2018 and the position is expected to start on September 1, 2018. Please apply at http://careers.ucalgary.ca/jobs/2744065/ Jonathan Lytton, PhD Professor & Head, Department of Biochemistry & Molecular Biology University of Calgary - Health Research Innovation Centre - Room GAC64 3280 Hospital Drive NW, Calgary, AB, Canada T2N 4Z6 T: 403-220-2893; F: 403-270-0313; E: jlytton@ucalgary.ca; W: ucalgary.ca/bmb/profiles/dr-jonathan-lytton

Leslie McGill <lmcgill@ucalgary.ca>

UExeter FieldAssist Bees

Social Insect Fieldwork Assistants in West Sussex, UK:

We seek two fieldwork assistants to help research social behaviour in the ground nesting sweat bee, Lasioglossum malachurum, from the start of June until mid-end of July 2018.

The assistants will be working alongside a Postdoctoral researcher and a PhD student at a rewilding estate in West Sussex, UK. L. malachurum is a small bee that nests in very small colonies (fewer than 10 individuals) in the ground, and has an insignificant sting. Work involves: observing foraging behaviour, handling and marking bees, setting up video cameras, uploading video footage and excavating nests from the ground. In warm weather, field assistants will work long days in the field; in bad weather there will be tasks to carry out back at the accommodation/opportunity for time off. Because the work involves recording colour marks on individual animals, the job would not be suitable for someone who is colour-blind. See our research group website for more information about the kind of work we do (http://biosciences.exeter.ac.uk/-staff/index.php?web_id=Jeremy_Field).

Experience of working with insects and a Degree (or working towards a Degree) in a Behaviour/Evolution/Ecology-related topic are desired. Flexibility around the start and end date of the assistant position is required. The successful applicants must have enthusiasm for fieldwork and be prepared to work hard. They will obtain excellent experience of cutting-edge social insect research.

Shared accommodation in Sussex is provided, but assistants are required to pay for their own food/personal expenses. Assistants receive 125 per week to cover costs.

Please contact Dr Tanya Pennell (t.pennell@exeter.ac.uk) and CC Prof. Jeremy Field (j.p.Field@exeter.ac.uk) to discuss these positions further.

Dr Tanya Pennell

College of Life and Environmental Sciences

University of Exeter

Cornwall

TR109FE

Email: T.Pennell@Exeter.ac.uk

Twitter: @TanyaPennell

“T.Pennell@exeter.ac.uk” <T.Pennell@exeter.ac.uk>

UFlorida DataManager SpatialEvolution

The MabLab at the University of Florida is recruiting a Data Manager to fill an immediate opening for the position of Biological Scientist in the lab. We are looking for an enthusiastic, highly motivated and responsible individual to join an exciting research team focused on spatial ecology. The Data Manager will be responsible for the group’s database system, and will assist with multiple projects investigating for instance animal fine-scale movement in urban areas, or migration and range dynamics in the context of climate change.

The primary mission of the Data Manager will be to manage the group’s database system: we run a PostgreSQL/PostGIS database system on a Linux server, which hosts telemetry data on wood storks, sea turtles, raccoons, and associated GIS layers. In the near future, we will be adding advanced data from albatrosses, including accelerometers and infrasound. The Data Manager will manage the database server (database design, manual and automated data entry, metadata, set permissions for users and groups, backups, development of web apps to access and display data, etc.). Additional responsibilities will include assisting members of the group with data processing, and maintaining our open source R packages (rpostgis, rpostgisLT, hab).

Familiarity with SQL is essential. Experience using PostgreSQL/PostGIS (or other SIG database systems) and R is a plus, as well as experience with Linux systems and database servers.

The candidate must be able to work independently and with others in a fast-paced environment, and should be comfortable working across agency boundaries (University of Florida, U.S. Fish and Wildlife Service, U.S. Geological Survey and the National Park Service, etc.), making excellent written and oral communication skills essential for this position.

* Qualifications: B.S. with experience in Data Science, Computing, GIS, Biology or a related field. Must be eligible to work in the United States.

* Salary: Commensurate with qualifications and past experience (typically $40-50k/year with benefits).

* Start Date: Flexible, as early as June 1st, 2018. This is a permanent position from the University of Florida.

* Closing Date: Review of applications will begin on May 15th, 2018, and will continue until the position is filled.

* Application: Apply on UF Jobs website (job #507275): http://explore.jobs.ufl.edu/cw/en-us/job/507275/-biological-scientist-ii-data-manager Applications should include: - a cover letter with information about professional interests, qualifications, dates of availability, and current contact information; - a resume; - names and phone numbers of three references.

For more information, don't hesitate to contact me! Mathieu Basille

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Mathieu Basille

basille@ufl.edu | https://mablab.org/ +1 954-577-6314 | University of Florida FLREC

≪ Le tout est de tout dire, et je manque de mots Et je manque de temps, et je manque d'audace. ≫ Paul Ãluard

basille@ufl.edu

UGothenburg PlantEvolution

Senior Lecturer in Plant Ecology Gothenburg University, Sweden Department of Biological and Environmental Sciences (BioEnv)

We are recruiting a Senior Lecturer in plant ecology with a focus on conservation biology in terrestrial habitats. The subject area includes different aspects of plant ecology (vascular plants/lichens/mosses), such as ecosystem functions and evolutionary processes, as well as anthropogenic effects on these systems by, for example, land exploitation or climate change.

* https://www.gu.se/omuniversitetet/aktuellt/lediga-jobb/Lediga_anstallningar-detaljsida/?id=2019 * https://www.gu.se/english/about_the_university/job-opportunities/vacancies-details/?id=2019 Closing day 11 June 2018 (can be prolonged under certain circumstances). Welcome to us at BioEnv!

Website: https://bioenv.gu.se/english Johan Uddling Fredin <johan.uddling@bioenv.gu.se>

UNebraskaLincoln 2ResTech DrosophilaEvol

The Meiklejohn lab at the University of Nebraska-Lincoln (https://meiklejohnlab.unl.edu) has two open positions for laboratory research technicians. Technicians will be responsible for contributing to ongoing scientific research in the lab, overseeing Drosophila stock maintenance, preparing Drosophila media, ordering reagents and supplies, and assisting in the training and coordination of undergraduate research in the lab. Research will focus on investigation of X-linked hybrid male sterility in Drosophila, using genetic, gene expression, and cytological methods to investigate spermatogenesis in sterile hybrid males. Applicants must have a BS, BA, or MA degree in biology or a related field. Relevant experience includes prior academic training in genetics and/or evolution, experience with Drosophila husbandry, familiarity with molecular biology techniques and strong organizational skills. Starting annual salary will be between $25 - $30,000 depending on experience, plus health care benefits. The expected start date will be between June and September 2018. Applications must be received by May 15 for full consideration, but the positions will remain open until filled. Interested applicants should send a cover letter describing their past research experience and why they are interested in the position, a resume or CV, and contact information for three references to cmeiklejohn2@unl.edu.

Colin Meiklejohn <cmeiklejohn2@unl.edu>

UNottingham TeachingEvolution

Applications are invited to the above role to undertake undergraduate teaching and provide advice as a member of the University of Nottingham Biology teaching team, within an established programme of study. The role holder is expected to contribute to teaching of organismal animal biology, including ecology and/or evolutionary biology. The role holder may also contribute to curriculum development in the School.

The role holder will have specific responsibility for identifying the learning needs of students and ensure that the content, methods of delivery and learning materials meet the defined learning objectives of undergraduate Biology courses.

The role holder will be involved in the development of new teaching and assessment practices and/or developing systematic methods for evaluating and disseminating these practices within the School/Faculty.

Candidates must hold a PhD in a relevant area of Biology, or the equivalent in professional qualifications and experience.

Candidates must be able to demonstrate evidence of excellent oral and written communication skills, including the ability to communicate with clarity on complex information. The role holder must also be able to demonstrate evidence of previous teaching experience at a Higher Education level.

This full time fixed-term post is available from 3rd September 2018 until 3rd September 2020. Job share arrangements may be considered.

The School of Life Sciences holds an Athena Silver SWAN Award, in recognition of our commitment to supporting and advancing women's careers in the life sciences (STEMM). You can read more about this initiative at http://www.nottingham.ac.uk/lifesciences/documents/athena-swan-silver-award.pdf Informal enquiries may be addressed Dr Tom Reader (tom.reader@nottingham.ac.uk).Please note that applications sent directly to this Email address will not be accepted.

The University of Nottingham is an equal opportunities employer and welcomes applications from all sections of the community. Biology http://jobs.nottingham.ac.uk/MED166118 < https://t.co/C0vSnrvdK1 >

Four other possitions are also open:

Pharmacology http://jobs.nottingham.ac.uk/MED166518 < https://t.co/beWcseFSYb >

Biochemistry http://jobs.nottingham.ac.uk/MED166018 < https://t.co/lXS0df2W46 >

Neuroscience http://jobs.nottingham.ac.uk/MED166418 < https://t.co/8t0AbIkPCW >

Molecular Cell Biology/Immunology/Microbiology/Virology http://jobs.nottingham.ac.uk/MED166218 < https://t.co/7FYrtoo3dA >

– Dr. Angus Davison Reader and Associate Professor in Evolutionary Genetics School of Life Sciences University Park University of Nottingham NG7 2RD

0115 8230322 angus.davison@nottingham.ac.uk angusdavison.org < http://www.angusdavison.org/ >

@angus_davison (and @leftysnail)

Angus Davison <Angus.Davison@nottingham.ac.uk>

UQueensland 4yr EvolutionaryBiol

Call for Expressions of Interest: Mid-Career Research Fellowships in Biological Sciences at the University of Queensland

The School of Biological Sciences at The University of Queensland is seeking expressions of interest from applicants interested in applying for the Australian Research Council Future Fellowship scheme. These government fellowships offer 4-years of salary and research funds to outstanding Australian and non-Australian mid-career researchers (details on the scheme can be found at: http://www.arc.gov.au/future-fellowships). UQ's School of Biological Sciences is seeking to support a small number of outstanding candidates in the anticipated 2018 round of this scheme. We will consider any applicants whose research compliments our School's existing research strengths but are particularly interested in candidates with strong quantitative skills. For selected candidates, we will be offering negotiated setup packages to help successful fellows establish their own research group as well as negotiated extensions of employment as teaching and research academics in the School following the completion of awarded fellowships.

The School of Biological Sciences (http://www.biology.uq.edu.au/) at The University of Queensland is internationally recognised, and is one of the largest and most productive Biology departments in Australia, with a thriving graduate student and postdoctoral community. The School has strengths in ecology, evolution, genetics, and conservation biology.

Research within the School is diverse, including both empirical and theoretical approaches in taxa ranging across microbes, animals and plants, in a range of marine, freshwater and terrestrial ecosystems. The School offers a highly collaborative environment, including a variety of non-academic and industry partnerships, and collaborations across institutions nationally and internationally.

If interested please submit a CV and a brief expression of interest (no more than 1 page) outlining how your research programme will complement research within the School, and meets the Future Fellowship scheme objectives of being innovative, internationally competitive research, building collaborations across industry or research, and generating economic, environmental, social and/or cultural benefits for Australia.

Please direct questions and submit expressions of interest to Dr Katrina McGuigan by 30 June 2018: k.mcguigan1@uq.edu.au

k.mcguigan1@uq.edu.au

USheffield ResAssist ButterflyAdaptation

24 month Research assistant position in the Department of Animal and Plant Sciences with Dr. Nicola Nadeau on a NERC-funded project investigating thermal and altitudinal adaptation in the neotropical Heliconius butterflies.

This exciting project aims to improve our understanding of thermal adaptation in tropical insects, particularly across altitudinal gradients. You will assist with rearing and phenotyping of butterflies to characterize both inter- and intraspecific differences in thermal adaptation at different altitudes in the Andes. This will be followed by generation and analysis of high-throughput genomic data to identify underlying genetic differences.

The rearing and phenotyping will be conducted in Ecuador, therefore you will be expected to spend significant amounts of time working in Ecuador. You will have an interest and enthusiasm for evolutionary research with good attention to detail and experience of accurate collection and handling of data.

The post will contribute to the research excellence of the Department of Animal and Plant Sciences through the generation of high profile research outputs.

You will have a good honours degree or equivalent experience in a biological discipline and experience of recording and checking numerical data in a research context. You will have an enthusiasm for evolutionary/ ecological/ entomological research and experience of rearing insects.

Further information and to apply: https://jobs.shef.ac.uk/sap/bc/webdynpro/sap/hrrcf_a_posting_apply?PARAM=cG9zdF9pbnN0X2d1aWQ9Mzc2Qjk3QjNERjc5MUVEODk2OUYwNDdGMzU1RjlGMjAmY2FuZF90eXBlPUVYVA%3d%3d&sap-client=400&sap-language=EN&sap-accessibility=X&sap-ep-themeroot=%2fSAP%2fPUBLIC%2fBC%2fUR%2fuos# For informal enquiries contact Nicola Nadeau using the details below: – Dr Nicola Nadeau Dept. of Animal and Plant Sciences Alfred Denny Building, University of Sheffield Western Bank, Sheffield S10 2TN, UK N.Nadeau@sheffield.ac.uk Tel: +44 (0)114 222 4717 http://nadeau-lab.group.shef.ac.uk/ "n.nadeau@sheffield.ac.uk" <n.nadeau@sheffield.ac.uk>

Vairao Portugal BiodiversityBioinformatics

Dear Colleagues,

I would like to inform you about the call for applications for a IT Specialist position, at the Research Center in Biodiversity and Genetics Resources (CIBIO-InBIO), Vairao, Portugal, which will be open until May 31th, 2018.

If possible, I would greatly appreciate to be able to count on your collaboration in the dissemination of this opportunity amongst potential candidates.

Thank you so much!

All the best,

CIBIO-InBIO's Science Communication and Outreach Office

CIBIO - Centro de InvestigaÃÂem Biodiversidade e Recursos Geneticos/ InBIO Laboratorio Associado, Universidade do Porto

Campus Agrario de Vairao

Rua Padre Armando Quintas

4485-661 Vairao

Portugal

***

IT Specialist

Reference: ICETA 2018-26

< http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId679 > Link to the call - http://www.eracareers.pt/opportunities/index.aspx?task=global < http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId679 > &jobId679

Main research field: Computer science

The CIBIO/InBIO, University of Porto, through ICETA, is seeking for a highly-qualified, self-motivated IT

Specialist (Reference ICETA 2018-26) to work on the project PORBIOTA Portuguese E- Infrastructure for Information and Research on Biodiversity 22127. This project will be a distributed e-infrastructure to manage biodiversity data and meta-data from multiple sources (data providers). Tailored according to the national needs (research, management, policy, governance, citizen science), but compliant with requirements of LIFEWATCH and other international initiatives, it aims to promote a national agenda of biodiversity survey and research, and to provide services to the administration, the scientific community and society.

Desired Skills and Experience:

Degree or MSc in Computer Science, Computer Engineering or related areas. Strong knowledge of Database design and SQL language is required. The jury will consider:

§proficiency in the usage of open-source database engines (PostgreSQL, MySQL, sqlite3) and SQL Procedural Languages.

§knowledge of spatial data types (e.g., PostGIS).

§demonstrated experience in scripting languages (e.g., Python, PHP, Javascript) for front- and back-end development.

§strong knowledge of database security, especially under UNIX/Linux database deployments.

Other competencies that may be valued are:

§knowledge of UNIX/Linux OS deployment and management.

§knowledge of UNIX/Linux network security.

§knowledge of OS level virtualization and containers.

§interest and willingness to learn new technologies to tackle challenges posed in the field of computational biology (especially big-data management and analysis).

Job Responsibilities:

The successful candidate will be involved in the design and development of the database infrastructure that will be the core of PORBIOTA facilities at CIBIO. His/her main job will consist in the design of databases to hold different types of biodiversity data (genetic, species occurrence, collections), in the development of tools aimed at the management of local databases, and in the implementation of tools for rapid data digitization. He/she will also be strongly involved in the development of the front-end tools that aggregate different data types for posterior analysis which will connect with PORBIOTA's main portal.

Type of contract: fixed-term contract

Starting date: June 2018

Duration: 24 months

Monthly salary: Indice 20 Tabela de RemuneraÃÂÃÂnica

Selection Criteria:

In a first stage, candidates will be ranked based on:

§Professional experience (40%).

§The relevance of academic degree(s) (20%).

§Software developed, published in SCI journals or available in open-access repositories (20%).

§Motivation letter (20%).

If necessary, on a second stage only the top-most ranked candidates will be selected for an interview. The final rank will be calculated by the weighted average of the interview (40%) and the original ranked mark (60%). The interview will focus on the motivation of the candidate and his or her knowledge on the subject of this call. It may also include a technical discussion and/or technical questions. The jury will not choose any of the candidates if they all fail to demonstrate their fit to the position.

Jury composition:

Presidente: Antonio MÃÂºrias do Santos, PhD

1 Âº Vogal Efectivo: Pedro Beja, PhD

2 Âº Vogal Efectivo: Paulo Celio Alves, PhD

1 Âº Vogal Suplente: Nuno Ferrand de Almeida, PhD

Application:

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YaleU AssociateDirectorBotanicalGarden

We welcome applications for the position of Associate Director of the Marsh Botanical Garden at Yale University. Sitting on eight acres, with six greenhouses, the mission of the Garden is to support the research and teaching of Yale faculty and students, and provide enjoyable and educational botanical experiences for the general public. The successful candidate will strategically execute Marsh Botanical Garden's mission through the growth and expansion of research and educational programing, fundraising, outreach, special events and tours. Responsibilities include horticulture, administration, outreach and communications, development/fundraising and financial oversight for program initiatives. This position requires a Ph.D. in botany, horticulture, or a related discipline and relevant field experience; or a Master's degree with at least five years of related experience.

Applications will be reviewed on a rolling basis, with the hope of extending an offer by mid-September 2018. Please apply using the Yale STARS online hiring system, with job code 49081BR. https://sjobs.brassring.com/TGnewUI/Search/Home/Home?partnerid=25053&siteid=5248#jobDetails=1248258_5248 – Erika J Edwards Professor of Ecology and Evolutionary Biology Yale University

edwardslab.org

"Edwards, Erika" <erika.edwards@yale.edu>

ZFMK UBonn ComparativeGenomics

We are looking for an evolutionary biologist or computational evolutionary biologist with a strong focus on comparative genomics. We are particulary interested in scientists working with non-model organisms and a willingness to contribute their expertise to various genomic projects in the research group.

Ad: Comparative Genomics The Center of Molecular Biodiversity Research (https://www.zfmk.de/en/zmb) at the Zoological Research Museum Alexander Koenig (ZFMK) seeks enthusiastic, creative, and productive applicants for a full time tenure track position in the field of comparative genomics. The evolutionary analysis of rapidly expanding genomic datasets requires development and implementation of sophisticated laboratory techniques, rigorous computational approaches, and theoretical work. The successful applicant is expected to develop a strong, independent, externally funded research program for a better understanding of the evolution of zoological biodiversity. We are particularly interested in candidates performing comparative genomic research and/or in candidates developing theoretical foundations of comparative genomics. We seek an innovative and accomplished scientist whose research program will complement and diversify existing departmental research areas including integrative taxonomy, phylogenomics, evolutionary biology and biodiversity research on animals.

Assessment Criteria: The ranking of eligible applicants will be based primarily on research expertise. Research expertise comprises genomics research merits as well as the applicantÂs potential to contribute to the future development of comparative genomics. In assessing research expertise, special weight will be given to large-scale comparative genomic studies and research on non-model animals. Special weight will also be paid to scientific independence and the ability, or expected ability, to attract external funding. The planned research of the applicant shall complement on-going research in the Center of Molecular Biodiversity Research. The candidate is expected to establish an international competitive research group, to successfully apply for research grants, to publish in international recognized journals, and to tightly collaborate with other research groups at the ZFMK.

Required qualifications: It is essential that the applicant has a - PhD in Evolutionary or Molecular Biology or a closely related field —— with strong emphasis on genomics;

- experience in working with non-model organisms (animals); - an internationally competitive publication record; - experience analysing DNA sequence and genome data (computational skills); - experience in staff management and student supervision; - motivation to work in a team and take responsibility; - excellent communication skills.

The ZFMK is a Zoological Research Museum of the Leibniz Association cooperating with the University of Bonn, funded by the Federal State of NRW and the federal government. The Center of Molecular Biodiversity Research has been established to foster molecular research spanning from genomics and speciation genetic research to developing high-throughput bar-coding applications.

We offer a highly motivating environment and ability to work independently. Salary and benefits are according to a public service position in Germany (TV-L E 13). An upgrade of salary and benefits to TV-L E 14, is possible and will be subject of the tenure evaluation. The ZFMK advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely disabled applicants will be given preference. The contract will start as soon as possible and will initially be restricted to three years. A tenured position will be subject to personal performance reviewed by a commission. Please send your application by email attachment, including a detailed CV, a research plan, a list of successful grant applications, names of three potential referees and five publications, until June 29th 2018 to Mrs. Heike Lenz (e-mail: h.lenz@leibniz-zfmk.de). In case of questions concerning the position please contact Prof. Dr. Bernhard Misof, Head of the Center of Molecular Biodiversity Research (e-mail: b.misof@leibniz-zfmk.de). For more information about the museum see http://www.leibniz-zfmk.de Bernhard Misof <bmisof@uni-bonn.de>

Other

DominicanRepublic FieldResAssist Lizards

A field expedition to the Caribbean tropics of Hispaniola to study *Anolis* lizard thermal physiology will be led by Brooke Bodensteiner (Virginia Tech PhD student, Muñoz lab) in June and July 2018. We are currently seeking motivated field assistants to join on the trip and participate in the field and experimental aspects of the study. For example, students will help Bodensteiner collect lizards, measure physiological traits, and record ecological data. The sites to be visited span both the west and east sides of the Dominican Republic, including tropical rain forest sites along the coast, xeric scrubland sites in the coastal inlands, and montane cloud forests. For students interested in learning more about the tropics, herpetology, and behavioral ecology, this will be a fun and exciting opportunity. Applicants should enthusiastic about tropical field biology and work well with others. We are looking for assistant available up to 8 weeks of field work, but commitment to the entire time is not necessary. Spanish language abilities and/or field experience are preferred, but not required. We will cover all travel and living expenses while in the Dominican Republic.

Please Contact: Brooke Bodensteiner at bodenbro@vt.edu with CV, availability, and Spanish proficiency.

Brooke Bodensteiner Department of Biological Sciences Virginia Tech http://brookebodensteiner.weebly.com/ bodenbro@vt.edu

Gabon VolunteerFieldAssist Primates

Mandrillus Project - Information for Volunteers

Volunteer Field Assistant Positions

Role description

The Mandrillus Project is a non-profit organisation aiming at longitudinally studying wild mandrills in Southern Gabon. We are currently recruiting Volunteer Field Assistants for our 2018-2019 field season. These positions combine practical research with training and are entirely field-based. The volunteers are trained by and work alongside local field assistants, field managers, sometimes students and researchers, contributing to the research activities of the Mandrillus Project. Following established protocols, the fieldwork will primarily involve daily follows of a natural population of mandrills on foot, collecting data on the behaviour of individually recognisable animals, together with the collection of non-invasive measurements and samples. Please visit the website of the project to get an idea of the scientific programs that are currently running (http://www.projetmandrillus.com/research-and-conservation.html).

Positions available

Two Volunteer Field Assistant positions are currently available, each running for six months from early-mid September to late February / mid March.

What we cover

Once the volunteers arrive in the field site, the Mandrillus Project covers all their work-related costs, including accommodation (private equipped room with air-con and private bathroom, shared kitchen) and a stipend for meals (about 200Â/month). The association will also cover the costs of the volunteers' travel insurance. On the successful completion of fieldwork, we also contribute a minimum of 150Â towards the cost of the volunteers' travel fees.

Who are we looking for?

These positions are open to all with an interest in animal behaviour and ecology . We are particularly keen to hear from applicants who:

* Are friendly, easy-going people, happy to live in small team at a remote field site * Are strongly motivated, reliable, honest and committed * Have good levels of physical fitness and stamina - you will be following the mandrills on foot several hours a day, 6 days per week, over mountainous terrain, in heat * Show good initiative, with a willingness to learn and show attention to detail * French is a plus but not eliminatory

What do volunteers get out of it?

* An amazing opportunity to share the lives of wild mandrills in an equatorial forest landscape * An opportunity to learn new skills and gain experience, especially those relevant to research in behaviour and ecology * An opportunity to be involved in a long-term project on African wildlife, hosted by an international research institution * An opportunity to use this field experience with the Mandrillus Project as a stepping stone on to future Masters and PhD degree courses * Experience a new culture and share knowledge with local assistants

Further information

For further details about these positions, including the work involved, our living conditions in the field, preparations prior to departure, and what to bring with you, please see below (and additional information will be provided to successful candidates).

How to apply

If you would like to apply, please prepare a CV and a detailed covering letter that should explain why you would like to work on the project. The CV should include the names of two referees with e-mail contact details.

Applications must be sent at marie.charpentier@umontpellier.fr by 5pm Tuesday 19 June 2018 . We will notify successfully shortlisted candidates until Wednesday 20 June, and interviews will be held in Montpellier (for local successful candidates) or by skype Friday 22 June . Applicants should keep this date free for interview, since no other dates will be available. Telephone/skype interviews will be possible for overseas applicants.

* * * * * *

The Study Site

Weather

Gabon has an Equatorial climate with little seasonality. Precipitations are important, almost every day from October to May, and days may be hot (up to 30Â°C), although the Lekedi Park benefits from a cooler weather because of its altitude (600m). The long dry season, from June to September, is characterized by cool weather (temperatures can fall below 18Â°C) with no precipitation.

Landscape

The Lekedi Park is characterized by a mix of savannas and gallery forests interspersed with rivers and riverbeds. Equatorial Marantaceae forests are found in the area.

Wildlife

The Lekedi park is home to a variety of wildlife including forest buffalos, several Apes (chimpazees, gorillas) and other primates (cephus, nictitans) and, of course, mandrills! Predators include, occasionally, leopards (but don't expect any encounter with them!). Birds and reptiles also abound.

Location

— / —

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

Help ScienceCommunicationResearch

Dear all,

My colleagues and I want to know more about how researchers deal with science communication and outreach activities when they need to talk about the 'unpopular' 99% of Earth's biodiversity, that is, the *invertebrates*. If you take part in such activities, we prepared a questionnaire that should take no more than 10 minutes of your time to answer. We'd be very grateful if you could could answer it (and maybe pass on to your colleagues).

Just follow this link: https://goo.gl/forms/r7rED8V3Pgwfrir53 Thank you very much! Kind regards, Rodrigo.

Rodrigo B. Salvador, PhD Museum of New Zealand Te Papa Tongarewa. *Website: *[LINK] < https://rodrigobsalvador.wordpress.com/ > Editor of *Strombus*, journal of the Conchologists of Brazil: [LINK] < http://www.conchasbrasil.org.br/strombus/default.asp > Editor of the *Journal of Geek Studies*: [LINK] < https://jgeekstudies.org/ >

salvador.rodrigo.b@gmail.com

Large microsatellite dataset

Dear EvolDir list

To perform simulations, I am looking for a dataset that fulfills as many of the following criteria as possible: - is part of a published paper - includes more than 20 microsatellite markers - includes wild populations (at least 5) - includes a reasonable number of individuals per population (at least 10, but if possible 20+) - investigated a conservation-relevant species (for example, inbred populations)

If you have any idea, please write me: christian.rellstab@wsl.ch

Thanks, Christian

Christian Rellstab

Biodiversity and Conservation Biology Ecological Genetics Swiss Federal Institute WSL Zürcherstrasse 111 8903 Birmensdorf Switzerland

Room: Bi MG C 39 Phone: +41 44 739 2542 E-Mail: christian.rellstab@wsl.ch https://www.wsl.ch/en/employees/rellstab.html Office days: Tuesday - Friday

"christian.rellstab@wsl.ch" <christian.rellstab@wsl.ch>

Milner Prize Lecture

Just 2 weeks left to nominate for the inaugural Milner Prize Lecture: http://www.milnercentre.org/milner-prize/ Candidates for the prize must be early career researchers in any field of evolutionary biology, who have begun their PhD study after January 1, 2011. In addition, nominees will be considered who are more than 7 years from the start of their PhD if they have had career breaks taken for family, caring or health reasons; the nature of the reason must be given. The nomination of the candidate may be by a colleague or self-nominated. The nominations should be sent as a single PDF file to Laurence Hurst, Director of the Milner Centre for Evolution (l.d.hurst@bath.ac.uk). The nomination should include a brief justification, the candidate's CV and list of publications (indicating three most significant papers), a short description of future research plans, and a letter from the candidate approving the nomination. A letter of reference from another colleague (or two in case of self-nomination) should be sent directly to Prof. Hurst.

Nominations and letters of support should arrive no later than May 15th, 2018. Please take care to limit the size of attachments (total < 10 MB) in any one email.

The nomination committee will evaluate the nominations and inform the winner approximately by the end of May 2018.

The prizewinner is expected to attend the Inaugural Conference of the Milner Centre for Evolution (18th-21st September 2018: http://www.milnercentre.org), where he or she will deliver the 2018 Milner Prize Lecture. The Milner Centre will cover registration, accommodation, and travel expenses (economy fare).

Laurence D. Hurst

Professor of Evolutionary Genetics Director of The Milner Centre for Evolution Department of Biology and Biochemistry University of Bath Bath Somerset, UK BA2 7AY

tel: +44 (0)1225 386424 fax: +44 (0)1225 386779 email: l.d.hurst@bath.ac.uk website: http://people.bath.ac.uk/bssldh/LaurenceDHurst/Home.html Laurence Hurst <L.D.Hurst@bath.ac.uk>

MolecularEcolPrize nominations

Nominations for Molecular Ecology Prize

We are soliciting nominations for the annual Molecular Ecology Prize.

The field of molecular ecology is young and inherently interdisciplinary. As a consequence, research in molecular ecology is not currently represented by a single scientific society, so there is no body that actively promotes the discipline or recognizes its pioneers. The editorial board of the journal Molecular Ecology therefore created the Molecular Ecology Prize in order to fill this void, and recognize significant contributions to this area of research. The prize selection committee is independent of the journal and its editorial board.

The prize will go to an outstanding scientist who has made significant contributions to Molecular Ecology. These contributions would mostly be scientific, but the door is open for other kinds of contributions that were crucial to the development of the field. The previous winners are: Godfrey Hewitt, John Avise, Pierre Taberlet, Harry Smith, Terry Burke, Josephine Pemberton, Deborah Charlesworth, Craig Moritz, Laurent Excoffier, Johanna Schmitt, Fred Allendorf , Louis Bernatchez, and Nancy Moran.

Please send your nomination with a short supporting statement (no more than 250 words; longer submissions will not be accepted) directly to Deborah Charlseworth (Deborah.Charlesworth@ed.ac.uk) by Friday 29 June 2018.

With thanks on behalf of the Molecular Ecology Prize Selection Committee"

"Rieseberg, Loren" <lriesebe@mail.ubc.ca>

NewCaledonia VolFieldAssist AvianEvolution

Volunteer field assistants

We are looking for 2 field assistants for a study on the co-evolutionary arms race between Fan-tailed Gerygone and Shining Bronze-cuckoo in New Caledonia. This is part of a long-term study conducted by the Behavioural Ecology Unit at the Museum and Institute of Zoology of the Polish Academy of Sciences.

Periods: 3-4 months, from September to December.

Location: fieldwork will be conducted at several field sites in Grande Terre, New Caledonia. These include lush tropical forests and savannah areas with abundant birdlife. There will be plenty of opportunities for birdwatching and for exploring New Caledonia.

Duties: searching for and monitoring nests during the breeding season, behavioural observations, video analysis. Field activities will require 6-8 working hours a day (5-6 days a week) and an early morning start.

Experience: experience with monitoring and banding birds, nest searching, mist-netting and fieldwork in tropical environments is highly desirable, but training will be provided. Fieldwork will be physically demanding and conducted in a variety of environments (tropical forest, savannah, dry grassland) sometimes in extreme weather conditions. Physical fitness, enthusiasm, self-motivation, ability to work in a group and shared living are a must. Knowledge of French and driving license are desirable although not necessary.

The project will cover travel expenses, accommodation and food costs. To apply, please email a short CV with a brief description of relevant field work/research experience to attisano@miiz.waw.pl (deadline 24/06/2018). Successful candidates will be interviewed in the last week of June.

For more information contact: Alfredo Attisano (attisano@miiz.waw.pl) or J??rn Theuerkauf (jtheuer@miiz.eu) or visit http://corenc.lagoon.nc . Dr. Alfredo Attisano Assistant Professor Museum and Institute of Zoology, PAS Wilcza 64, 00-679, Warsaw Poland

Alfredo Attisano <attisano@miiz.waw.pl>

Preprint service survey

Dear All

Some of us are thinking about starting a pre-print service devoted to ecology and evolutionary biology. We'd love to know what you think of this idea (good, bad, or otherwise). So, if you can spare a minute, please take our BRIEF survey: https://goo.gl/ZpJiPx If you don't know what a pre-print is, please read below for more info: Pre-prints are spreading rapidly in ecology and evolutionary biology; the posting rate is doubling every year (see: http://www.sciencemag.org/news/2017/09/-are-preprints- future-biology-survival-guide-scientists). Pre-prints are old news in physics but are new in most other disciplines. Discipline-specific pre-print services have emerged recently in fields ranging from biology, geology, psychology, economics, and engineering. Right now, most biology pre-prints are posted on a single site (Biorxiv), but biology is a vast field and it may make sense to create different pre-print services for different sub-fields.

So what is a pre-print and why would someone post one? A typical pre-print is a manuscript posted by authors prior to submission to a journal. In the short-term, this allows for peer comments that can improve the manuscript before formal peer review, provides early exposure for the manuscript, establishes priority, and provides an opportunity to garner citations before publication (a pre-print gets a doi). After publication, pre-prints are still useful because a pre-print is available to anyone, not just people who can get past a pay wall. This open-access is not only desirable for maximum visibility of the science, but is required by many funding bodies. Finally, pre-prints have become compatible with later publication in a journal, as most prominent journals, and a rapidly growing list of other journals, accept manuscripts that are posted as pre-prints. Some people would like pre-print services to ultimately replace journals. Others see pre-prints as a useful addition to the current publishing landscape. Either way, pre-prints appear here to stay. We are considering helping to found a pre-print service devoted to papers from ecology and evolutionary biology. The first step in this process is determining the level of interest. We would greatly appreciate it if you would complete the short survey at this link: https://goo.gl/ZpJiPx Tim Parker Fiona Fidler Shinichi Nakagawa

Dr Shinichi Nakagawa (Associate Professor / ARC Future Fellow) Deputy Director of Research, Evolution & Ecology Research Centre, EERC (Visiting Scientist at Garvan Institute of Medical Research) Room 5102, Biological Sciences Building (E26) School of Biological, Earth and Environmental Sciences, BEES The University of New South Wales Randwick NSW 2052, Sydney, Australia Mobile: 0422 655 854 Office : 0293 859 138 Website: http://www.i-deel.org/ Shinichi Nakagawa <s.nakagawa@unsw.edu.au>

RoyalSociety PhotographyCompetition

Following the success of our 2017 Royal Society Publishing photography competition, we are doing it all over again this year! As always, the competition is run in collaboration with our journals and celebrates the power of photography to communicate science and the role images play in making science accessible to a wide audience. This competition is split into 5 categories, including behavior, and is free to enter. The overall winner will receive a prize of ????500 (or currency equivalent) and winners of the categories not chosen as the overall winner will receive ????250 (or currency equivalent). The closing date for entries is 31st August. Full details can be found at https://royalsociety.org/journals/-publishing-activities/photo-competition/how-to-enter Felicity Davie Royal Society Publishing T +44 20 7451 2647 Submit an image to the 2018 Royal Society Publishing photography competition - https://royalsociety.org/-journals/publishing-activities/photo-competiti on/how-to-enter The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG http://royalsocietypublishing.org Registered Charity No 207043

"Davie, Felicity" <Felicity.Davie@royalsociety.org>

SharingTravel AGASymposiumHawaii Jul

Share a car/travel post conference: AGA Symposium Hawaii, July 2018

Dear Colleagues,

I am looking for 1-3 people interested in sharing a car at KOA airport (I'm arriving July 21, 9 pm) for the duration of the conference or for a few of days after the conference, or both. I am planning to stay 3-4 extra days on the Island to hike in state parks and do some scuba. I'm planning to camp, but will consider renting a place if others prefer that. yampolsk@etsu.edu

Lev Yampolsky

Professor Department of Biological Sciences East Tennessee State University Box 70703 Johnson City TN 37614-1710 Cell 423-676-7489 Office/lab 423-439-4359 Fax 423-439-5958

"Yampolsky, Lev" <YAMPOLSK@mail.etsu.edu>

Smithsonian Panama ResIntern ButterflySpeciation

Research Internship (with stipend): Butterfly behaviour and speciation in the tropics

We are seeking a research intern to work at the Smithsonian Tropical Research Institute (STRI) in Panama from the end of June 2018 for a period of at least one year. The internship will focus on behaviour and diversification in Heliconius butterflies.

The intern will work as part of a team involving collaboration between Ludwig-Maximilians-Universität, Munich (http://www.evol.bio.lmu.de/research/merrill/-index.html) and STRI (https://stri.si.edu/scientist/-owen-mcmillan). The intern will join a vibrant and highly international community of scientists studying the origins and maintenance of tropical diversity (see also: http://www.heliconius.org).

The project is based in Gamboa, Panama and the intern will be assisting a project investigating the genetic basis of behavioural isolation between Heliconius species. The project involves breeding butterflies, managing crossing experiments and conducting behavioural assays. The internship is a learning experience and there will be opportunities to develop independent projects. Applicants must be able to work both with a group and independently, and be committed to working full time in Panama for the duration of the project. A knowledge of Spanish and the ability to drive would be useful but are not essential.

A stipend of US$1000/month will be provided to cover accommodation and living costs in Panama; we will also cover the cost of an airfare to Panama where necessary.

To apply, please send an up-to-date CV (including the names and contact details of two referees), and a cover letter explaining why you would be a good fit for this position. Please combine the CV and cover letter in one single pdf file with the file name in the format of YOURLASTNAME_STRI intern.pdf. Please send applications to Chi-Yun Kuo (kuo@bio.lmu.de); questions can be directed to Chi-Yun Kuo or Richard Merrill (merrill@bio.lmu.de). Please use the subject header: "PANAMA INTERN" before 26thMay 2018. Online interviews will be held the following week.

Dr. Richard Merrill Emmy Noether Group Leader

Division of Evolutionary Biology Faculty of Biology Ludwig-Maximilians-Universität München Grosshaderner Strasse 2 82152 Planegg-Martinsried

phone: +49 (0)89 / 2180-74160 (Panama: (+507) 64267029)

@dickmerrill merrill@bio.lmu.de http://-www.evol.bio.lmu.de/research/merrill/index.html
merrill <merrill@biologie.uni-muenchen.de>

Software DAMBE update

Dear All,

DAMBE has been updated to Version 7 (new version was uploaded last week).

Three features are relevant to evolutionary biologists:

1) Simultaneous imputation of missing distances and phylogenetic reconstruction

2) More accurate estimation of the shape parameter of gamma distribution. This is a simple way of estimating alpha from a continuous-gamma model, based on Gu

and Zhang (1997). Alpha from a discrete-gamma model tend to underestimate alpha. It uses a simultaneous method to estimate site-specific number of substitutions, making use of information from all sites instead of a single site.

3) An improved LPB93 method. The K80 model in the original is replaced by the F84 model for correcting multiple hits at 0- fold, 2-fold and 4-fold sites. To avoid inapplicable cases, the original independent estimation is replaced by simultaneous estimation. Let me know if you wish to have implementation details and comparisons.

A short tutorial is available for using these three methods: http://dambe.bio.uottawa.ca/software_download/Using_New_Functions.pdf If you use DAMBE, please cite:

Xia X. 2018. DAMBE7: New and improved tools for data analysis in molecular biology and evolution. Mol Biol Evol. https://doi.org/10.1093/molbev/msy073 For those who have not used DAMBE before, an incomplete list of functions can be found at:

http://dambe.bio.uottawa.ca/DAMBE/dambe.aspx Best Xuhua http://dambe.bio.uottawa.ca http://science.uottawa.ca/biology/people/xia-xuhua “Xuhua.Xia@uottawa.ca” <Xuhua.Xia@uottawa.ca>

Teaching Macroevolution

Dear friends,

I am organizing a dicussion with the Biology students about evidences of Macroevolution.

If you have good examples, articles, good videos for teaching and maybe a good published review, could you please send me?

Thanks for any help!

Prof. Dr. J. C. VOLTOLINI Grupo de Pesquisa e Ensino em Biologia da ConservaÃÂ- ECOTROP Universidade de Taubaté, Departamento de Biologia Taubaté, SP. E-Mail: jcvoltol@uol.com.br * Grupo de pesquisa ECOTROP CNPq:

http://dgp.cnpq.br/buscaoperacional/detalhepesq.jsp?pesqÂ37155809735635 * CurrÃÂ'culo Lattes: http://lattes.cnpq.br/8137155809735635 * Assessoria EstatÃÂ'stica: http://assessoria-estatistica.blogspot.com.br/ * Fotos de Cursos e Projetos: https://www.facebook.com/ecotrop/photos_albums VOLTOLINI <jcvoltol@uol.com.br>

UCambridge FieldAssist InsectEvolution

Position announcement Subject: Cambridge, UK. Summer field assistant position open

ABOUT I’m a graduate student in Prof. Rebecca Kilner’s lab at the Department of Zoology, University of Cambridge. We’re excited about starting a new project on resource partitioning and community structuring in burying beetles from May to October 2018 and I’m seeking a research assistant interested in conducting related experiments in the field with me.

DATES AND DATA COLLECTION We will be collecting data in the field from 4:30 pm through to 11:30 pm on the following sets of dates: 25th May to 1st June 7th June to 14th June 20th July to 27th July 3rd August to 10th August 21st September to 28th September 5th October to 12th October Though there are some night time excursions in the picture, we should be safe and sound at the Department’s Madingley field station!

EXPERIENCE The position is open to anyone interested in sampling insects or carrying out hypothesis-driven experiments in the field, who is going to be in Cambridge for *one or more* of the sets of dates I’ve listed. Driving experience is an added advantage!

CONTACT If you are interested in getting involved and will be available in Cambridge for *one or more* of the sets of dates mentioned above, do write to me at si299@cam.ac.uk to further discuss the project, logistics and funding.

Please don’t hesitate to get in touch if you have any questions.

Swastika Issar <si299@cam.ac.uk>

ULausanne VirtualCompBiolSeminar AnnaSapfoMalaspinas May18

Dear all,

We are pleased to announce the next speaker at the SIB Virtual Computational Biology Seminar Series:

Anna-Sapfo Malaspinas, Population Genomics Group, University of Lausanne & SIB Monday 28 May 2018 at 15:00 - Genopode Auditorium A - UNIL campus "Genome Odyssey : theatre as an effective way to teach scientific concepts to children"

The seminar will also be broadcast live for those unable to attend it physically (https://collab.switch.ch/-sib-cbss/). For more information about these seminars as well as the upcoming speakers list and previous screencasts, please visit the SIB virtual seminar series webpage: http://www.sib.swiss/training/-virtual-seminars-series Important: If you want to remain informed about our upcoming seminars, please subscribe to the dedicated mailing list:http://lists.isb-sib.ch/mailman/listinfo/sib-virtual-seminars Looking forward to seeing you all there.

Best regards, Diana Marek

Diana Marek <Diana.Marek@sib.swiss>

UMainz FieldAssist ArizonaAnts

UMainz.FunctBasisLifespFecundity

The Institute of Organismic and Molecular Evolution at the University of Mainz is searching for a field / research assistant (65% TVL E13) for the research project

The functional basis of lifespan and fecundity in Temnothorax ants

We invite applications for a field / research assistant (2 months, extension possible) for an ant collection trip to the Chiricahua Mountains Arizona followed by transfer of ant colonies to lab nests at the Johannes Gutenberg University of Mainz, Germany. Our project aims at understanding the evolution of life history traits such as lifespan and fecundity and their functional transcriptomic basis. Our model systems are Temnothorax ants, in which workers and queen lifespan vary between one to over twenty years. Field work includes searching for ant colonies in rock crevices and transfer to vials with an aspirator. The position requires a Master degree in Biology. Candidates with an interest in an academic career in Evolutionary Biology will be preferred, as it is likely that the successful candidate could may be able to continue to work on this project for his / her PHD. In this project, we will use experiments, RNA-seq and RNAi gene knockdowns and epigenetic inhibitors to study the regulation and connectivity of gene regulatory pathways linked to longevity and fecundity. We are searching for a highly motivated student with a strong background in evolutionary genetics and behavioral ecology. Previous research experience with social insects, ant collection, transcriptomics are advantageous, but not required. Students from every nationality are encouraged to apply. The working language of the laboratory is English. For more information on the position, especially the long-term perspectives, please contact us.

Interested candidates should send an application (as a single pdf e-mail attachment) containing a letter of motivation, a brief statement of their research experience and interests, a curriculum vitae (including grades of their B.Sc and M.Sc), and the names and email address of 2 potential referees to Prof. Dr. Susanne Foitzik (foitzik@uni-mainz.de) or Dr. Barbara Feldmeyer (barbara.feldmeyer@senckenberg.de).

Deadline for applications is May 25th 2018. Skype-interviews will be scheduled on June 5th 2018, on-site interviews about 2 weeks later. Fixed starting date due to the field season in Arizona would will be August 11th 2018.

Prof. Dr. Susanne Foitzik foitzik@uni-mainz.de

Dr. Barbara Feldmeyer barbara.feldmeyer@senckenberg.de

"B.Feldmeyer" <b.feldmeyer@googlemail.com>

PostDocs

AarhusU ComputationalPhylogenetics

The department of Bioscience, Aarhus University, Denmark invites applications for a 2-year postdoc position, offering applicants the opportunity to join an exciting international network developing new methods for phylogenetic synthesis.

Job description:

You will work on a pipeline for building comprehensive phylogenetic trees for large evolutionary lineages, synthesising all available molecular data. Read more about the research ideas here: https://doi.org/10.1002/ajb2.1041. You will be part of the PhyloSynth network (http://-phylosynth.github.io/), a recently initiated collaboration of computer scientists and evolutionary biologists with the common goal of developing an open, modular Tree of Life pipeline. Having grown out of the botanical community, PhyloSynth first and foremost aims to apply this pipeline to the evolutionary lineage of land plants, but our intention is to develop methods that are broadly transferable to other parts of the Tree of Life.

You will have the opportunity to work flexibly and collaboratively across the remit of PhyloSynth, leading and/or contributing to the development of pipeline modules. A special focus of the postdoc will be developing solutions for integration of publically available data (Genbank/INDSC) with newly generated genomic data, in close collaboration with the Plant and Fungal Trees of Life (PAFTOL) project at the Royal Botanic Gardens, Kew (https://www.kew.org/science/who-we-are-and-what-we-do/strategic-outputs-2020/plant-and-fungal-trees-life). Part of your research may also include macroevolutionary analysis of the reconstructed trees. You will be expected to lead at least 2 papers per year (including software notes), as well as software packages that comply with PhyloSynth's ambition of openness and interoperability. You will actively participate in PhyloSynth networking activities, including visits to collaborating groups, and public outreach.

Your profile:

You are a bioinformatician, a computer scientist, or a biologist with strong programming skills. Experience with biological sequence data and/or phylogenetic methods is highly desirable, as is a track record of developing well-documented software. You have a PhD degree or equivalent, or submitted your PhD thesis for assessment before the application deadline. You are expected to have strong collaborative skills, proven abilities to publish at a high international level, and good skills in English. International applicants who do not have English as their first language must prove strong English language writing skills and fluency.

Supervisor: Associate Professor Dr Wolf Eiserhardt (wolf.eiserhardt@bios.au.dk, +45 8715 6136)

Place of employment: You will be part of the Section of Ecoinformatics & Biodiversity (ECOINF), Department of Bioscience, Aarhus University, Ny Munkegade 114, DK-8000 Aarhus C, Denmark. ECOINF is an ambitious, collaborative and highly international research group. Postdocs and PhD students are encouraged to collaborate within the group, across departments and with other universities. More information about the people and research activities of the group can be found at http://bit.ly/ecoinfAU . To apply please visit: http://www.au.dk/en/about/vacant-positions/-scientific-positions/stillinger/Vacancy/show/974533/-5283/ The deadline for applications is 31/05/2018. The position is available from 01/06/2018 or as soon as possible hereafter.

"Wolf L. Eiserhardt" <Wolf.Eiserhardt@gmx.net>

ARS-USDA Illinois FungalEvolutionaryBiology

Postdoctoral Position in Fungal Evolutionary Biology
NCAUR-ARS-USDA, Peoria, Illinois

We are searching for a highly-motivated postdoctoral associate with strong molecular and/or bioinformatic research experience with fungi or other microorganisms who can effectively utilize existing and incoming genome datasets to develop sequence-based classification tools for Fusarium, and to make inferences about evolutionary patterns and processes in this agriculturally important fungal genus. This position is part of the NSF-funded project "A Phylogenetic Revisionary Monograph of the Genus Fusarium" with colleagues at The Pennsylvania State University. Scientists in the Mycotoxin Prevention and Applied Microbiology (MPM) Research Unit at the USDA in Peoria have an outstanding record of discovery and publication regarding Fusarium biology, chemistry and evolution, and over 20,000 Fusarium cultures are available. Current Fusarium research projects in the MPM Research Unit include phylogenomics of the genus, population genomics of key Fusarium pathogens and toxin producers, and the evolutionary dynamics of secondary metabolite gene clusters. Thus, opportunities exist for the postdoc to engage in these and other areas of interest. MPM scientists have generated genome datasets for more than 500 phylogenetically diverse Fusarium isolates and additional datasets will be developed for all known Fusarium species during this project. It will provide the postdoctoral associate with the opportunity to develop high-impact bioinformatics resources, and to utilize outstanding data resources for addressing key questions in fungal trait evolution. The postdoc will be working both with MPM scientists and an international community of PIs, Senior Personnel and project participants. They will participate in all phases of the project from design to publication. Salary and benefits are excellent, and because the position will be managed through the Oak Ridge Institute for Scientific Education (ORISE), it is open to both US and non-US citizens. This full-time position is funded for 3 years with annual renewal contingent on satisfactory performance. The anticipated start date is flexible, and could be as early as July 2018. The successful candidate must hold a PhD in Biology or related field by appointment start date, be proficient in both written and oral English, and have experience in genome analyses and/or an excellent background in evolutionary biology. To apply, please email a single PDF to Kerry O'Donnell (kerry.odonnell@ars.usda.gov) that includes: (1) a cover letter with a short description of why you are interested in and qualified for the position, (2) a current CV that includes a list of peer-reviewed publications, and (3) names and contact information for three references. This position will remain open until filled.

"ODonnell, Kerry - ARS" <Kerry.ODonnell@ARS.USDA.GOV>

Barcelona 2PDF 1PhD EvolutionaryBioinformatics

The Evolutionary and Functional Genomics Lab led by Josefa Gonzalez is seeking two highly motivated postdoctoral researchers and one PhD student to join our research team at the Institute of Evolutionary Biology (CSIC-UPF) in Barcelona, Spain (http://-gonzalezlab.eu).

Postdoctoral Bioinformatics position The postdoctoral researcher will be responsible for the in silico characterization of the potential regulatory role of transposable element insertions in natural populations of Anopheles mosquitoes, and in available human genome sequences. Among others, the tasks involved in the postdoctoral research project will be the identification of transcription factor binding motifs and epigenetic marks present in the candidate adaptive insertions, de novo assembly of genome sequences, and de novo transposable element annotation. The postdoctoral researcher will work in close collaboration with a PhD student and a Postdoctoral researcher.

A PhD in Evolutionary Biology or a related field, good programming skills (command line usage, bash scripting), and good writing skills are required. Although not required, genome assembly and genome annotation experience will be considered as well.

We offer a full-time position for 2 years with the possibility of extension. Salary will depend on the experience of the candidate. The candidate will join a research team of four postdoctoral students, three PhD students, and a lab technician. Besides lab group meetings, the candidate will also join the Comparative and Computational IBE Research Program meetings. The lab also offers extensive networking opportunities as we are co-leading the European Drosophila Population Genomics Consortium (droseu.net) and the Spanish excellence network in adaptation genomics (adaptnet.es).

Application Please send your CV (including the contacts of potential references) and a brief letter of motivation to: josefa.gonzalez@ibe.upf-csic.es

Application deadline 19th June 2018. Expected starting date 1^st September 2018, alternative dates can be discussed.

ERC Postdoctoral Bioinformatics position The postdoctoral researcher will work on a project funded by a European Research Council Consolidator Grant that aims at identifying the genetic basis, the molecular mechanisms, and the functional traits relevant for environmental adaptation. The postdoctoral researcher will be responsible for the in silico characterization of candidate adaptive mutations identified in natural populations of Drosophila melanogaster. Among others, the tasks involved in the postdoctoral research project include the integration of several genomic datasets obtained in our laboratory: RNA-seq, ChIP-nexus, ChIP-seq for histone marks, ATAC-seq, and HiC.

A PhD in Bioinformatics or a related field, good programming skills, and good writing skills are required. Experience with state-of-the-art approaches to analyze the different genomic techniques used in the lab is required. Previous postdoctoral experience will be considered.

We offer a full-time position for 2 years with the possibility of extension. Salary will depend on the experience of the candidate. The candidate will join a research team of four postdoctoral students, three PhD students, and a lab technician. Besides lab group meetings, the candidate will also join the Comparative and Computational IBE Research Program meetings. The lab also offers extensive networking opportunities as we are co-leading the European Drosophila Population Genomics Consortium (droseu.net) and the Spanish excellence network in adaptation genomics (adaptnet.es).

Expected starting date is September 2018 but alternative dates can be discussed.

Application Please send your CV (including the contacts of potential references) and a brief letter of motivation before the 19^thJune 2018 to: josefa.gonzalez@ibe.upf-csic.es. Please include "ERC-Postdoctoral position" in the subject of your e-mail.

PhD position The PhD thesis will investigate the role of transposable elements in environmental adaptation in Anopheles mosquitoes. The tasks include de novo assembly of Anopheles genomes, de novo annotation of transposable elements in the newly assembled genomes, and identification of signatures of selection in the Anopheles genomes. The PhD student will work in close collaboration with a Postdoctoral researcher and will interact with other PhDs and postdoctoral researchers in the group.

A master in Bioinformatics or a related field, good programming skills, and good writing skills are required. Previous research experience will be considered. The lab offers extensive networking opportunities as we are co-leading the European Drosophila Population Genomics Consortium (droseu.net) and the Spanish excellence network in adaptation genomics (adaptnet.es).

Application Please send your CV (including the contacts of potential references)

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Belgium Biodiversity

The Royal Belgian Institute for Natural Science is looking for a master or Postdoc in molecular ecology for a contract of limited duration.

<October 2018-September 2019>

ANTARCTIC BIOLOGICAL AND MICROBIAL DATA MANAGER (m/f)

who will join the Antarctic team of the Biodiversity and Ecosystems Data and Information Centre part of OD Nature.

This team is in charge of the management of biodiversity and ecosystem data resulting, for example, from the federal monitoring programmes of the marine environment or from research projects in marine and Antarctic sciences.

AntaBIS (www.biodiversity.aq) is a BelSPO (www.belspo.be)-funded project that aims at constructing a dedicated Antarctic biodiversity virtual Laboratory in the framework of the EU Lifewatch program, providing tools for the discovery and analysis of Antarctic biodiversity data.

Biodiversity.aq creates new ways of exploring and understanding Antarctic biodiversity by linking various online resources. Biodiveristy.aq contributes Antarctic biodiversity Data to global initiates such as the Ocean Biogeographic Information System (www.iobis.org) and the Global biodiversity Information Facility (www.gbif.org). The Register for Antarctic (Marine) species (www.marinespecies/RAMS) provides access to Antarctic taxonomic data and forms the taxonomic backbone for our other portals. The data portal (data.biodiversity.aq) allows users explore and download Antarctic biodiversity. Our Microbial Antarctic Resource System (mARS.biodiversity.aq) is a unique platform that allows researcher to explore next generation sequencing data and environmental data (http://antabis.bedic.be/mars/).

We seeks an enthusiastic data manager to assist in the construction of this Antarctic biodiversity virtual laboratory. The successful candidate will be responsible for publication of various types of biodiversity data. The main focus will be on enriching the content of the mARS portal and the further development and maintenance of this portal.

The Data Manager Officer will be offered a one-year, full time position starting October 1st, 2018 or as soon as possible, and will be based at the Royal Belgian Institute of Natural Sciences (www.naturalsciences.be). She/he will work under the supervision of the Project Promoter and in close collaboration with the AntaBIS data scientist. There is potential to extend the duration of the position but this will depend on available funding and positive evaluation.

The successful candidate will work for 12 months in the context of one of the Belgian Federal contributions to EU Lifewatch (www.lifewatch.be) This work will be done in collaboration with a wide variety of international collaborators. The work handles the data management component of this project, and focusses mostly on the microbial Antarctic Resource System (mARS) mARS.biodiversity.aq.

Tasks:

The tasks involve:

- the development, the maintenance and the management of the mARS database (PostgreSQL,) and of it's query interfaces
- harvesting of data in public repositories (e.g. genbank SRA) , contacting data providers and users; communications in English,
- quality control of the data (environmental and DNA sequence information) using relevant data standards (e.g. Darwincore, TDWG) , their archiving, their reporting

and their scientific exploitation,

- Publication of data in mARS, OBIS and GBIF

- In collaboration with AntaBIS staff and partners:

- identify existing tools for the analysis of (microbial) Antarctic biodiversity data;

- evaluate online workflows using these tools and in particular their benefit to the Antarctic (microbial) research community

- participation in national and international projects dealing with marine data management.

Profile:

Diploma:

Candidates must hold a PhD or a Master degree in science or applied sciences, with a strong preference for a background bioinformatics or Antarctic Microbial biology. They will demonstrate a wide analytical insight and a strong interest in the technical side of data management.

Technical skills:

Musts are:

Candidates should have a strong taste for bioinformatics; a good knowledge in data management and relational database, geospatial tools, biodiversity informatics standards.

Experience with scientific programming (preferably using R and/or Python) as well as the use of software project hosting and version control systems such as GitHub or Gitlab

Having excellent networking and communication skills in English is absolutely required; a good working knowledge of additional European language(s), in particular Dutch and/or French, is an asset;

Enthusiasm and an outstanding ability to collaborate in a

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brian@helix biology mcmaster caUIllinois Chicago EcoEvoDevo

A postdoctoral position focusing on eco-evo-devo is available in Alexander Shingleton's laboratory at the University of Illinois, Chicago.

The project uses Drosophila as a model to understand how the environment regulates development to generate phenotypic plasticity and how this regulation evolves. Research in the Shingleton Lab spans multiple disciplines including developmental genetics, physiology, bioinformatics, mathematical modeling, ecology and evolutionary biology, and the project will incorporate many of these. The specific project is to elucidate the mechanisms that regulate sex-specific differences in the phenotypic plasticity of body size, in particular in response to changes in different aspects of developmental nutrition. The project is, however, open ended, and the successful candidate will be encouraged and expected to take the research in a direction that matches their particular skills and career goals. The postdoc is funded for three years.

You should hold a PhD in biology and must be comfortable exploring biological processes at multiple levels of organization. The ideal candidate will have extensive experience in Drosophila developmental genetics but individuals with researchers with expertise in the developmental physiology of other insects are also encouraged to apply. Your exact field of research to date is less important than your demonstrated record of publication and tenacity. Nevertheless, you should have a solid background in statistics and/or bioinformatics and either be proficient in R or willing/able to learn R to an advanced level through self-study. Candidates who are also interested in mathematical modeling of biological processes are particularly encouraged to apply.

The Shingleton Lab offers a dynamic work environment with excellent opportunities for independent and collaborative research. We have a track record of mentoring undergraduate research and postdocs with an interest in working with undergraduates will find a particularly welcoming environment.

The lab is moving to UIC in August 2018 and will be within the Ecology and Evolution Group in the Department of Biological Sciences. The department is home to a diverse and dynamic set of research groups who study a wide-variety of biological questions, utilizing a correspondingly wide-variety of tools and techniques. The department is located in the center of Chicago. More details on the lab, department and university can be found here:

shingletonlab.org bios.uic.edu uic.edu

The start date is somewhat flexible, but ideally will be around September 1, 2018. Review of applications will begin immediately and continue until the position is filled.

To apply send your CV and the name and contact details of three references to awshingleton@shingletonlab.org

"Shingleton, Alexander" <shingleton@mx.lakeforest.edu>

Caltech Genomics Convergence Symbiosis

Postdoctoral position in genomics of convergence and social symbiosis (Parker Lab)

A postdoctoral position is available to study the genomic basis of evolutionary convergence in the lab of Joe Parker at the California Institute of Technology.

Work in the Parker lab is focused on the evolution of complex phenotypes, principally in the context of symbiosis. We use a unique system to explore this phenomenon: the convergent evolution of symbioses between rove beetles and social insects. Rove beetles (family Staphylinidae) are the largest metazoan family, and include multiple remarkable lineages that have evolved to become "social parasites" stealth impostors that infiltrate ant or termite societies, employing radical behavioral, anatomical and chemical adaptations. We have found that many of the most extreme symbiotic phenotypes have evolved convergently numerous times in distantly related lineages. We are a now seeking a postdoctoral candidate to probe the genomic basis of complex phenotypic convergence in this system. Our goals are twofold: i) Pinpoint shared or unique molecular changes that drive the evolution of social symbiosis in rove beetles; ii) Make basic inferences into the long-standing question of how complex phenotypic changes can arise repeatedly and predictably over deep evolutionary timescales.

Aspects of this work will involve two study systems: 1) A deep-time system encompassing symbiont lineages from across the rove beetle subfamily Aleocharinae that are separated by up to 100 million years. 2) A recently-evolved system in which multiple rove beetle lineages have convergently evolved symbioses with a single ant genus in the South Western US. This latter project involves potential fieldwork at sites in Southern California and Arizona. The successful candidate will spearhead genome sequencing of free-living and symbiotic species from across phylogeny, and use comparative genomic tools to understand patterns of genome evolution. There is potential for collaboration with Caltech labs using machine learning and single cell profiling, and the candidate will also lead genome/transcriptome assembly and annotation of several higher quality reference genomes to facilitate functional genetic studies in laboratory model rove beetle species. Depending on the candidate, the project may involve wet lab work to functionally test loci with possible causal roles in symbiosis, or involve collaboration with others to this end.

The following papers illustrate the rove beetle-ant system:

Parker, J., Eldredge, K.T., Thomas, I.M., Davis, S., Coleman, R.T. (2017) Hox-Logic of Preadaptations for Social Insect Symbiosis in Rove Beetles. bioRxiv, 198945

Maruyama, M., and Parker, J. (2017) Deep-Time Convergence in Rove Beetle Symbionts of Army Ants. Current Biology, 27, 920926 PMID: 28285995

Yamamoto, S.â euro —, Maruyama, M. and Parker, J. (2016) Evidence for Social Parasitism of Early Insect Societies by Cretaceous Rove Beetles.Nature Communications, 7: 13658 PMID: 27929066

Candidates

Applications are encouraged from talented and motivated individuals who have a Ph.D. or are nearing completion of their Ph.D. with experience in genome and transcriptome sequencing, genome assembly, annotation, comparative genomics and genome evolution. Interest or experience in machine learning and/or single cell profiling are desirable. Top candidates will have a strong track record of research productivity, excellent communication skills, enthusiasm for basic research and a collegial approach to science. Candidates should send a cover letter, a detailed curriculum vitae, and names and contact details for three references to joep@caltech.edu Start Date and Project Duration

The start date is flexible and depends on the candidate. Preference is for candidates who can start in 2018, or early-mid 2019 at the latest. The position is funded for two years at least and potentially longer depending on progress.

The California Institute of Technology

Caltech is consistently ranked among the top research universities in the world and hosts a diverse and collaborative scientific community. Caltech is located in Pasadena, California, a vibrant city 10 miles northeast of downtown Los Angeles and minutes from the Parker lab's fieldwork sites in the San Gabriel mountains. More info about the Parker lab: https://www.be < http://www.bbe.caltech.edu/content/joseph-parker >etles.caltech.edu

We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, or national origin, disability status, protected veteran status, or any other characteristic protected by law.

– Joe Parker, Ph.D. California Institute of Technology Division of Biology and Biological Engineering 1200 E. California Blvd. MC 216-76

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CSIRO Australia DipteranMicrobiomes

Available: 3 Year Postdoctoral Fellowship Studying the Microbiomes of Flies (Diptera)

https://www.postdocjobs.com/posting/7051482 Best wishes

Dr David Yeates Director, Australian National Insect Collection National Research Collections Australia CSIRO National Facilities and Collections Adjunct Professor, The Australian National University Phone: +61 2 6246 4282 | Fax: +61 2 6246 4264 David.yeates@csiro.au | Mobile: 0402592845 Address: Clunies Ross Street, Acton, ACT 2601 | GPO Box 1700, Canberra, ACT 2601 Researcher ID A-9917-2008 PLEASE NOTE

“David.Yeates@csiro.au” <David.Yeates@csiro.au>

CSIRO EnvironmentalGenomicsOfAge

FSP Postdoctoral Fellowship - Rapid Epigenetic Age-estimators

- Launch your research career in the frontier science of Environmental Genomics - Be mentored by world-leading research scientists - Join CSIRO’s Environomics Future Science Platform

The position Animal age is a fundamental aspect of population biology relevant to many fields ranging from wildlife conservation to fisheries management. Yet, most animals lack an accurate and practical non-invasive method for estimating age. Changes in DNA methylation levels has recently been used to estimate the age of animals, but there is still extensive technical and theoretical work to be done to streamline the development of epigenetic age assays for new species and to understand how the estimates can be used. We are seeking a postdoctoral scientist to join the Environomics Future Science Platform to undertake important developmental work in this exciting frontier of applied science.

The Environomics Future Science Platform is a new CSIRO science program exploring the limits of what is possible at the interface between genomics and environmental science. Environomics is bringing together expertise from across CSIRO and the university sector in molecular biology, ecology, and big data science. Environomics is developing the next generation of tools for environmental science that will allow us to see beyond the landscape to the genescape, transforming our ability to manage biodiversity and make use of the genetic resources locked inside.

Location: Perth WA, Australia Salary: AU$83K-AU$91K plus up to 15.4% superannuation Tenure: Specified term of 3 years Reference: 56718

To be successful you will need: - A doctorate (or will shortly satisfy the requirements of a PhD) in a relevant discipline area, such as molecular biology, cell biology or molecular ecology.

Please note: To be eligible for this role you must have no more than 3 years postdoctoral research experience. - High level written and oral communication skills. - A record of publications in quality, peer reviewed journals. - Extensive experience relative to career stage of working with molecular biological analysis of non-model organisms. - Demonstrated ability to analyse complex molecular biological, population biological or ecological data sets. - A record of innovation and creativity in self-directed research. - Demonstrated capacity to incorporate novel ideas into a project with goals determined by others.

The Commonwealth Scientific and Industrial Research Organisation (CSIRO) We imagine. We collaborate. We innovate. At CSIRO, we do the extraordinary every day. We innovate for tomorrow and help improve today for our customers, all Australians and the world. We do this by using science and technology to solve real issues. Diversity is the compass that navigates our innovation. We provide an inclusive workplace that respects, values and actively pursues the benefits of a diverse workforce.

How to apply: For full details about this position, and to apply visit: https://jobs.csiro.au/job/Perth%2C-WA-FSP-Postdoctoral-Fellowship-Rapid-Epigenetic-Age-estimators/473103600/ Applications close: 11:59pm AEDT, 20 May 2018

"Noni.Lauder@csiro.au" <Noni.Lauder@csiro.au>

EawagSwitzerland EvolutionStickleback

A postdoctoral position in evolutionary ecology is available in the research group of Blake Matthews, at Eawag's Center for Ecology, Evolution, and Biogeochemistry, near Luzern Switzerland.

The position is part of an SNF funded project entitled 'Eco-evolutionary dynamics in aquatic ecosystems', whose aim is to understand the interactions between rapid trait evolution, community dynamics, and ecosystem functions. The project focuses on stickleback as a model system, and involves a combination of genomics and quantitative genetics of functional traits, large-scale experiments in mesocosms and ponds, and field-work in natural populations in Southern Greenland.

We are interested in candidates with broad interest in evolutionary community ecology. Interest and prior experience with field ecology would be an asset, as would experience with fish ecology, ecosystem dynamics, and/or the genomics of adaptation. Independently developing research within the framework of the project is encouraged.

Eawag's Center for Ecology, Evolution & Biogeochemistry (CEEB) is located on the shore of Lake Lucerne and is a strong nucleus of Eawag research groups aimed at integrating evolutionary biology, community ecology, and ecosystem science http://www.eawag.ch/forschung/cc/ceeb/index_EN. The Postdoc will interact with a diverse range of researchers studying community ecology, evolutionary biology, ecological genetics, ecosystem science, and applied environmental science.

The project is led by Blake Matthews, and involves collaborations with other research groups at CEEB, including Ole Seehausen, Jakob Brodersen, and Philine Feulner. The starting date is flexible, although early 2019 is preferred. The position is for 2 years, and there is potential for an extension.

Screening of applicants will begin immediately, with a closing date of 1 Sept 2018.

For further information please contact Blake Matthews by email, blake.matthews@eawag.ch. Lab homepage: http://homepages.eawag.ch/~matthebl/Welcome.html Publication list: https://scholar.google.ch/citations?user=KPOcG_sAAAAJ&hl=en We look forward to receiving your application. Please submit your application (including CV, motivation letter, and the names and contact information for three references) via the Eawag Jobs & Career webpage, any other way of applying will not be considered. The link below will take you directly to the application form.

https://apply.refline.ch/673277/0618/pub/1/index.html Matthews, Blake blake.matthews@eawag.ch http://homepages.eawag.ch/~matthebl/Welcome.html Eawag, Aquatic Ecology Department Center for Ecology, Evolution & Biogeochemistry Seestrasse 79 6047, Kastanienbaum Switzerland

"Matthews, Blake" <Blake.Matthews@eawag.ch>

GlasgowU EvolBiolParasite

A post-doc position is available in the Institute of Biodiversity, Animal Health and Comparative Medicine at the University of Glasgow to investigate the effect of drug treatment on the genetic composition of Onchocerca adult worms and their offspring. The project will use ddRAD-Seq data, targeted resequencing and whole genome sequencing to undertake sib-ship analysis of larval stages and adult worms. We aim to develop methods that can be used to differentiate between reinfection and repopulation post-treatment in O. volvulus infected humans with the long-term goal of improving the ability to test macrofilaricidal drug efficacy.

The project is funded for 20 months in the first instance with the potential for a further two years funding, if the work is successful. This project is fundamentally laboratory and analysis based, but there is the potential for fieldwork in countries such as Ghana and Cameroon, project and post holder dependent.

Candidates should have a PhD in biology or epidemiology with expertise in genetics/ genomics and experience with population genetic approaches (e.g. ddRAD-Seq, WGS etc); knowledge of appropriate programming languages (e.g. Linux, R, Python or equivalent); excellent interpersonal, communication and problem-solving skills.

Appointment at level 6 or 7 depending upon experience (level 6/7 ??28,9098-??31,604/??34,520-38,833). Enquiries to Dr Poppy Lamberton, poppy.lamberton@glasgow.ac.uk. Closing date 28 May 2018 (please see University vacancy 021058 for full job description, https://www.gla.ac.uk/explore/jobs/).

Mark Paterson <Mark.Paterson@glasgow.ac.uk>

IZWBerlin EvolutionaryDemography

The Department of Evolutionary Ecology of the IZW Berlin (http://www.izw-berlin.de/welcome.html) offers a Scientist position for 3 years in one of the following areas: EVOLUTIONARY DEMOGRAPHY, assessment of effects of the external and social environment on physiology, behaviour and life history of individuals and the demography of groups and populations using theoretical, comparative, modelling and/or empirical studies; analysis of the influence of life history traits and demography on population viability and processes relevant for species conservation; METABARCODING, assessment of biodiversity patterns, pathogen load and microbial composition based on composite samples using next-generation sequencing; construction of genomics libraries for metabarcoding and RAD-Seq analysis and analysis of metabarcoding data in collaboration with a central NGS facility (https://begendiv.de/); field work and supervision of students in the collection of samples and in the analysis of data; HUMAN-WILDLIFE CONFLICT: assessment of factors underlying human-wildlife conflicts; quantification of economic and ecological aspects of human-wildlife conflicts; analysis of stakeholder interests and interactions; study of the efficacy of mitigation schemes; bridging biological and social sciences. REQUIREMENTS: Completed Dr. or PhD degree in biology or similar subjects; Background in wildlife ecology, social sciences or evolutionary ecology; Excellent programming skills in R and a solid background in statistical analyses and modelling; Reliability, high motivation and efficiency; Ability to work independently and as part of a team; Proficiency in English (oral and written); Excellent track record of publications. For informal enquiries, contact PD Dr. Christian Voigt (voigt@izw-berlin.de). For more information about the position and application details, see https://short.sg/j/-2156225. APPLICATION DEADLINE: JUNE 15, 2018

Dr Oliver Höner

Department of Evolutionary Ecology Leibniz Institute for Zoo and Wildlife Research (IZW) Alfred-Kowalke-Straße 17 10315 Berlin GERMANY Fon. + 49 - 30 5168 516 Fax + 49 - 30 5126 104

Twitter: @HyenaProject Website: https://hyena-project.com ORCID iD: orcid.org/0000-0002-0658-3417

:: Evolutionary wildlife research for conservation ::

“Hoener, Oliver” <hoener@izw-berlin.de>

Liverpool LepResistanceGenomics

We are seeking to recruit a Postdoctoral Research Associate with expertise in computational population genetics, statistics and informatics to join an international research team working to uncover the molecular genetic basis of resistance to Bt-maize in the African maize stemborer moth. You will be based in Liverpool, working closely with Ilik Saccheri (PI) and Al Darby (Co-I). Responsibilities will include: de novo assembly of a reference genome; identifying resistance and tolerance loci; assessing genetic diversity at these loci in natural populations; and analysing resistance allele frequency changes in time. You should have a PhD in population/evolutionary biology, bioinformatics or statistics, and experience of genomic analysis. The post is available until 31 January 2021 (with likely extension to 3yrs from start of contract), ideally starting in October 2018. For additional details and to apply go to https://recruit.liverpool.ac.uk/ and search for Job Ref 009147 (closing date: 21 May 2018). Informal enquiries to saccheri@liv.ac.uk.

<I.J.Saccheri@liverpool.ac.uk>

LuzernSwitzerland EvolutionaryEcolGenomics

A postdoctoral position in evolutionary ecology is available in the research groups of Blake Matthews and Ole Seehausen, at Eawag’s Center for Ecology, Evolution, and Biogeochemistry, near Luzern in Switzerland.

The position is funded as part of the project SeeWandel: Life in Lake Constance- the past, present and future, which investigates the combined effects of multiple stressors on the Lake Constance Ecosystem (www.seewandel.org).

The postdoc project focuses on the evolutionary ecology of stickleback, including foraging behavior, life history evolution, and the genomics of adaptation.

We are interested in candidates with broad interest in evolutionary ecology. Interest and prior experience with field ecology would be an asset, as would experience with fish behavior and genomics. Independently developing research within the framework of the project is encouraged, as is collaborating with other project partners.

Eawag's Center for Ecology, Evolution & Biogeochemistry (CEEB) is located on the shore of Lake Lucerne and is a strong nucleus of Eawag research groups aimed at integrating evolutionary biology, community ecology, and ecosystem science http://www.eawag.ch/forschung/cc/ceeb/index_EN. The Postdoc will interact with a diverse range of researchers studying community ecology, evolutionary biology, ecological genetics, ecosystem science, and applied environmental science.

The project is jointly led by Blake Matthews, Piet Spaak, and Ole Seehausen. The starting date is flexible, but start dates in 2018 (or early 2019) are preferred. The position is for 2 years.

The closing date for applications is 8 June, 2018.

For further information please contact Blake Matthews by email, blake.matthews@eawag.ch Lab homepage: http://homepages.eawag.ch/~matthebl/Welcome.html Publication list: https://scholar.google.ch/citations?user=KPOcG_sAAAAJ&hl=en We look forward to receiving your application. Please submit your application (including CV, motivation letter, and the names and contact information for three references) via the Eawag Jobs & Career webpage, any other way of applying will not be considered. The link below will take you directly to the application form.

https://apply.refline.ch/673277/0616/pub/1/index.html Matthews, Blake blake.matthews@eawag.ch http://homepages.eawag.ch/~matthebl/Welcome.html Eawag, Aquatic Ecology Department Center for Ecology, Evolution & Biogeochemistry Seestrasse 79 6047, Kastanienbaum Switzerland

"Matthews, Blake" <Blake.Matthews@eawag.ch>

Madrid PlantMicrobeInteraction

Postdoctoral position in plant-microbe interaction: Interactions between bacteria and viruses in co-infected hosts: effects on host resistance and on the evolution of pathogen virulence.

Madrid, Spain

Project Summary:

In agro and natural- ecosystems, plants simultaneously interact with multiple microbes and eventually some of them successfully infect producing a disease. The knowledge on specific mechanisms and events underlying the outcome of a plant-pathogen interaction has fundamentally arisen from studies in a single host-single pathogen frame. It has been suggested that multiple infections are a major force driving pathogen evolution, but with the exception of virus-virus interactions, the effect of coinfection on disease production and pathogen evolution has been scarcely documented at the experimental level. The general objective of this proposal is to understand the effects of interactions between viruses and bacteria, in coinfected plants, on plant resistance and on the pathogens infectivity and virulence. This objective will be tackled using tomato (Solanum lycopersicum) coinfected with the bacteria Pseudomonas syringae pv, tomato (PsPto) and the RNA virus tomato mosaic virus (ToMV). The designed approach, combining the analysis of multiple infections outcome and pathogen evolutionary studies under different selective pressures would be pioneer in the area, and will open new avenues for the design of novel preventive and control strategies that may increase the sustainability of plant disease control. The research project, and is collaboration between the "Plant-virus interaction and co-evolution" and "Phytopathogenic bacteria" groups. For further information on the groups visit their web pages: http://www.cbgp.upm.es/index.php/en/scientific-information/interactions -of-plants-with-environment-ipm/plant-virus. http://www.cbgp.upm.es/index.php/es/informacion-cientifica/interaccion- de-las-plantas-con-el-medio-ipm/phytopathogenic-bacteria

RESEARCHER PROFILE

Postdoctoral researcher

MAIN RESPONSABILITIES

Designing and performing experimental approaches to tackle the project objectives; Involvement in general task related to the lab work routine; Active participation in periodic laboratory meetings; Manuscript preparation and publishing; Presentation of work in international conferences.

SPECIFIC OFFER REQUIREMENTS

Applications must include a detailed CV and the name of at least two scientists to provide references.

REQUIRED QUALIFICATIONS

Applicants are expected to hold a PhD or equivalent qualification in Biology in the area of host-pathogen interactions. A record of publications in a related field is desirable. Fluency in English is required.

ELIGIBILITY CRITERIA

We seek candidates with a background in host-pathogen interactions with a solid foundation in molecular evolution and NGS data analyses techniques. Previous experience in plant-microbe interactions will be considered. Applicants must be able to work independently and demonstrate good communications skills.

Applications: http://www.cbgp.upm.es/index.php/es/-form Deadline: June 12th, 2018

Contact: humanresources.cbgp@upm.es

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Fernando GarcÃa-Arenal Catedratico de la Universidad Politecnica de Madrid Centro de BiotecnologÃa y Genomica de Plantas (CBGP, UPM-INIA) Universidad Politecnica de Madrid (UPM) - Instituto Nacional de Investigacion y TecnologÃa Agraria y Alimentaria (INIA) Campus de Montegancedo-UPM 28223-Pozuelo de Alarcon (Madrid) Spain Phone: (34) 91 336 4550/4539 Phone: (34) 91 715 77 21 Fax: (34) 917157721 fernando.garciaarenal@upm.es www.cbgp.upm.es Twitter: @CBGP_Madrid FaceBooK: @cbgpupm CBGP Severo Ochoa

Fernando García-Arenal <fernando.garciaarenal@upm.es>

MaxPlanckEvolBiol BehavioralEvolutionMice

A position for an advanced postdoc in the field of behavioral studies in house mice is available in the group of Diethard Tautz (Max-Planck Institute for Evolutionary Biology, Department of Evolutionary Genetics, Ploen, Germany). The postdoc will be in charge of running a dedicated facility to study mice under semi-natural conditions. The department runs also a mouse house that harbors a collection of outbred house mouse populations from the wild, as well as inbred strains. These serve as a basis to study the natural behavior of mice using both, standardized behavioral tests, as well as semin-natural conditions. Previous studies in the facility have dealt with questions of assortative mating, the role of ultrasonic vocalization, as well as the role of anxiety and personality on teeriotoriality and reproductive success. We are currently in a phase to develop the next round of experiments and the postdoc will have the chance to bring in interests and project ideas for own career development.

Qualification: PhD and postdoc experience in behavioral biology and ecology in mammals (preferably mice). Proven scientific record with first author papers in the discipline.

Salary will be according to the TvöD 13-14 scale (depending on experience), including social benefits and pension scheme. The position is initially for three years, but can be extended.

The Max-Planck Institute for Evolutionary Biology in Ploen has developed in the past years into a major center for basic research on evolutionary topics, ranging from evolutionary genetics, evolutionary ecology, experimental evolution to evolutionary theory. It runs together with the nearby University of Kiel an international graduate program (IMPRS in Evolutionary Biology) and a Master program in Molecular Biology and Evolution. Scientists come from all over the world and the working language is english. Ploen is a small village in a beautiful postglacially shaped landscape with all the amenities of a touristically active area. Two major cities (Kiel and Luebeck) as well as the Baltic Sea are only 30-40min away, Hamburg is about 90min away (all well connected by train).

Applications should include a CV and a publication list (including papers in press or submitted), a statement of motivation, as well as two names for obtaining letters of reference. Applications should be sent by email with documents attached as pdf files to Diethard Tautz (tautz@evolbio.mpg.de).

Prof. Dr. Diethard Tautz Max-Planck-Institut fuer Evolutionsbiologie Abteilung Evolutionsgenetik August-Thienemannstrasse 2 24306 Ploen (Germany) Tel.: 04522 763 390 Fax: 04522 763 281 tautz@evolbio.mpg.de http://www.evolbio.mpg.de/-15929/evolutionarygenetics Diethard Tautz <tautz@evolbio.mpg.de>

McGillU RA PDF ViralEvolution

We are recruiting a Research Assistant with molecular biology experience to study viral evolution. The RA will assume a hands-on role in a scientific team responsible for uncovering novel host-virus interactions in virus infection (Hepatitis C, Dengue virus, Zika virus, as well as several negative-strand RNA viruses). The RA will help complete a research grant investigating novel modes of HCV contamination in clinical settings. The scientist will also collaborate with the research team to develop new assays for investigating RNA structure, interrogating RNA-protein interactions, and support the activities of the research team. The candidate will manage several aspects of the research laboratory including but not limited to: ordering, inventory, database management, training, maintenance of cell lines, preparation of virus stocks, and general lab management.

The RA will be an active member of a project team, communicate results at project team meetings, and be involved in preparation of manuscripts for publication in peer-reviewed journals. The candidate should be able to: exercise scientific judgment and independence; plan and execute research strategies in a goal-oriented fashion; troubleshoot; generate, analyze and interpret data; and contribute ideas, novel techniques or resources to advance project goals.

Minimum M.Sc. Degree (Biological Sciences)

1-3 years relevant experience

Experience in Mammalian cell culture and molecular biology a must.

website: www.saganlab.com Interested candidates should send a cover letter, CV and contact information for three references to:

Selena M. Sagan <selena.sagan@mcgill.ca> Subject: PDF, McGill U Post-doctoral Fellow McGill University, Montreal, Canada Department of Microbiology & Immunology

We are recruiting a postdoctoral fellow (PDF) to pursue a research project focused on inhibition of viral entry and/or development of novel diagnostic strategies for several positive-sense and negative-sense RNA viruses. Viral evolution (Zika virus) and/or directed evolution projects will be pursued. Experience in mammalian cell culture and molecular biology is a must. Experience and knowledge in virology, RNA biology, lentiviral vector preparation, cell sorting, and biochemistry would be considered an asset.

The PDF will be an active member of a project team, communicate results at project team meetings, and be involved in preparation of manuscripts for publication in peer-reviewed journals. The candidate should be able to: exercise scientific judgment and independence; plan and execute research strategies in a goal-oriented fashion; troubleshoot; generate, analyze and interpret data; and contribute ideas, novel techniques or resources to advance project goals.

The ideal candidate is a highly motivated and collaborative team player, with excellent organizational, analytical, verbal/written communication and computer skills. Candidates must be comfortable working with infectious materials.

Primary and/or co-authroed publications in high impact journals Flexible and able to work under pressure to meet deadlines Excellent written and oral communication skills in English are required

Interested candidates should send a cover letter, CV and contact information for three references to:

Selena M. Sagan <selena.sagan@mcgill.ca>

“Selena Sagan, Dr” <selena.sagan@mcgill.ca>

MichiganStateU DrosophilaQuantGenomics

Multiple postdoctoral positions are available in quantitative genetics and genomics in Drosophila melanogaster at Michigan State University in the laboratory of Wen Huang (https://msu.edu/~huangw53/)

Our laboratory is broadly interested in the genetics of complex quantitative traits using Drosophila as a model. Laboratory approaches include classical genetics, molecular biology, genomics, statistics, and bioinformatics therefore trainees are expected to receive training in these areas.

This advertisement invites applications from candidates with background in experimental and/or quantitative biology. Candidates with a recent Ph.D. and experience in Drosophila genetics, molecular biology, bioinformatics are strongly encouraged to apply. Potential projects include mapping developmental and environmental regulatory variation at single cell and single base resolution, development of massively parallell assays to assess effects of regulatory variation, experimental evolution under different diets, development and application of statistical methods for explaining and predicting quantitative trait variation. Postdocs are also encouraged to propose projects that fit their own interest and align with directions of the lab.

Candidates are encouraged to inquire or apply by sending current CV and a brief introduction explaining background, experience and career plan to the PI (Wen Huang: huangw53@msu.edu).

whuang.ustc@gmail.com

MNH Stockholm NematodeSystematics

Please share.

A two-year postdoctoral position is available in the Department of Zoology, Swedish Museum of Natural History, Stockholm. This position is a part of the project "Systematics of poorly known marine nematodes of the class Chromadorea from Sweden" funded by the Swedish Taxonomy Initiative. The main goal of the project is to describe the diversity of marine nematodes in Sweden by focusing on poorly studied genera and families from the class Chromadorea, including descriptions of new taxa. Molecular data obtained during the project will be used to analyse phylogenetic relationships within the class Chromadorea and to expand the reference dataset used in metabarcoding.

The successful candidate will have a recent (max 3 years old) PhD in Zoology, Ecology, Nematology or related disciplines, with experience in morphology-based and molecular systematics and identification of free-living nematodes. A relevant record of scientific publications and proficiency in English are expected. Experience in light microscopy and scientific illustration are highly desirable.

Complete announcement for this position is available at:

http://www.nrm.se/download/18.3462f76c16281c50be07abed/1523876868434/Postdoktor+ZOO.pdf Oleksandr Holovachov Senior curator, Department of Zoology Swedish Museum of Natural History Box 50007, SE-104 05, Stockholm SWEDEN Email (work): oleksandr.holovachov@nrm.se Email (private): holovachov@gmail.com ResearchGate LinkedIn Twitter World Database of Free-Living Marine Nematodes World Register of Marine Species - Nematoda Dyntaxa Swedish Taxonomic Database - Nematoda

Oleksandr Holovachov <Oleksandr.Holovachov@nrm.se>

Montpellier France EvolutionaryGenomics

A two-year post-doctoral position is open at Institut des Sciences de l'ÂEvolution (ISEM), Université de Montpellier, France, to study evolutionary genomics of natural sex reversal in a mouse species.

In natural populations of the African Pygmy mouse (/Mus minutoides/), two types of X chromosomes coexist, one of which (named X*) is feminizing, producing a very high proportion of fully fertile X*Y females. Therefore, the X* is a new type of sex chromosome, completely unique among mammals: a third sex chromosome that behaves like a**female heterogametic**W chromosome. This induces a drastic change in the modes of transmission of sex chromosomes, which in this system can thus be either strictly female (X*), or bisexual (X and Y). We study in the lab differences of life-history traits associated with the different sexual types (XX, X*X and X*Y females, XY males), in order to understand how this new mode of transmission contributes to the evolution of sex-linked phenotypic differences and of potential antagonism over their control.**

The post-doc will study the genomic aspects of this question, by analyzing various available datasets:

-Participate in the /de novo/ assembly and annotation of the X and X* chromosomes.

-Analyse differential gene expression between sexual types from RNA-seq data.

-Analyse population genomics data.

The results will contribute to understand the evolutionary forces driving the birth, building and spread of a new mammalian sex determination system, to**test theories of the role of sexual antagonism in the evolution of sex chromosome architecture, and to decipher the genetic basis of this novel sex determining program.

The post-doc will work in Montpellier at Institut des Sciences de l'ÂEvolution (with Frederic Veyrunes and Pierre Boursot), in close collaboration with The Earlham Institute, Norwich, UK (David Thybert) and the Institut de Génétique Humaine, Montpellier (Francis

Poulat).

The candidate should have strong proven skills in bioinformatics for genomic data analyses (genome and transcriptome sequences). A background in biology (molecular or evolutionary biology) would be a plus.

The candidate should preferably have defended his/her PhD no longer than 4 years before the start of the post-doc, and should preferably not have worked in Montpellier during the last two years.

Salary will be according to the rules of Université de Montpellier, up to 2200 Euros/month net, depending on experience.

Starting date: from September 2018 to January 2019 at the latest.

Deadline for application: June 30, 2018.

Send a CV, a motivation letter and the coordinates of at least two references to frederic.veyrunes@umontpellier.fr <mailto:Frederic.veyrunes@umontpellier.fr>and pierre.boursot@umontpellier.fr

– Frederic VEYRUNES, PhD Chargé de Recherche CNRS Institut des Sciences de l'ÂEvolution de Montpellier ISEM UMR5554 Université Montpellier, FRANCE Département "Génome" Equipe "Sexe & Spéciation" http://www.isem.univ-montp2.fr/veyrunes_frederic + 33 (0)4 67 14 46 33 (office) + 33 (0)4 67 14 36 22 (fax) + 33 (0)6 50 13 51 28 (mobile)

Frederic Veyrunes <frederic.veyrunes@univ-montp2.fr>

NINA Trondheim PDF PhD SalmonEcoEvo

Two positions in quantitative ecology and evolution of salmon: PhD student or Postdoctoral fellow on sea survival Postdoctoral fellow on eco-evolutionary dynamics modelling

The Department of Aquatic Ecology at the Norwegian Institute for Nature Research (NINA) is inviting applications for two positions: a PhD student or postdoctoral fellow position, and a Postdoctoral fellow position. Both are 3-year positions with possibilities for an extended period and/or for a permanent position in NINA.

NINA is Norway's leading institution in applied ecological research and has approximately 250 employees. The Department of Aquatic Ecology, located in Trondheim, Norway, has more than 50 scientists, postdocs, PhD students and research assistants. More information about NINA can be found at www.nina.no . Job description (repeated under): https://www.nina.no/-Aktuelt/Nyhetsartikkel/ArticleId/4508/PhD-student-or-Postdoctoral-fellow-on-sea-survival-Postdoctoral-fellow-on-eco-evolutionary-dynamics-modelling PhD student or Postdoctoral fellow on sea survival:

Research Project: The successful candidate will work on aspects related to sea survival and will be closely connected to the project "ATLANTIC SALMON AT SEA - factors affecting their growth and survival" recently granted by the Research Council of Norway's MILJÃFORSK program. This project aims at understanding the factors underlying temporal and spatial variation in the survival of Atlantic salmon at sea. This includes environmental, developmental and genetic factors (using molecular data). The candidate will work in close collaboration with the postdoctoral fellow working on eco-evolutionary dynamics modelling (see below). The position is funded by a strategic institute initiative at NINA. We will employ either a PhD student, or a Postdoctoral fellow, dependent on qualifications of the applicants.

More information about the ATLANTIC SALMON AT SEA project can be found at https://-www.forskningsradet.no/prosjektbanken/#/project/-NFR/280308/Sprak=en . Main tasks: *Statistical analysis of time-series data. *Stochastic population modelling.

Academic Qualifications: Required: *Master's degree in biology, statistics or similar for PhD student, or PhD on the same topics for postdoc. Desired: *Strong statistical skillset. *Experience in R programming.

Postdoctoral fellow on eco-evolutionary dynamics modelling:

Research Project: The successful candidate will be funded through the project "The effect of life-history genes on eco-evolutionary dynamics (EcoEvoGene)", recently granted by the Research Council of Norway FRIPRO program. This project aims at understanding how the genetic basis of life-history variation affects the interplay between population dynamics and life history-evolution in a wild Atlantic salmon population. The candidate will work in close collaboration with the PhD student or Postdoctoral fellow working on sea survival.

The successful candidate will be expected to spend significant time (6 to 12 months) at University College Cork, Ireland, to work with Thomas Reed and Phillip McGinnity.

More information about the EcoEvoGene project can be found at https://www.forskningsradet.no/-

prosjektbanken/#/project/NFR/275862/Sprak=en . Main tasks: *Construct a pedigree for the salmon population in the Imsa River using high-density SNP data. *Develop a stochastic population model for the Imsa salmon population. *Develop an eco-evolutionary model for the Imsa salmon population.

Academic Qualifications: Required: *PhD in ecology, evolutionary biology, biostatistics or similar. *Strong statistical skillset. *Experience in R programming. Desired *Experience with stochastic matrix population models. *Experience with estimating natural selection. *Experience with GWAS or QTL analyses. *Experience in C++ programming or other programming languages. *Knowledge on quantitative genetics, stochastic population dynamics and population genetics.

General information for both positions:

Personal skills: *Ability for independent work displaying initiative and careful creative thought. *Analytical and academic approach to research questions. *Good collaborative/social skills. *Applicants must be proficient in English, both written and spoken. *Proficiency in Norwegian is not required but is advantageous.

NINA offers *State regulated salary levels (annual salary for PhD is NOK 459 100 to 508 800, and annual salary for postdoc is NOK 579 300 to 590 000). *Good pension and insurance schemes. *Flexible working hours.

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Omaha Zoo ConservationGenetics

Omaha's Henry Doorly Zoo & Aquarium Department of Conservation Genetics based in Omaha, Nebraska, is seeking one post-doctoral researcher with interest/expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

Duties and Responsibilities (include but not limited to): The successful applicant will be proficient in the construction genomic libraries and in solution hybridization methodologies for high throughput sequencing as well as all relevant analysis of large datasets, and manage next-generation sequence workflows. The researchers will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and taxa from Madagascar. Assembly of whole genomes is in-progress, but will likely require additional analysis pertinent to specific research projects. Interested candidates should be highly motivated, organized, independent, and have extensive experience with molecular genomics and bioinformatics, and be able to efficiently write and revise manuscripts. Data on a variety from a variety of species has already been generated, thus candidates will be able to quickly start analysis and manuscript preparation. Travel to Madagascar to support the field programs of Omaha Zoo and the Madagascar Biodiversity Partnership to Madagascar is required for a single three-week interval once a year.

WORKSKILLS: Strong people skills, detailed oriented, willingness to learn and contribute, follow directions, meets deadlines

Basic Qualifications: The applicant should hold a PhD in bioinformatics, computer science, molecular genomics or related field and have more than one year of experience in high-throughput genome sequence analysis. Applicant should be experienced at software related to next generation sequencing data and be able to manipulate genomic data for phylogenetics and phylogeography. Our group's focus is large-scale sequencing for phylogenetics, phylogeography and evolutionary studies of lemurs (specifically the genera Daubentonia Lepilemur, Microcebus, Propithecus, and Varecia) and tortoises (genera Astrochelysand Pyxis) from Madagascar. Thus, previous experience in genome assemblies, annotation and analysis of a variety of next generation sequencing (NGS) pipelines is preferable. The ideal candidate will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds, and have outstanding written and verbal communication skills. The successful applicant must be interested in interdisciplinary science and field research and have a solid publication record that illustrates ability to conduct novel, independent research.

Preferred Qualifications Candidate should have 3+ years of experience in molecular biology, genetics, or bioinformatics. The position requires proficiency in programming (perl or python) and bash scripting using Linux operating systems. Applicants are also expected to be familiar with bioinformatics tools, should be able to implement complex computational pipelines, incorporate genomics databases and have extensive and creditable laboratory experience with constructing genomic libraries. The applicant will need to work closely with two full time technicians to manage NGS lab work, as well as with a full time bioinformatician. While in Omaha the researchers will work with a variety of Malagasy graduate students, and is expected to assist with the progression of a variety of projects, and assist with completion of their degrees and peer-reviewed manuscripts. Based on all these above duties requires a candidate with excellent interpersonal skills, and the ability to train and teach both national and international audiences is necessary. Candidates must also be able to jump between a variety of projects, based on needs of the research group.

Time Frame These positions will be part of an on-going team of rotating postdoc fellows. This position is expected to begin in mid-2018. Initial appointment will be for two years, with possibility to extend to three years.

Application Please submit your CV with the contact information for 3 professional references, a letter describing your interests and goals, and copies of a few publications. Please apply at: http://www.omahazoo.com/careers/ Learn more at: https://madagascarpartnership.org/ Must be legally entitled to work in the USA. Visa sponsorship is not currently available.

Genetics Department <genetics@omahazoo.com>

Paris EvolutionAntibioticResistance

We are looking for a post doctoral researcher to model vaccination and niche competition effects in the gut for microbiota engineering, to target antibiotic-resistant bacteria. Antibiotic multi-resistant (AMR) bacteria that frequently inhabit the intestinal tract of humans and livestock are a serious threat. Our recent work demonstrates that intestinal antibodies, raised by inactivated oral vaccines, enforce the targeted strain to undergo "enchained growth", forming large clonal clumps, which change the effective population size, important for evolution of resistance. During the project, a protocol combining vaccination with introduction of a niche competitor, for targeted drug-free removal of an individual bacterial strain from the microbiota of mice, will be developed, and extended to domestic pigs. Combining mathematical models and quantitative dynamic data will provide a solid framework for subsequent large-scale trials and extension to more diverse bacterial species and hosts.

The postdoc will analyze experimental data to extract information about the bacterial populations dynamics. He/she will develop biophysical models of the microbiota dynamics and evolution in the gut, integrating immune dynamics and competition, and animal size and physiology. Beyond the direct applications to the experiments of the project, the goal is to gain a better understanding on how the physical conditions in the gut interplay with the microbiota dynamics and evolution.

The postdoc will be based in Sorbonne Universite, Paris, under the supervision of Claude Loverdo, and the work will be in close collaboration with Emma Slack, ETH Zurich. The postdoc will be integrated to the theory team of the Laboratoire Jean Perrin, a young and dynamic biophysical lab, in the center of Paris. The postdoc duration is 12+ months, start date negotiable from September 2018, with salary according to experience.

The candidate should have a PhD (or have it completed before the start of the position), in relevant field, and a strong experience in modeling.

If you are interested please send us a CV and a short email motivating your interest in the position.

Claude Loverdo claude.loverdo@upmc.fr Emma Slack emma.slack@micro.biol.ethz.ch

Most relevant publications: - K.Moor, M.Diard, M.E.Sellin, B.Felmy, S.Y.Wotzka, A.Toska, E.Bakkaren, M.Arnoldini, F.Bansept, A.Dal Co, T.Voller, A.Minola, B.Fernandez-Rodriguez, G.Agatic, S.Barbieri, L.Piccoli, C.Casiraghi, D.Corti, A.Lanzavecchia, R.R.Regoes, C.Loverdo, R.Stocker, D.R.Brumley, W-D.Hardt, E.Slack. High-avidity IgA protects the intestine by enchaining growing bacteria. Nature 544:498–502 (2017)

- M.Diard, E.Bakkaren, J.K.Cornuault, A.Hausmann, K.Moor, M.E.Sellin, C.Loverdo, A.Aertsen, M.Ackermann, M.De Paepe, E.Slack, W-D.Hardt. Inflammation boosts bacteriophage transfer between Salmonella spp. Science 355:1211–1215 (2017)

- F.Bansept, K.Schumann-Moor, M.Diard, W-D.Hardt, E.Slack, C.Loverdo, Enchained growth and cluster dislocation : a possible mechanism for microbiota homeostasis, bioRxiv:298059

Claude Loverdo <claude.loverdo@upmc.fr>

Penn Stanford RapidAdaptation

Postdoctoral positions in rapid adaptation

We are seeking to hire postdoctoral associates interested in the genomic, functional and mechanistic basis of rapid adaptation, using Drosophila spp. as genetic model systems. Projects include (1) manipulation of identified genes using CRISPR and other methodologies, combined with functional analyses in both the laboratory and field; (2) genomic and phenotypic analysis of natural populations as well as manipulative experiments in our field facility (https://web.sas.upenn.edu/paul-schmidt-lab/orchard/). The general context for this work is the ongoing collaboration between the Schmidt laboratory at Penn and the Petrov laboratory at Stanford; there are extensive opportunities for integration across labs as well as development of independent projects.

Inquiries may be addressed to Paul Schmidt (schmidtp@upenn.edu) or Dmitri Petrov (dpetrov@stanford.edu), or in person at the Drosophila Research Conference, the Population, Evolutionary and Quantitative Genetics Conference, or at Evolution Montpellier 2018.

RIKEN Japan GenomeEvolution

We are seeking to hire a postdoc in Life Sciences at RIKEN iTHEMS (Interdisciplinary Theoretical and Mathematical Sciences).

Candidates with expertise in genome evolution are especially encouraged to apply.

For informal enquiries about the position, please contact Jeffrey Fawcett (jeffrey.fawcett@riken.jp).

—- Seeking a Postdoctoral Researcher or Research Scientist(W868)

Laboratory

RIKEN Interdisciplinary Theoretical and Mathematical Sciences Program (http://www.riken.jp/en/research/labs/ithems/) (Program Director: Tetsuo Hatsuda)

Research field and overview

'Interdisciplinary Theoretical and Mathematical Sciences (iTHEMS) program' (program director: T. Hatsuda) promotes interdisciplinary collaborations and creation of new interdisciplinary fields through the interactions among researchers in mathematics, theoretical sciences, and computational sciences. Also, iTHEMS aims at nurturing young scientists who cross the boundaries between different disciplines. For more information, please refer to RIKEN Interdisciplinary Theoretical and Mathematical Sciences Program (iTHEMS) Website (http://www.riken.jp/en/research/labs/ithems/).

Job description

iTHEMS is seeking a research scientist in life sciences. Successful applicant is expected not only to pursue his/her own top-level researches in life sciences but also to lead interdisciplinary collaborations among different fields such as mathematics, physics, chemistry, life sciences, engineering, computational sciences, information sciences, and social sciences, under the concept of iTHEMS. This time, we encourage junior applicants who have research experiences in mathematical biology, bioinformatics, systems biology, evolutionary biology, genome biology etc. and can collaborate with iTHEMS Senior Research Scientists, Dr. Jeffrey Fawcett and Dr. Takashi Okada. For more details, send an e-mail to the contact person below.

Contact information/Send application to

e-mail to ithems_app[@]ml.riken.jp with Subj: iTHEMS Researcher (inquiry: Life Sciences).

Further details can be found at:

http://www.riken.jp/en/careers/researchers/20180426/

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– Jeffrey Fawcett

Senior Scientist, RIKEN iTHEMS Tel: +81-48-462-1111 (ext.3086) E-mail: jeffrey.fawcett@riken.jp

Jeffrey Fawcett <ja_fawc@yahoo.co.jp>

ScandinavianResearchSchool Biosystematics

Considering a postdoc in systematic biology in Scandinavia?

ForBio - the Scandinavian Research School in Biosystematics is organising a training program for outgoing and incoming postdoctoral fellows to apply for European

Commission H2020 MSCA Individual Fellowships.

The training program is open to potential incoming fellows to, and outgoing fellows from, research groups in systematic biology in Scandinavia, including systematics, taxonomy, phylogenetics, biogeography, etc. The target group are academically-engaged senior PhD students, postdocs and junior researchers. This covers the IF programs ER-ST (Standard European), ER-CAR (Career Restart Grant), ER-SE (Society and Enterprise), ER-RI (Reintegration), and GF (Global). We aim to have a mixed group of incoming and outgoing fellows.

The program runs from June 1st to the submission deadline of the H2020 MSCA-IF call on September 12th 2018. The training includes match-making between fellows and hosts, coaching, an intensive 3-day workshop at the University of Oslo, writing support, peer review, and liaison with EU coordination offices.

For more information about teachers, target group, course plan, costs and registration, see: http://-www.forbio.uio.no/events/courses/2018/MSCAIF.html For potential hosts for incoming fellows see here (http://www.forbio.uio.no/events/courses/2017/msca-if-hosts.html), but also consider any relevant host at the University of Oslo, NTNU Trondheim, University of Bergen, University of Tromsø, Gothenburg University, Uppsala University, Stockholm University, The Natural History Museum of Denmark, University of Copenhagen, Swedish Museum of Natural History, University of Aarhus, etc etc. SE (Society and Enterprise) fellowships can include mobility to research agencies, SMEs and NGOs.

Registration: Fellows should register online and provide contact information of their host before May 15th. Registered fellows will be evaluated and notified by May 21st regarding acceptance and participation in the training program. Make sure the reserve the dates 18-20 June for the workshop.

If you have any questions, contact Hugo de Boer (hugo.deboer@nhm.uio.no) for more information.

Hugo de Boer

Natural History Museum University of Oslo P.O. Box 1172 Blindern 0318 Oslo, Norway Phone: +47 22851875

Leader of ForBio - the Scandinavian Research School in Biosystematics www.nhm.uio.no/english/-about/organization/research-collections/people/-hugode/ www.forbio.uio.no/ Hugo de Boer <h.d.boer@nhm.uio.no>

SGN Frankfurt ModellingBiodiversity

Job offer ref. #11-18005

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. SGN conducts natural history research with almost 800 employees and research institutions in six federal states. Within SGN, the Senckenberg Biodiversity and Climate Research Centre (BiK-F) explores the interactions between biodiversity, climate, and society. For the working group Quantitative Biogeography we invite applications for a

Vegetation / Ecosystem Modeller (m/f) (full time position, 3 years)

The applicant should work with different aspects of the development and applications of regional to global dynamic vegetation models, most likely based on the Lund-Potsdam-Jena General Ecosystem Simulator (LPJ-GUESS). Possible research topics include the role of higher tropic levels, the importance of plant trait variability for ecosystem functioning and resilience, forest and/or livestock management, linkages between ecosystem/habitat changes and biodiversity change (ranging from longer-term evolutionary and extinction dynamics to the current protection of biodiversity), feedbacks on the climate system (e.g. via changes in the carbon cycle, the land surface, fire and trace gas emissions), and more applied climate impact research. Priorities will also depend on the interests of the applicant, the development of the research field and success in related research proposals by the working group. The applicant is not expected to work on all the topics above. Instead, it is intended that one or two of them should become main focus areas. Model parameterization and evaluation should be based on state-of-art methods for linking models with various observational and experimental datasets.

Your tasks • Advance the field of dynamic vegetation and ecosystem modelling in a relevant topic • Collaborate with other members of the research group and the whole of Senckenberg • Contribute to a better understanding of the interactions between biodiversity (from the genetic to the ecosystem level) and climate • Write manuscripts and publish results in international journals • Contribute to scientific outreach activities

Your profile • PhD degree in Biology, Biogeography, Environmental Modelling, Geoecology, Ecology, Earth System Science or related subjects such as Environmental Physics • Substantial experience with computer programming, preferably in C/C++ • Experience in vegetation or ecosystem modelling • Knowledge of plant physiology and ecology • Good overview over biodiversity and climate research • Documented ability to publish scientific papers in international journals • Research experience in interdisciplinary working environments • Excellent written and oral communication skills in English

What is awaiting you? • Interesting basic research with high relevance for society • Work in interdisciplinary teams from bio- and geosciences, as well as social sciences • The opportunity to strengthen your experience in the above-mentioned research fields • Flexible working hours - annual special payment - company pension scheme - Senckenberg ID card for free entry in museums in Frankfurt - a holiday of 30 days/year

Salary and benefits are according to a full time public service position in Germany (TV-H E 13, 100%). The contract shall start as soon as possible and will be initially limited for 3 years. A prolongation with the opportunity to carry out a habilitation (senior lecture equivalent) is envisioned, but depends on performance and funding. A possible prolongation is dependent on performance and funding. The Senckenberg Gesellschaft für Naturforschung supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please send your application, mentioning the reference of this job offer (ref. #11-18005) until May 31st, 2018 by e-mail (attachment in a single pdf document) and including a letter outlining your suitability and motivation, a detailed CV, two relevant publications, a 1-4 page text outlining how you would address one to two of the potential research topics listed above, all transcripts and grades, two relevant publications, and contact details of two potential references to:

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt am Main

E-Mail: recruiting@senckenberg.de

For scientific inquiries please get in contact with Prof. Dr. Thomas Hickler, thomas.hickler@senckenberg.de.

Mit freundlichen Grüßen /Best Regards

Jessica Helm Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung

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SGN Frankfurt PhylogenomicsMetagenomics

PostDoc (m/f) - Soil Invertebrate Phylogenomics - Metagenomics (100%)

https://tbg.senckenberg.de/wp-content/uploads/2018/05/ref12-18007_postdoc_soil-_invertebrate.pdf Job offer ref. #12-18007 The Senckenberg Gesellschaft fuÌr Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG) is a joint venture of the Senckenberg Gesellschaft fuÌr Naturforschung (SGN), Goethe-University Frankfurt, Justus-Liebig-University Giessen and Fraunhofer Institute for Molecular Biology and Applied Ecology IME aiming to intensify biodiversity genomics in basic and applied research. We will establish a new and taxonomically broad genome collection to study genomic and functional diversity across the tree of life and make genomic resources accessible for societal-demand driven applied research.

The Senckenberg Gesellschaft fuÌr Naturforschung and the LOEWE-TBG invite applications for a PostDoc (m/f) - Soil Invertebrate Phylogenomics - Metagenomics (100%)

Your tasks - Assembly of high-copy genes from shallow genome sequencing data - Phylogenomic inferences - Inference of phylogenetic trait conservatism - Taxonomic / functional assignment of invertebrate metagenomes

Your profile - PhD in bioinformatics, evolutionary studies or related areas - Experience in de novo mitogenome (and other high-copy gene) assembly - Experience in phylogenomics / phylogenetics - Ability to assemble / troubleshoot bioinformatic pipelines and to deal with large amount of data (i.e. ability for shell and script programming) - Excellent communication skills in written and oral English - Team player who successfully interacts with graduate students and colleagues - Interdisciplinary training and background is welcome

What is awaiting you? - A dynamic team of scientists at the new LOEWE Centre Translational Biodiversity Genomics (including ecologists, evolutionary biologists, bioinformaticians, applied scientists, etc.) - Close collaboration with scientists working on a similar project at the Laboratoire d'EÌcologie Alpine (LECA Grenoble, France) - Interdisciplinary networking with biodiversity and climate scientists at the Senckenberg Research Institute - Possibility to co-supervise undergraduate and graduate students and to gain teaching experience - Flexible working hours - annual special payment - company pension scheme - Senckenberg ID card for free entry in museums in Frankfurt - a holiday of 30 days/year

Place of employment: Frankfurt am Main Working hours: Full time (40 hours/week) Type of contract: initially limited for 2 years Salary: according to the German collective agreement TV-H (pay grade E 13)

Salary and benefits are according to a full time public service position in Germany (TV-H E13). The position is available as of January 1st, 2019, but can begin later if necessary.

The Senckenberg Gesellschaft fuÌr Naturforschung supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft fuÌr Naturforschung.

Please send your application, mentioning the reference of this job offer (ref. #12-18007) by e-mail (attachment in a single pdf document) until August 31st, 2018 (or until the position is filled), and include a cover letter detailing your research interests and experience, a detailed CV, copies of your certificates (transcripts and grades), a list of publications, contact details of two referees to: Senckenberg Gesellschaft fuÌr Naturforschung Senckenberganlage 25 60325 Frankfurt am Main E-Mail: recruiting@senckenberg.de

For more scientific information, please contact Dr. MikloÌs BaÌlint, Miklos.Balint@senckenberg.de.

– Dr. Miklós Bálint Senckenberg Biodiversity and Climate Research Centre Georg-Voigt-Str. 14-16 60325 Frankfurt Germany

https://tbg.senckenberg.de/bodenmetagenomik/ http://www.bik-f.de/root/index.php?page_id=238 http://scholar.google.co.uk/citations?user=NeS7d8oAAAAJ +49 (0)69 7542 1856

Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Uwe Fritz, PD Dr. Ingrid Kröncke; Präsidentin: Dr. h.c. Beate Heraeus; Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Die Welt baut ihr Museum - bauen Sie mit! www.die-welt-baut-ihr-museum.de

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StockholmU EvolutionaryGenomics

Researcher in Evolutionary Genomics A postdoctoral researcher position in evolutionary genomics is currently available at Stockholm University and Science for Life Laboratory in the research group of Dr. Tanja Slotte. Deadline for applications is June 1, 2018.

Full ad https://bit.ly/2jQPA6p Project description The position is associated with the European Research Council (ERC) funded project SuperGenE: Supergene evolution in a classic plant system - genomic studies of distyly.

The aim of this project is to investigate the genomic architecture underlying the balanced floral polymorphism distyly in wild Linum species. Specifically, we will identify the genomic region (termed supergene) that governs distyly in Linum and test whether this supergene exhibits evolutionary genetic similarities to sex chromosomes. For this purpose, we will conduct evolutionary genetic analyses of cutting-edge genomic data to comprehensively investigate the tempo and mode of recombination suppression, the impact of natural selection, and regulatory evolution at the supergene in three distylous species. We will also investigate the genetic basis and population genomic consequences of three losses of distyly that are likely associated with a change in the breeding system.

Main responsibilities The position involves research in the ERC project SuperGenE. The researcher will conduct evolutionary genetic analyses of genomic and gene expression data. The position may also include sampling of natural plant populations in the Mediterranean region.

Qualification requirements A PhD degree and training in evolutionary genetics or population genomics is required.

Experience of bioinformatic analyses of large-scale genomic or gene expression data is beneficial. Experience of evolutionary genetic studies of sex chromosome evolution is beneficial, but not required.

Assessment criteria In the appointment process, special attention will be given to research skills, in particular pertaining to evolutionary genetics/population genetics. Excellent proficiency in English (the working language of the group) is required. The researcher needs to be able to work well in a collaborative environment, as well as independently. Finally, creativity and drive, and an aptitude for problem-solving are personal characteristics that are desirable.

Terms of employment The position involves full-time employment for a maximum of two years, with possibility of extension. Start date immediately or as per agreement.

Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Infrastructure and environment The researcher will be based in the Slotte lab (https://tanjaslottelab.se), a part of the Dept. of Ecology, Environment and Plant Science, Stockholm University (http://su.se/deep/english/). We are located at Science for Life Laboratory in Stockholm (http://www.scilifelab.se), which holds considerable expertise in high-throughput sequencing technology and bioinformatics. The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with both genomicists, evolutionary biologists and ecologists at SciLifeLab and Stockholm University.

Contact Further information about the position can be obtained from Dr. Tanja Slotte, tanja.slotte@su.se.

Application Full ad and application at: https://bit.ly/-2jQPA6p

Deadline for application: June 1, 2018.

“tanja.slotte@su.se” <tanja.slotte@su.se>

StockholmU EvolutionCognition

Postdoctoral Fellow in the Evolution of Cognition and the Brain

at the Department of Zoology, Stockholm University, Sweden

Deadline for application: May 29, 2018.

A postdoctoral position focused on cognitive evolution is available in Alexander Kotrschal's research group in the Department of Zoology at Stockholm University. The project uses the guppy (Poecilia reticulata) as a model to comparatively and experimentally investigate the factors driving cognitive evolution. As such, the project spans over multiple disciplines including field collections, artificial selection, assays of behaviour and detailed tests of cognitive ability, brain imaging and neural density estimations, and analyses of the genomic architecture that orchestrates changes in brain anatomy and cognitive ability.

The project will use both animals from wild populations with known differences in ecology, and from a selection experiment. These animals will be subjected to relevant assays of behaviour, brain anatomy and genomics. The overall aim of the project is thus to increase our understanding of the evolutionary relationship between brain anatomy, cognitive ability and the genome.

The work will mostly be lab-oriented but includes at least one field trip to Trinidad. The project will require hard work but at the same time provide excellent opportunities for personal initiatives and development towards pursuing a successful academic career. An important task will be to undertake selection experiments followed by the collection and analysis of complex data. The project is undertaken in a brand new section of the large tropical freshwater fish labs in the Department of Zoology with established assays of brain anatomy, several different aspects of cognitive abilities, swimming parameters, personality, individual and collective behaviour, etc.

The successful candidate will be part of an international team consisting of an Ethologist (Alexander Kotrschal, Stockholm University), Evolutionary Biologist (David Reznick, University of California & Trinidad), Genome Biologist (Alison E. Wright, University of Sheffield), and Information Technology researcher (Kristiaan Pelckmans, Uppsala University) that investigate the evolution of cognition, brain anatomy and the genome via state-of-the-art methods.

In the appointment process, special attention will be given to research skills in cognitive evolution, with excellent analytical ability and experience from quantitative analyses of behaviour and other traits of interest. Experience in working with aquatic animals in the lab is especially meriting.

The position involves full-time employment for a maximum of two years, with the possibility of extension under special circumstances. Start date July 2018 or as per agreement.

For more information on the position and to apply follow this link:

https://www.su.se/english/about/working-at-su/-jobs?rmpage=job&rmjob=5639&rmlang=UK

Questions? Please contact Dr Alexander Kotrschal, alexander.kotrschal@zoology.su.se

For more information about research in the Kotrschal lab see: https://www.su.se/profiles/akotr-1.218779 Alexander Kotrschal <alexander.kotrschal@zoologi.su.se>

UArizona EvolutionaryGenomics

The Matzkin Lab at the University of Arizona, Department of Entomology (www.matzkinlab.org) is currently recruiting a postdoc to work on a variety evolutionary genomics projects focusing on the genomic diversification of cactophilic Drosophila. I am seeking a highly motivated and creative individual with strong computational and evolutionary genetics skills to join our evolutionary and ecological genomics lab. Postdoc will be based at The University of Arizona, Department of Entomology and will have the opportunity to interact with investigators at the BIO5 Institute and Department of Ecology and Evolutionary Biology.

The postdoc will be involved in all research aspects of the assigned projects and will have the opportunity to develop projects in consultation with Dr. Matzkin. Critical and independent thinking is very important for this position, as well as having the ability to analyze data, develop pipelines and genomic tools, write manuscripts and proposal writing. Postdoc will interact with the graduate and undergraduate students in the Matzkin lab at the University of Arizona as well as having the opportunity to be involved in outreach activities.

The postdoctoral researcher will be required to maintain up-to-date records of all experiments, analysis and data collected. The postdoc will report to Dr. Matzkin on a weekly basis on the progress of projects and experiments. The postdoc will be required to have an active participation in writing publication manuscripts based on the research produced in the lab. The postdoctoral research will also be responsible in creating and maintaining a database of the genomic data as well as assisting in creating a web platform to disseminate the information to the broader community.

The candidate is expected to have a PhD in evolutionary biology, genomics, computational biology or related field. Postdoc must have excellent writing, communication and critical thinking skills with at least 1-3 publications (in print or submitted). Prior experience working with Drosophila a plus but not necessary. The position is available to start immediately. Funding for the position is for one year, with the possibility of extension pending additional funding.

Apply at https://uacareers.com/postings/29309. (Posting number P20575). You will need to submit a 1) cover letter briefly outlining the candidate's fit to the position and future goals 2) curriculum vitae 3) contact information (email and phone) for three references, preferably including doctoral advisor and/or postdoctoral advisor (if relevant) and 4) no more than three relevant publication PDFs. Please contact Luciano Matzkin (lmatzkin@email.arizona.edu) if you have additional questions about the position.

Outstanding UA benefits include health, dental, vision, and life insurance; paid vacation, sick leave, and holidays; UA/ASU/NAU tuition reduction for the employee and qualified family members; access to UA recreation and cultural activities; and more! The University of Arizona has been recognized on Forbes 2015 list of America's Best Employers in the United States and has been awarded the 2015 Work-Life Seal of Distinction by the Alliance for Work-Life Progress! For more information about working at the University of Arizona, please www.whyua.com . Dr. Luciano M. Matzkin Associate Professor University of Arizona Department of Entomology BIO5 Institute Department of Ecology and Evolutionary Biology 520-621-1955 Marley 641F www.matzkinlab.org "Matzkin, Luciano Matias - (lmatzkin)" <lmatzkin@email.arizona.edu>

UBath EvolutionaryPaleontology

Applications are invited for a two-year position as a Postdoctoral Research Associate, as part of a research project on mass extinction and recovery, and with particular emphasis on the Cretaceous-Paleogene (K-Pg) boundary. The project, led by Dr. Nicholas Longrich, is part of a 5-year project funded by the Leverhulme Foundation and based at the Milner Centre for Evolution (https://themilnercentre.org/) at the University of Bath. The Milner Centre is a new, researcher-led initiative doing fundamental research in evolution and answering major questions in evolutionary biology. Supported by a 5 million donation to create a new building, our goal is to create an internationally excellent centre for evolutionary biology and establish Bath as a leader in the field, producing great science and excellent researchers.

The project goal is to understand the severity, selectivity, and recovery from mass extinction, and the role of extinctions in driving evolution. Earth's history is punctuated by mass extinctions - severe, global, and rapid events that wiped out vast numbers of species. The dynamics of these extinctions are incompletely understood. How many species were lost? How did survivors differ from victims? How did the ecosystem recover? How did extinction affect the distribution of species on Earth? Do recoveries simply replace lost diversity, or do they lead evolution to pursue different directions? To answer these questions, we are undertaking a series of studies of the K-Pg transition. We will study new Cretaceous and Paleogene fossils from terrestrial ecosystems in North America and marine vertebrates in Morocco, synthesize data from the literature on the diversity and distribution of invertebrates, and use molecular clocks to search for signals of adaptive recovery in the Cenozoic. The project will also extend this work to other extinction events to understand the degree to which mass extinctions are governed by common patterns and processesot.

As part of the project, we seek a postdoctoral researcher with a strong relevant research background in palaeontology, evolutionary biology, and/or geology. The researcher appointed will be involved in both leading and collaborating in research within the project, including identifying new collaborative and funding opportunities. They will also have a significant role as deputy leader of the laboratory, including day-to-day running of the lab, leading meetings, supervising postgraduates and junior researchers and recruiting new members. Skills in this area, in addition to a strong research background, are thus important for this role.

Please include with your application:

- Full CV including publication list
- Cover letter, discussing research experience and goals, and what you will bring to this project
- Contact details for three references

For more details and to apply, see https://www.bath.ac.uk/jobs/Vacancy.aspx?ref=CA5851 Nick Longrich <N.R.Longrich@bath.ac.uk>

UBern PDF PhD EvolutionBehaviour

PhD position (3 years) in animal behaviour and behavioural genetics

At the Division of Animal Welfare, University of Bern, Switzerland, we are seeking a PhD student who is eager to investigate causes of variation in animal research. The project is funded by the Swiss National Science Foundation (SNSF); its ultimate goal is to develop experimental designs for improving the external validity and reproducibility of animal research. The successful candidate will work in a small team together with faculty, two postdocs, and a lab technician and will participate in the training and mentoring of undergraduate students.

The PhD project will include single and multi-laboratory studies using laboratory mice to investigate how different sources of biological variation affect variation within and between studies, and to test whether systematic heterogenization of study populations improves the external validity and reproducibility of animal research. Outcome variables will include behavioural, physiological, and epigenetic measures.

Candidates need a University degree in biology or biomedical sciences. Since the project involves multiple approaches covering a diverse array of techniques, students with various skill sets are encouraged to apply. A background in animal behaviour or behavioural genetics will be essential. Experience in working with laboratory rodents and familiarity with rodent behavioural testing, as well as sound knowledge in experimental design and statistics are desirable. Some wet-lab experience will be beneficial.

Proficiency in German language is not required but a willingness to learn basic German will facilitate living in Bern and positively affect social life. We offer an attractive academic environment, opportunities to develop the own academic career, a 3-year contract, and a competitive salary based on the Swiss National Science Foundation (SNSF) scheme.

Please send your application letter together with a motivation statement, your CV, copies of relevant study certificates, and contact details of one or two reference persons (reference letters are not required at this stage) in a single pdf-file to: hanno.wuerbel@vetsuisse.unibe.ch.

The deadline for application is June 20, 2018. The intended project start is September 2018 (negotiable). Please indicate your preferred and earliest possible start date in the application letter. For informal enquiries, please contact Prof. Hanno Wurbel: hanno.wuerbel@vetsuisse.unibe.ch.

Postdoctoral position (3 years) in quantitative behavioural genetics

At the Division of Animal Welfare, University of Bern, Switzerland, we are seeking a postdoctoral scientist who is eager to investigate causes of variation in animal research. The project is funded by the Swiss National Science Foundation (SNSF); its ultimate goal is to develop experimental designs for improving the external validity and reproducibility of animal research. The successful candidate will work in a small team together with faculty, another postdoc, a PhD student, and a lab technician and will participate in supervision of the PhD student and training of undergraduate students.

We will employ a multi-faceted approach comprising conceptual and quantitative statistical modelling based on existing datasets, systematic review and meta-analysis of published data, and experimental studies using laboratory mice to investigate how different sources of biological variation affect variation within and between replicate studies. Outcome variables will include behavioural, physiological, and epigenetic measures.

Candidates need a University degree and PhD (or equivalent) in biology or biomedical sciences. Since the project involves multiple approaches covering a diverse array of techniques, candidates with various backgrounds and skill sets are encouraged to apply. An understanding of sampling theory and statistics, and reasonable programming and computational skills will be essential. Knowledge in quantitative genetics and epigenetic analyses (DNA methylation and histone modification) are desirable. Experience in behavioural and physiological phenotyping of mice and in systematic reviews and meta-analyses will be beneficial.

Proficiency in German language is not required but a willingness to learn basic German will facilitate living in Bern and positively affect social life. We offer an attractive academic environment, opportunities to develop the own academic career, a 3-year contract, and a competitive salary based on the Swiss Cantonal University scheme.

Please send your application letter together with a motivation statement, your CV, publication list, copies of relevant study certificates, and contact details of one or two reference persons (reference letters are not required at this stage) in a single pdf-file to: hanno.wuerbel@vetsuisse.unibe.ch. We encourage applications of people with unusual career tracks.

The deadline for application is June 20, 2018. The intended project

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UCalifornaSanDIego VirusEvolution

The Virus Evolution Group at University of California, San Diego is looking to hire a postdoctoral researcher interested in virus evolution. We are a computational group with interest in a broad range of viruses. Much of our work focuses on HIV molecular epidemiology, and this position will be funded in part by an NIH R01 to study HIV molecular transmission networks in a public health setting. Opportunities for independent research trajectories will also be encouraged.

Candidates should have demonstrated productivity in evolutionary biology, computational biology, or a relevant field.

To apply, please send (i) a brief Cover Letter detailing research interests, (ii) your CV, and (iii) contact information for references to jwertheim@ucsd.edu.

Women and members of under-represented minorities are strongly encouraged to apply.

Joel Wertheim

Division of Infectious Diseases and Global Public Health Department of Medicine University of California, San Diego

"jwertheim@ucsd.edu" <jwertheim@ucsd.edu>

UCalifornia Berkeley HumanEvolGenetics

Recruitment Period Open date: April 16th, 2018 Next review date: May 1st, 2018 Apply by this date to ensure full consideration by the committee. Final date: May 17th, 2018 Applications will continue to be accepted until this date, but those received after the review date will only be considered if the position has not yet been filled.

Description Description: The Moorjani Lab (https://moorjanilab.org/) at University of California, Berkeley has a post-doctoral position available for motivated candidates with background in statistical Human Evolutionary Genetics and/or data science.

Our lab focuses on using statistical and computational approaches to study questions in human genetics and evolutionary biology. A central aim in the lab is to understand the impact of evolutionary history on genetic variation and to apply this knowledge to learn about human history and biology. To this end, we use genetic data from ancient specimens and present-day species to learn about: (1) when key events (such as introgression and adaptations) occurred in human history, (2) how different evolutionary processes such as mutation rate evolve across primates, and (3) how we can leverage these patterns to identify genetic variants related to human adaptation and disease. The research in the lab involves both development of new methods and large-scale genomic data analysis.

Responsibilities: A successful candidate will develop and apply computational approaches to large genomic datasets to characterize patterns of population history and evolution. The main responsibilities include conducting research, attending regular lab meetings and journal clubs, and preparing research results for publication and presentations at scientific meetings. Opportunities may also exist for mentoring graduate and undergraduate students.

Minimum/Basic Qualifications required at the time of application: - Completion of all doctoral degree requirements except the dissertation in genetics, computational biology, biostatistics, Human Evolutionary Genetics or related fields.

Additional Qualifications (required by start date): - PhD or equivalent degree in genetics, computational biology, biostatistics, Human Evolutionary Genetics or a related field. - Knowledge of statistics and Human Evolutionary Genetics theory. - Demonstrated record of research productivity and publications. - Programming experience (e.g. C/C++, Python/ Perl, R or other programming languages)

Preferred Qualifications: Experience with large-scale genomic data analysis.

Salary: This is a full-time position. Salary is commensurate with qualifications and experience.

How to apply: To apply, please go to the following link: http://apptrkr.com/1205272 Applicants should submit the following materials: - A cover letter - A curriculum vitae - Statement of Research (One-page summary of research interests) - Contact information for 3 references

Letters of reference are not required at this time. We will seek your permission before contacting your references. All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are provided via a third party (i.e., dossier service or career center), to the UC Berkeley statement of confidentiality: http://apo.berkeley.edu/evalltr.html . This position will be open until filled. The anticipated start date is May 2018. The appointment is for a duration of one year with the possibility of annual renewal up to three years. Please address inquiries to Maria Ruiz, maruiz@berkeley.edu.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: http://policy.ucop.edu/doc/4000376/NondiscrimAffirmAct . Job location Berkeley, CA Requirements Documents - Curriculum Vitae - Your most recently updated C.V. - Cover Letter - Statement of Research - One-page summary of research interests References3 references required (contact information only) jeid-7f45ca7c3d12a84888fdf9c7ca1dbc27

Jessica Godoy <jessica@jobelephant.com> Jessica Godoy <jessica@jobelephant.com>

UCalifornia LosAngeles PlantSystematicsEvolution

The research group of Felipe Zapata in the Department of Ecology and Evolutionary Biology (EEB) at the University of California, Los Angeles (UCLA) is looking for a highly motivated, creative postdoc. The main focus of the group is evolutionary and systematic biology, particularly studies aimed at learning about the origin and evolution of biodiversity, reconstructing the history of populations, species, and clades, and generating/testing hypotheses about processes promoting taxonomic and phenotypic diversification.

The postdoc could work on a variety of projects using different types of data. Specifics of the research projects are flexible, but could include: population and speciation genomics to study how populations/species differentiate and multiply; spatial analyses of eco-phenotypic and genomic data to learn about the nature of species; testing alternative hypotheses on speciation and diversification at different phylogenetic scales; generating/testing hypotheses to study the evolution of genomes and phenotypes in lineages with contrasting eco-phenotypic variation; and developing computational tools for comparative biology (in the context of the projects described above). The research group conducts empirical work with a main focus on angiosperms from the Andes, central America, and the California Floristic Province. The research group is small but is growing, and the postdoc will have the opportunity to play a critical role in the intellectual growth and development of the group.

The EEB department at UCLA is an exciting place to conduct research in evolutionary and systematic biology, with numerous research groups focused on similar areas (e.g., Alfaro, Barber, Campbell-Staton, Jacobs, Lohmueller, Sears, Shaffer, Smith, Sork). Outside EEB, UCLA offers several opportunities for learning, collaborating, teaching, and mentoring in one of the largest and most diverse public universities in the US.

Los Angeles is a vibrant and multicultural city, and it provides a welcoming environment to everyone. The research group of Felipe Zapata is a safe space and is committed to increasing diversity in the scientific community. Applications from diverse candidates with overlapping scientific interests are strongly encouraged.

Qualifications: Ph.D. in evolutionary biology, systematic biology, organismic biology, plant biology, or similar fields. Strong and genuine interest in organisms is required (there will be opportunities to do field work, lab work, and herbarium work). Background in scripting/programming is a big bonus (but it can be learned).

Salary will be competitive and only recent graduates with no previous postdoctoral experience will be considered for this position. Start date is flexible, but ideally sometime in summer/fall of 2018. The position is for one year, with potential for renewal for up to one additional year.

To apply, please follow the instructions posted here: [goo.gl/forms/k06fxmBCsgvehVnG2]

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

Felipe [fzapata@ucla.edu] – Felipe Zapata Department of Ecology and Evolutionary Biology University of California, Los Angeles zapatalab.org

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: UC Nondiscrimination & Affirmative Action Policy < http://policy.ucop.edu/doc/4000376/NondiscrimAffirmAct >.

Felipe Zapata <fzapata@ucla.edu>

UCSF Berkeley StatisticalGeneticsOfInfectionNetworks

New postdoctoral position in statistical genetics to develop Bayesian methods for inference of malaria infection networks. Joint postdoc with Bryan Greenhouse at UCSF and Rasmus Nielsen at UC Berkeley. See https://drive.google.com/file/d/1bC14PL7ePaB5v4ZPx_1qbqesm6gKXx-6/view . Rasmus Nielsen <rasmus_nielsen@berkeley.edu>

UEdinburgh QuantitativeGenetics

Postdoctoral Researcher in Quantitative Genetics

Salary Range: 31,342 - 37,394 Closing Date: 18 June 2018

Background: The Centre for Tropical Livestock Genetics and Health (CTLGH) was established through a collaborative framework agreement between the University of Edinburgh (acting through its Roslin Institute), Scotland's Rural College (SRUC), and The International Livestock Research Institute (ILRI). CTLGH is hosted and managed by the Roslin Institute on behalf of other partners and currently operates in 2 major locations/nodes: Edinburgh (Scotland) and Nairobi (Kenya). CTLGH provides a framework for the founding partners and other stakeholders to mobilize the latest advances in genetics and genomics science to develop innovative tools and solutions to drive tropical livestock productivity and resilience, particularly in small holder farming systems in LMICs (low and middle income countries). Under the auspices of CTLGH, the parties are funded by the Bill & Melinda Gates Foundation (BMGF), the UK Department for International Development (DFID) and the UK BBSRC to support programmes under the following initiative: Genomic Tools to Improve the Productivity of Tropical Livestock and Increase Climatic Resilience, Adaptation, and Mitigation for the Benefit of Smallholder Farmers in Sub-Saharan Africa.

Job purpose: CTLGH and its founding partners are seeking to appoint a post-doctoral researcher within the research group led by John Hickey at The Roslin Institute. This post-doctoral researcher will work with the CTLGH team and its partners, with the broader set of researchers at The Roslin Institute and with the African Dairy Genetic Gains (ADGG) team to develop tools and technologies to enhance genetic improvement for small-holder production systems in low and middle income countries.

Specifically, post-doctoral researcher will develop novel breeding program designs that are suited to the ADGG context, develop novel statistical methods and data generating methods (e.g., imputation) that are suited to the ADGG context, perform data analysis of the large and expanding ADGG data set and perform stochastic simulations to understand underlying phenomena and model future outcomes.

Key Contacts/Relationships The successful candidate will work alongside computational biologists, animal and plant breeders, quantitative geneticists and software engineers and have access to high performance computing clusters. Working to derive solutions at the interface between academia and industry, the post-holder will lead on research planning and management of key projects, guided by the group's outputs and deadlines.

The post-holder will join the Genetics and Genomics department at The Roslin Institute, a world-class centre for research on quantitative genetics of populations, particularly in managed populations such as livestock, companion animals, forests and crops.

For more information about:

* The research group please visit http://www.alphagenes.roslin.ed.ac.uk . * The Roslin Institute please visit https://www.ed.ac.uk/roslin * CTLGH please visit http://www.ctlgh.org/ * ADGG please visit https://www.ilri.org/node/40458 Informal enquires can be made to John Hickey while formal applications should be done through the website of The Roslin Institute.

https://www.ed.ac.uk/roslin/working/opportunities/vacancies/research-fellow-043857 HICKEY John <John.Hickey@roslin.ed.ac.uk>

UGlasgow SticklebackEpigenetics

We seek a postdoctoral research associate to work on the genomic and epigenetic basis of phenotypic variation in populations of sticklebacks. Uniquely these populations are derived from Icelandic geothermal sites where temperatures have been elevated for extended periods. Samples have already been collected from several field sites and lab crosses are underway. Candidates will be considered from a wide range of backgrounds and the position will involve the use of bioinformatic analyses of 'omic' data to facilitate population genomic and QTL approaches. Support comes from a NERC highlight topic fund awarded to Kevin Parsons, Shaun Killen, Jan Lindstrom, and Neil Metcalfe. Further involvement comes from Liverpool Genomics.

We are a lab focused on the evolutionary, ecological, and developmental basis of adaptive change. The atmosphere at Glasgow is highly social with a number of research groups within the institute, and a number of special interest reading groups. The post will last approximately 20 months with the possibility of an extension.

Further details can be found here:

http://www.jobs.ac.uk/job/BJK584/research-assistant-associate/ Informal inqueries can be made to: Kevin.Parsons@glasgow.ac.uk

Dr. Kevin Parsons Senior Lecturer Institute of Biodiversity, Animal Health, and Comparative Medicine University of Glasgow

https://sites.google.com/site/kevinparsonslab/home http://www.gla.ac.uk/researchinstitutes/bahcm/staff/kevinparsons/ Kevin Parsons <Kevin.Parsons@glasgow.ac.uk>

UGothenburg Sweden BirdsMacroevolution

Apply by: 2018-05-15

Project description Birds are one of the most charismatic and well-studied group of animals, yet we know very little about how humans have affected their global patterns of diversity and evolutionary history. This project is part of a larger initiative funded by the Swedish Research Council titled "Is biodiversity understandable from contemporary distributions?" with Søren Faurby (goo.gl/9S6nuP) as a PI and Tim Blackburn (goo.gl/9LWXfk; a bird macro-ecologist at University College London) and Manuel Steinbauer (goo.gl/UEiG7T; an island biologist at Friedrich-Alexander University Erlangen-Nürnberg) as co-applicants. The work will involve close collaboration with this team as well as additional researchers at Gothenburg University, especially members of the Antonelli Lab (http://antonelli-lab.net/).

Earlier work by the PI has discovered substantial biases in macro-scale analyses of mammals, when conclusions are drawn based only on present-day distributions (e.g. http://onlinelibrary.wiley.com/doi/10.1111/-ddi.12369/full; http://www.pnas.org/content/113/4/-868.short; http://onlinelibrary.wiley.com/doi/10.1111/-ecog.02287/abstract). The goal of this project is to investigate whether those biases are restricted to mammals (which could be particularly sensitive to anthropogenic impacts), or are more general and affect other organisms.

Job assignments Retrieving and analyzing information on the taxonomy of extinct birds

Estimating and analysing potential present-natural distribution of all bird species and the differences between these and contemporary patterns

Employment The employment is a full-time position for 18 months. The physical placement will be at the University of Gothenburg, Department of Biological and EnvironmentalScience but may include shorter stays at University College London or Friedrich-Alexander University Erlangen-Nürnberg.

Full details can be found at https://www.gu.se/english/-about_the_university/job-opportunities/vacancies-details/?id=2001 - Søren Faurby http://antonelli-lab.net Sören Faurby <soren.faurby@bioenv.gu.se>

UHeidelberg SingleCellEvolGenomics

EXPERIMENTAL POSTDOC POSITION: SINGLE-CELL EVOLUTIONARY GENOMICS

Center for Molecular Biology (ZMBH), Heidelberg University, Germany

The position: The Kaessmann lab is looking for an ambitious and highly qualified postdoctoral researcher interested in unravelling the molecular and cellular basis of the evolution of species-specific organ phenotypes in mammals based on single-cell experiments.

Background: A primary goal in biology is to understand the molecuÂbasis of phenotypic evolution, most notably that of humans and other mammals. Most phenotypic differences between species are likely due to regulatory mutations that affect gene expression. Our lab has therefore previously generated comprehensive sets of RNA-seq data and various other high-throughput "omics" (e.g., epigenomic, metabolomic, proteomic) datasets for a large collection of tissues from representative mammals and performed integrated analyses of these data to study the expression (regulatory) evolution of mammalian genomes across gene types, lineages, organs, developmental stages, chromosomes and sexes (see e.g. Brawand et al. Nature 2011, Necsulea et al. Nature 2014, Cortez et al. Nature 2014; selected publications are listed below).

We have recently begun to bring all of previous "evo-devo" work to the cellular level and thus illuminate how evolutionary changes in cellular composition and underlying gene regulatory networks have led to the emergence of species- or lineage-specific organ anatomies and functions.

The project: The first aim for this postdoctoral position is to develop and apply single-cell sequencing protocols for profiling transcriptomes and epigenomes across various tissues and developmental stages from selected mammalian and other vertebrate species. The second goal, which will be based on results from the first aim, is to utilize cellular and/or animal systems (derived from different species and tissues) in conjunction with genome engineering techniques to identify key regulatory mutations that underlie the evolution of distinct cellular phenotypes.

The candidate: The ideal candidate has experience and strong experimental skills in molecular and cell biology; preferably related to RNA biology, genome editing techniques (e.g., CRISPR/Cas), high-throughput assay development and/or pluripotent stem cells (e.g., iPS cells). Expertise in genetic engineering of mice or other organisms, developmental biology, the biology of specific organs (e.g., the brain), and/or genome-scale work (experimental and/or bioinformatic) is a plus. The candidate should ideally be driven by a passion for evolutionary biology.

The position requires the ability to independently take responsibility for the project, as well as strong teamwork and communication skills, problem-solving abilities, reliability, attention to detail and effective time management.

Research environment and location: The postdoc will be supported by research technicians and will work closely together with bioinformaticians and other wet lab scientists in our interdisciplinary group. The language of our institute (ZMBH) is English and hosts scientists from around the world. The institute is located in Heidelberg, a picturesque cosmopolitan city that offers a very stimulating, diverse and collaborative research environment thanks also to neighboring cutting-edge institutions, in particular the European Molecular Biology Laboratory (EMBL) and German Cancer Research Center (DKFZ). In fact, the postdoctoral project will be carried out in the framework of collaborations with groups and core facilities from these two institutions.

For more information, please refer to our websites at http://www.zmbh.uni-heidelberg.de/Kaessmann Please submit a CV, statement of research interest, references, a list of publications or other research output to Henrik Kaessmann (h.kaessmann@zmbh.uni-heidelberg.de).

—- Prof. Dr. Henrik Kaessmann Group leader in the DKFZ-ZMBH Alliance ZMBH - Center for Molecular Biology Heidelberg University Im Neuenheimer Feld 282 69120 Heidelberg Germany —-

Selected recent publications of the Kaessmann lab:

Guschanski, K., Warnefors, M., and Kaessmann, H. (2017) The evolution of duplicate gene expression in mammalian organs. Genome Res. 27: 1461-1474.

Marin, R., Cortez, D., Lamanna, F., Pradeepa, M.M., Leushkin, E., Julien, P., Liechti, A., Halbert, J., Brüning, T., Mössinger, K., Trefzer, T., Conrad, C., Kerver, H.N., Wade, J., Tschopp, P., Kaessmann, H. (2017) Convergent origination of a Drosophila-like dosage compensation mechanism in a reptile lineage. Genome Res. 27: 1974-1987.

Warnefors, M., Mössinger, K., Halbert, J., Studer, T., VandeBerg, J.L., Lindgren, I., Fallahshahroudi, A., Jensen, P., Kaessmann, H. (2017) Sex-biased microRNA expression in mammals and birds reveals underlying

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ULausanne 2 TheoPopGenomics

Two postdoctoral positions in theoretical population genetics and population genomics are available in the research group of Jérôme Goudet in the Department of Ecology and Evolution, University of Lausanne. The postdocs will join a team working on Population Genomics and the understanding of the interplay of population structure, trait architecture, and— selection using different approaches, from theory and the development of statistical tools to field observations. For details, see—http://www.unil.ch/dee/goudet-group Research scope and skills sought

The first postdoc's research will built on a recent paper by Weir and Goudet (http://www.genetics.org/content/206/4/2085) and will investigate the properties of population specific statistics, and derive their expected values under specific demographic scenarios.—

The ideal candidate will have a PhD in (theoretical) population genetics, statistics, physics or applied mathematics, an interest for evolutionary questions and excellent communication skills. A good knowledge of C++ and R are essential. The successful candidate should also have good interpersonal skills and an ability to interact with others. Although not a requirement, some knowledge of French would be an asset.—

The second postdoc will expand and mine an existing data set of ~100 whole genome sequences from European barn owls (Tito alba), with the goal to answer several questions about the past demography and selective pressures this species had experimented while colonizing Europe after the last glaciation.

The ideal candidate will have a PhD in population genomics, excellent communication skills, and a technical skill set that includes at least one of the following: generation and analyses of population genomic NGS data; evolutionary, population genomics or demographic modelling; quantitative genetics and GWAS; programming, bio-informatics, experimental design and statistics. Experience and an interest in working with birds could be an advantage. The successful candidate should also have good interpersonal skills and an ability to work in a team. Although not a requirement, some knowledge of French would be an asset.

Job information The position is envisaged at 100% for an initial period of one year, with a possible renewal of one to three years, depending on funding. Most of the postdoc's time will be dedicated to research, but a contribution to teaching is expected, including the possibility of supervising master students.

— The starting date is flexible, but funding is available immediately.— Workplace : University of Lausanne, Dorigny What the position offers you We offer a nice working place in a multicultural, diversified and dynamic academic environment, opportunities for professional training. Possibilities of continuous training, a lot of activities and other benefits to discover.

Your application

Informal enquiries for further details of the aims of the project should be sent to Jérôme Goudet (jerome.goudet@unil.ch). Formal applications should include (in Word or Pdf.) a cover letter detailing your research interests, experience and motivation for applying, a CV, and the names of two or three referees. Applications should be uploaded through the University of Lausanne platform, and sent as a single pdf to jerome.goudet@unil.ch.

Theoretical population genetics: https://bit.ly/-2wAqzFK Population genomics: https://bit.ly/-2wA4gjn Applications received by June 3rd 2018 will receive full consideration.—

Jérôme Goudet Dept. Ecology & Evolution Biophore, UNIL-Sorge CH-1015 Lausanne http://www.unil.ch/-dee/goudet-group mail:jerome.goudet@unil.ch Tel:+41 (0)21 692 4242

jerome.goudet@unil.ch

UMassBoston Phylogenetics DeadlineExtended

Dear list.

We have extended the deadline to apply for a postdoctoral research position in my lab until May 25.

Note that the emphasis is on PCM development in R, but anyone working on the development & application of phylogeny methods should feel welcome to apply.

Please see more information below:

Postdoctoral fellowship in phylogenetic comparative method development (in R)

Applications are invited for a postdoctoral fellowship in the Revell lab at the University of Massachusetts Boston to work on phylogenetic comparative method development in R. Qualifications should include experience developing new theoretical approaches and/or applying methods in software.

This is a re-advertisement of a postdoc that I posted last year (but didn't fill), with two important updates:

1. The position is for a *minimum of 2 years* (given satisfactory progress, etc.) rather than for one year as previously advertised.

2. The postdoc is for *phylogenetic comparative method development in particular*, rather than phylogeny methods more broadly. [But see comment above.]

I consider phylogenetic comparative methods to include anything related to the use of phylogenies to make evolutionary inferences (rather than the estimation of phylogenetic trees) - but please contact me if you'd like clarification (liam.revell@umb.edu).

More information along with a link to apply is available on my blog: https://goo.gl/h97tKV . Note that the application deadline has been extended until May 25, 2018.

– Liam J. Revell, Associate Professor of Biology University of Massachusetts Boston & Profesor Asociado, Programa de Biología Universidad del Rosario web: http:/-/faculty.umb.edu/liam.revell/

UMinnesota FungalEvolution

Post-Doctoral Research Associate Position- Evolution of virulence in a rust fungus

A post-doctoral position in the Figueroa group at the University of Minnesota (https://plpa.cfans.umn.edu/-people/faculty/melania-figueroa) is available beginning in July 2018. The appointee will join an international project investigating the biology of the pathogenic rust fungus, Puccinia coronata f. sp. avenae, which inflicts significant yield losses in oat. The overarching goal of the project is to determine the role of sexual recombination in the epidemiology and pathogenicity evolution. The incumbent will participate in discovery of effectors in P. coronata f. sp. avenae. It is imperative that the postdoctoral researcher is available to travel internationally in fulfillment of research responsibilities and is expected to publish research results in refereed journals, present their research findings at national and international scientific meetings, and assist in preparation of nationally competitive grant proposals. Opportunities for teaching and supervisory experience are also available.

Interested candidates should submit application via the University of Minnesota Office of Human Resources website (https://humanresources.umn.edu/jobs, Job ID # 322783) which must contain 1) a CV, 2) a cover letter describing their qualifications, relevant experience and research interests and 3) names and contact information for 3 references. In addition to this, candidates should send the full application package as a single PDF file to Dr. Melania Figueroa (figue031@umn.edu). Please label the e-mail subject with: “oat rust-postdoc”.

Job Duties:

- Prepare material for next-generation sequencing of various oat crown rust populations.
- Conduct computational analyses on resequencing data of rust isolates to address questions delineated by the project.
- Communicate findings and interpretations to PI and team
- Prepare peer-review manuscripts and assists in the development of grant applications
- Travels to visit project collaborators and present work at scientific conferences
- Supervise undergraduate and graduate researchers in the group

Required Qualifications: Ph.D. in Plant Pathology, Evolutionary Biology, Genetics and Molecular Biology, and/or Bioinformatics (by the start of employment). Individual may be immediate post-degree or returning for additional training, updating, and/or retooling. Limited to fields for which post-degree training is necessary for career entry.

The successful applicant must demonstrate:

1) Experience with Linux and high performance computing environments.

2) Ability in applying statistical or machine learning methods in computational biology.

3) Experience in handling large genome-scale datasets.

4) Record of research achievement in population genetics and computational biology. Therefore, background knowledge in comparative/population/evolutionary genomics should be evident.

5) Experience with scripting/programming in Python, Perl, C++, R or similar and handling relational databases.

6) Strong track record of publications in the field or related disciplines.

7) Ability to work independently as well as within a research group.

8) Excellent oral and written communication skills.

Preferred Qualifications:

1) Background in plant-microbe interactions studies, particularly involving rust fungi

2) Experience in effector biology and functional validation of effector genes

3) Experience in genetic association studies

4) Ability to design new projects and foster new collaborations

Capacity to mentor and supervise students

Note: This position cannot be used to grant permanent residency for international appointees.

Melania Figueroa Assistant Professor Department of Plant Pathology University of Minnesota 495 Borlaug Hall 1991 Upper Buford Circle St. Paul, MN 55108 USA

email: figue031@umn.edu phone: 612-624-2291 http://plpa.cfans.umn.edu Melania Figueroa <figue031@umn.edu>

UMinnesota PopulationGenomicsSilphium

The Brandvain lab [goo.gl/EiEgDN] at the University of Minnesota is looking for a postdoc interested to combine the study of natural variation with ongoing domestication in Silphium integrifolium.

The work is a collaboration with evolutionary geneticitsts (me + nolan kane), crop breeders (kevin smith & brent hulke, david van tassel), and agronomists (craig sheaffer) which utilizes population and quantitative genomics of natural and early generation domesticates to aid in the domestication of Silphium integrifolium as a sustainable perennial crop plants.

There is much opportunity for creative basic and applied questions, and the ideal candidate would be interested in question in evolutionary genomics and plant breeding. Potential directions include genome assembly from w. oxford nanopore technologies, whole genome heritability and prediction, studies of , minion

A background in some combination of R, python, sequence analysis and/or assembly, population and/or quantitative genetics would be useful

Email ybrandva@umn.edu with informal inquiries

To apply, email ybrandva@umn.edu with (1) a cv (2) A statement of interest - who you are, what you're interested in, what you've done and why you're interested in this opening and (3) contact info for two letter writers

Start date SOON, Due date: SOONER

ybrandvain@gmail.com

UMontana EvolutionaryGenomics

Postdoctoral Research Associate - Evolutionary Genomics, University of Montana

The Miller Lab in the Division of Biological Sciences at the University of Montana, Missoula (http://hs.umt.edu/dbs/labs/miller) is hiring a postdoctoral research associate in the area of evolutionary genomics. The nature of the project is flexible but should investigate the mechanisms responsible for the origins and maintenance of bacterial diversity. Recent projects have focused on the mechanisms of gene duplicate retention in bacteria with exceptionally high duplication rates, the population genomics of local adaptation along an environmental gradient and the maintenance of variation by ancient balancing selection (http://www.nature.com/articles/s41559-017-0435-9). A Ph.D. in biology or a related field is required, and the successful candidate will demonstrate a strong background in molecular evolution and genomics as well as proficiency with Python and/or Perl.

The Division of Biological Sciences at the University of Montana (hs.umt.edu/dbs) is home to a diverse and highly interactive faculty, and the Miller lab is housed in newly constructed space dedicated to genomics research. Missoula is a great college town located in the heart of the Rocky Mountains with an exceptional quality of life. For more information on this position and our research, please contact Scott Miller at scott.miller@umontana.edu.

To apply, please visit http://umjobs.silkroad.com and click the job title for this position (Tracking Code 1811-254) under All Openings. Candidates must apply online and will be asked to upload the following application materials: a cover letter describing research interests and qualifications, a CV, and the names and contact information for three references. The appointment is a 12-month Letter of Appointment with flexible start date, renewable for up to two years with a possible extension to a third year.

University of Montana is an ADA/EOE/AA/Veteran's Preference Employer

"Scott.Miller@mso.umt.edu"
<Scott.Miller@mso.umt.edu>

UMontana Phylogenomics

Postdoctoral Research Associate 'V Phylogenomics, University of Montana

A postdoctoral position on species diversification and genome evolution in mammals is available in the laboratory of Jeffrey Good at the University of Montana, Missoula. The position is part of an NSF-funded collaboration to integrate comparative genomics with quantitative morphology to investigate the most species-rich radiation of mammals: Old World rats and mice (murines). Representing >10% of all living mammals, murines radiated over the last ~14 million years as the group repeatedly colonized Eurasia, Africa, and Indo-Australia. The two most powerful mammalian model organisms (mouse and rat) emerged from this radiation, providing fundamental genetic and genomic resources for a broad range of basic and applied research. We will leverage and expand these unique resources to assess phenotypic and genotypic convergence and evaluate relationships among lineage diversification, phenotypic novelty, and molecular evolution. The successful candidate will collect and analyze exome and whole genome sequence data to explore patterns and processes of genetic diversification across this remarkable radiation. We seek a candidate with a strong background in phylogenetics, evolution, and genomics. A Ph.D. in biology or a related field is required. Candidates with previous experience collecting and analyzing phylogenomic data are strongly encouraged to apply.

The University of Montana offers a vibrant research community. The Good lab shares newly constructed molecular and computational space with five other outstanding research groups, as part of an entire floor dedicated to evolutionary genomics research. Missoula is a great college town located in the heart of the Rocky Mountains of western Montana. For further information on this position and our research please visit the Good Lab website (thegoodlab.org) and email Dr. Good directly at jeffrey.good@umontana.edu. All applicants are encouraged to contact Dr. Good prior to applying.

To apply, please visit http://umjobs.silkroad.com and click the job title for this position under "Current Openings". Candidates must apply online, and will be asked to upload the following application materials: a cover letter describing your research interests and qualifications, a CV, and the names and contact information for three references. Applications will be reviewed upon receipt and the position will remain open until filled. The start date will be flexible contingent on the needs of the preferred candidate.

ADA/EOE/AA/Veteran's Preference Employer

– Jeffrey M. Good, Ph.D.

Associate Professor Division of Biological Sciences The University of Montana 32 Campus Drive, HS104 Missoula MT 59812 Phone: 406-243-5771 Fax: 406-243-4184 Website: http://www.thegoodlab.org/ Jeffrey Good <jeffrey.good@mso.umt.edu>

UNorthCarolina Charlotte CnidarianVenomEvolution

Postdoctoral position in genomics and transcriptomics of venom in cnidarians (Reitzel Lab)

A postdoctoral position is available to study genetic diversity and expression of venom genes in cnidarians in the lab of Adam Reitzel at the University of North Carolina at Charlotte.

Work in the Reitzel lab is focused broadly on the ecology and evolution of sea anemones. For this NSF-funded position, I am seeking a postdoctoral candidate to probe the genomic diversity and expression dynamics of venom genes in sea anemones from different populations and closely related species. Our goals are twofold: i) Determine the extent of genetic diversity for venom genes throughout a species' geographic range and over shallow evolutionary time; ii) Characterize differences in expression of these venom genes when these anemones experience different biotic and abiotic conditions.

Aspects of this work will primarily involve the anemone Nematostella vectensis, which has a broad geographic range in estuaries throughout North America. This project involves a direct collaboration with Dr. Yehu Moran's lab (Hebrew University, Jerusalem) to understand the function and potency of these venom proteins on prey and predators. Depending on the candidate, the project may involve field work and wet lab work but the focus will be primarily on generation and analysis of high throughput sequence data from existing samples. The selected candidate will have the opportunity to explore independent research directions during their time that contribute to a broader understanding of the evolution and ecology of venom.

Candidates

Applications are encouraged from individuals who have a Ph.D. or are nearing completion of their Ph.D. with experience in genome and transcriptome sequencing, annotation, comparative genomics and genome evolution. Interest or experience in venom research are desirable but not required. Top candidates will have a strong track record of research productivity and interest in collaborative science.

Candidates should send a cover letter, a detailed curriculum vitae, and names and contact details for three references as a single pdf file to: areitze2@uncc.edu. In the subject line, please use “Venom Postdoc Applicant”.

Start Date and Project Duration

The start date is ideally on or before July 1. The position is funded for one year at least and potentially longer depending on progress.

Contact

Adam Reitzel, Ph.D. Department of Biological Sciences University of North Carolina at Charlotte Charlotte, NC 28223 Email: areitze2@uncc.edu Web: https://sites.google.com/site/thereitzellab/ areitze2@uncc.edu

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UOxford AdaptiveDivergenceGenomics

NERC-funded Postdoc in the genomics of adaptive divergence and phenotypic plasticity on Senecio plants on Mt Etna, Sicily.

===The Department of Plant Sciences, University of Oxford is seeking to recruit a Postdoctoral Research Assistant.

This is an 18 month contract funded by the NERC. This grant is jointly held by Professors Simon Hiscock Dmitry Filatov and Jon Bridle (University of Bristol).

The work is to be conducted in the Department of Plant Sciences, University of Oxford, South Parks Road, Oxford, OX1 3RB in collaboration with research groups at the Universities of Bristol, Catania and Naples. The research topic is 'The genomic basis of phenotypic plasticity and adaptation in two closely related species of Senecio (ragworts) on Mt Etna, Sicily'.

The postholder will complete the final stages of the bioinformatic analyses of draft genomes for three Senecio species, analyses of transcriptomes from the study plants on Mt Etna, followed by analysis of candidate genes and preparation of associated manuscripts.

The postholder should have: i) a PhD or equivalent (or be very close to completion) in evolutionary biology, ii) a strong publication record in evolutionary genetics/genomics, iii) excellent quantitative skills, including experience in evolutionary genetic and bioinformatics analyses, iv) high motivation with intellectual curiosity and rigour, v) ability to work independently and manage multiple tasks, vi) ability to manage the day-to-day running of a research project, including supervision of research students, vii) excellent oral and written communication skills.

Desirable skills: experience of standard molecular biology techniques, experience of research in plant evolutionary biology, experience in high-throughput sequence data analysis in any species, expert knowledge of one or more scripting or programming languages (e.g. Perl, Python, Ruby, C++ or Java etc.).

Informal enquiries should be directed to Simon Hiscock: simon.hiscock@obg.ox.ac.uk.

The closing date for applications is 12.00 noon on Wednesday 30 May 2018.

Please see

https://www.recruit.ox.ac.uk/pls/-
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d=Y&p_refresh_search=Y&p_recruitment_id4363

For more details

Jon Bridle <Jon.Bridle@bristol.ac.uk>

UOxford MicrobialGenomics

Data Scientist in Microbiology and Postdoctoral Research Assistant in Molecular Microbiology

Big Data Institute, University of Oxford

Applications to be received by noon UK time Wednesday 6 June 2018.

Grade 7: 31,604 - 38,833 p.a. One year fixed term.

The Big Data Institute (BDI) at the University of Oxford is a new interdisciplinary research centre aiming to develop, evaluate and deploy efficient methods for acquiring and analysing biomedical data at scale and for exploiting the opportunities arising from such studies.

The Data Scientist role, split between the BDI and London, will be part of a team developing systems for continuous record linkage between Public Health England and other population health records. The aims are to design record linkage algorithms, manage front ends for viewing the data source, and analyse and interpret results. We're looking for a graduate or equivalent experience in computer science, data science, statistics, or any other relevant subject with a strong quantitative component. Knowledge of databases like SQL and computer programming are needed.

The Molecular Microbiology role, based mainly at the John Radcliffe Hospital Microbiology Department, will be part of a team researching Staphylococcus aureus infection using RNA sequencing, genome wide association studies, and biochemical and immunological assays of bacterial behaviour. The aims include designing microbiological protocols, researching bacterial molecular genetics and data analysis. We're looking for a PhD or equivalent experience in a relevant subject such as microbiology, immunology, genetics or biochemistry. Experience designing protocols and basic microbiological and immunological skills are required.

To apply or for more details on the Data Scientist role:

https://www.recruit.ox.ac.uk/pls/hrisliverecruit/erq_jobspec_details_form.jobspec?p_id4850

For the Molecular Microbiologist role:

https://www.recruit.ox.ac.uk/pls/hrisliverecruit/erq_jobspec_details_form.jobspec?p_id4744

– Associate Professor Daniel Wilson Wellcome Trust/Royal Society Sir Henry Dale Fellow Big Data Institute Robertson Fellow University of Oxford www.danielwilson.me.uk Daniel Wilson <daniel.wilson@bdi.ox.ac.uk>

UPennsylvania HumanComplexTraitEvolution

Postdoc position: Human complex trait evolution

Advisor: Iain Mathieson, Department of Genetics, Perelman School of Medicine, University of Pennsylvania, Philadelphia PA, USA.

We are looking for a computational postdoctoral researcher to work on a project using both ancient and modern DNA to investigate the evolutionary history of complex traits in humans. The project includes both methods development and data analysis. While specific goals are flexible according to your interests, broadly we are trying to address the following questions:

- What is the evolutionary history of complex-trait-associated alleles? - How have the effects and strength of natural selection changed over human history? - How has the distribution of common disease risk alleles been affected by demography and selection?

Researchers with interest or experience in human genetics, and a PhD or equivalent in computational biology, computer science, statistics, population/statistical genetics, or another relevant field are encouraged to apply. Programming experience (ideally in R or Python) is required, and some experience with ancient DNA, genome-wide association studies, and statistical population genetics would be helpful but not necessary.

Review of applications will start June 1st 2018 and continue until the position is filled. Start date is ideally September 2018, but flexible.

To apply, please email your CV, contact details of two or three referees, and a cover letter with a brief description of your research interests and highlighting up to three of your research achievements (papers, software, or other) to Iain Mathieson <mathi@pennmedicine.upenn.edu>. Please feel free to contact me with informal enquiries.

The Perelman School of Medicine strives to foster a vibrant, inclusive environment and fully embrace diversity. Minorities/Women/Individuals with disabilities/Protected Veterans are encouraged to apply.

Pontus Skoglund <pontus.skoglund@gmail.com>

UPuertoRico EvolutionaryFuncGenomics

REQUISITES The applicant must have a recent obtained (five year or less) PhD or equivalent in a biological sciences discipline and significant experience in molecular genetics and developmental biology, bench techniques including PCR, cloning, and sequencing library prep. Strong preference will be given to applicants with any of the following skills: analysis of short-read data in a Linux environment, construction and implementation of enhancer-reporter constructs, and CRISPR/Cas9 genome editing.

JOB DESCRIPTION Postdoc in evolutionary and functional genomics. We are seeking to hire a postdoctoral fellow for up to three years to work at the intersection of functional genomics and evolutionary developmental biology. The postdoc will work as part of a collaborative effort to determine what kind of genomic changes drive color pattern diversity in butterflies. The successful candidate will join the Riccardo Papa lab and be hired through the University of Puerto Rico, but will be physically based in the Robert Reed Lab at Cornell University. The postdoc will join a large group of researchers and directly interact with an international collaborative team that includes the Arnaud Martin Lab at George Washington University, the Owen McMillan Lab at the Smithsonian Tropical Research Institute, and the Brian Counterman Lab at Mississippi State University. The postdoc's research will specifically focus on regulatory evolution of the wing pattern morphogen gene WntA, which underlies development of the major central wing patterns. The regulation of this gene has diversified dramatically within and between species, and population genetic work shows that variation in expression can be traced to regulatory regions adjacent to WntA. We are now working to ask the questions (1) what are the cis-regulatory elements that drive the evolution of WntA expression, (2) how did these regulatory elements first arise, and (3) how are these elements evolving to produce morphological variation? We are asking this question both within species (Heliconius mimicry) and between species (the family Nymphalidae). Our primary experimental approach is to combine whole-genome comparative assays of regulatory element activity (ATAC-seq) with functional validation (CRISPR and reporter constructs). The successful candidate will be encouraged to visit and work in collaborating labs depending on specific experimental goals. The postdoc will produce first-author publications representing their own intellectually independent work.

TO APPLY Please submit IN A SINGLE PDF FILE: (i) a cover letter including motivation and research interests, (ii) a full CV that includes all requisites for the position, and (iii) contact information for two references electronically, and (iv) copies of all academic degrees**(diplomas and certifications) to butterflypostdoc@gmail.com and rpapa.lab@gmail.com. Review of applications will start immediately and will continue until the position is filled. Inquiries about the position can be directed to butterflypostdoc@gmail.com and rpapa.lab@gmail.com. APPLICATIONS SUBMITED WITH INCOMPLETE INFORMATION WILL NOT BE CONSIDERED.

**The selected candidate must present an official copy of all academic records

Riccardo Papa Associate Professor, Department of Biology Director of High Throughput Sequencing Facility University of Puerto Rico - RÃo Piedras Julio GarzÃa DÃaz (JGD) 213 Rio Piedras, San Juan PR 00931 tell: 787-764-0000 ext 4827(office) or 7764(lab) fax: 787-764-3875 Lab WebPage (under construction): http://www.wix.com/ricpapa/ Papa-Riccardo-Lab Topicos 2013 (Genomic Frontiers in Modern biology): http://biotopicsuprrp.weebly.com/index.html

Riccardo Papa <rpapa.lab@gmail.com>

USheffield ButterflyAdaptation

We are recruiting a postdoc to work with Dr. Nicola Nadeau on a 3-year NERC-funded project on thermal and altitudinal adaptation in the neotropical Heliconius butterflies. This exciting project aims to improve our understanding of thermal adaptation in tropical insects, particularly across altitudinal gradients. It will involve intensive rearing and phenotyping of butterflies to characterize both inter- and intra-specific differences in thermal adaptation at different altitudes in the Andes. This will be followed by generation and analysis of high-throughput genomic data to identify underlying genetic differences. The rearing and phenotyping will be conducted in Ecuador, therefore you will be expected to spend significant amounts of time working in Ecuador with partner organisations. You will have a strong commitment to evolutionary research with skills in at least one of: analysis of large genomic data sets; analysis of quantitative trait variation; or insect ecophysiology. The post will contribute to the research excellence of the Department of Animal and Plant Sciences through the generation of high profile research outputs. You will hold a PhD or equivalent experience in evolutionary biology and will have experience of research in evolutionary genetics and analysing large data sets.

Further information and to apply: https://jobs.shef.ac.uk/sap/bc/webdynpro/sap/hrrcf_a_posting_apply?PARAM=cG9zdF9pbnN0X2d1aWQ9Mzc2Qjk3QjNERjc5MUVEODk2OUY0Mz client=400&sap-language=EN&sap-accessibility=X&sap-ep-themeroot=%2fSAP%2fPUBLIC%2fBC%2fUR%2fuos# For informal enquiries contact Nicola Nadeau using the details below: – Dr Nicola Nadeau Dept. of Animal and Plant Sciences Alfred Denny Building, University of Sheffield Western Bank, Sheffield S10 2TN, UK N.Nadeau@sheffield.ac.uk Tel: +44 (0)114 222 4717 http://nadeau-lab.group.shef.ac.uk/ "n.nadeau@sheffield.ac.uk" <n.nadeau@sheffield.ac.uk>

USydney 3PDF 2PhD EvolutionaryPhilosophy

Three post-doctoral positions and two postgraduate fellowships in the Theory and Methods in Bioscience group at the University of the Sydney.

The skills required for these positions lie at the intersection of philosophy and the biosciences. While all current members of the Theory and Methods in Bioscience group are appointed in the Department of Philosophy, the possibility exists for a candidate to be appointed in the School of Life and Environmental Sciences within the Faculty of Science if such an appointment is more suitable given their career trajectory.

Postdoctoral Research Associate (Ref No. 651/0418F)

Postdoctoral Research Associates (Two Positions) Department of Philosophy, School of Philosophical and Historical Inquiry Faculty of Arts and Social Sciences Reference No. 651/0418F

Full time, fixed-term position for 3 years by negotiation, with the possibility of further offers for up to 2 additional years. Remuneration package from 106k p.a. to 114k p.a. (which includes base salary, leave loading and up to 17% superannuation)

These positions are part of the ARC Laureate Project A Philosophy of Medicine for the 21st Century. The appointees will work with Chief Investigator Professor Paul E. Griffiths and collaborators to develop a new vision of health and disease which can accommodate developments in contemporary biology and to make the discipline of philosophy an active participant in identifying new directions for integrative biomedical research.

Specific research topics will include:

* - Exploring and developing accounts of biological function and biological normativity through their application to data and theory in current biology and medicine * - Implications of life history theory and the developmental origins of health and disease paradigm for conceptions of health and disease * - Implications of genetic conflict perspectives and recent work on biological individuality for health and disease

The research will be conducted in close collaboration with the biomedical research community at the University of Sydney.

Closing Date May 13th

All applications must be submitted via the University of Sydney careers website. Visit sydney.edu.au/recruitment and search by the reference number to apply.

Postdoctoral Research Associate (Ref No. 659/0418F)

Postdoctoral Research Associate Department of Philosophy, School of Philosophical and Historical Inquiry Faculty of Arts and Social Sciences Reference No. 659/0418F

Full-time, fixed-term position for 3 years, remuneration package 106k p.a. to 114k p.a. (which includes base salary, leave loading and up to 17% superannuation)

The University of Sydney has received a grant from The John Templeton Foundation to explore the conceptual foundations of health and disease and of biological normativity, entitled Constructing Objective Biological Criteria of Health

The Research Fellow will work with Project Leader Professor Paul E. Griffiths and Co-Project Leader Dr Pierrick Bourrat to develop a new vision of function and purpose in living systems which reflects developments in contemporary biological theory

Specific research topics will include:

* - Evolutionary and other approaches to function and purpose * - Theories of the organism in light of contemporary biology * - Biological individuality * - Evolution of human cognition and its pathologies, with special attention to niche-construction perspectives on human evolution

The research will be conducted in close collaboration with the biomedical research community at the University of Sydney.

Closing Date May 13th

All applications must be submitted via the University of Sydney careers website. Visit sydney.edu.au/recruitment and search by the reference number to apply.

PhD scholarship in History and Philosophy of Nutrition Science

This PhD scholarship is part of the ARC Laureate project 'A Philosophy of Medicine for the 21st Century'. The research will use philosophical and historical perspectives on nutrition and related sciences to contribute to efforts to create an integrated multidisciplinary approach to nutrition. The position will be based in the Theory and Methods in Biosciences research group at the Charles Perkins Centre and jointly supervised by Laureate Fellow Prof. Paul Griffiths and Charles Perkins Centre Nutrition Theme Leader Prof. David Raubenheimer.

Applicants should have either a degree in history and/or philosophy of science and demonstrated interest in the biological and biomedical sciences or a degree in a relevant biological/biomedical field and a demonstrated interest and ability in the history and philosophy of science.

Applicants can apply for admission as a PhD candidate in either the Department of Philosophy (School of Philosophical and Historical Inquiry, Faculty of Arts and Social Sciences) or the School of History and Philosophy of Science (Faculty of Science). The successful candidate

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UToronto BacterialEvolutionaryGenomics

* Postdoctoral Position in Bacterial Evolutionary Genomics at the University of Toronto*

A postdoctoral position is available in the laboratory of David S. Guttman in the Department of Cell & Systems Biology at the University of Toronto, Ontario, Canada. The position is part of a CIHR/NSERC Collaborative Health Research Project team grant focused on using population genomic data to predict antimicrobial susceptibility of Pseudomonas aeruginosa infecting the cystic fibrosis lung. The candidate will employ evolutionary and comparative genomic, genome-wide association, and machine learning methods to identify resistance factors and predict antimicrobial susceptibility from an extensive longitudinal collection of strains.

Interested applicants should have a Ph.D. (or be very close to completion) in population, evolutionary, or statistical genetics or genomics. A strong background is evolutionary biology, mathematics and / or statistics is required. Some computational background is a desired, but training is available. The positions is available for a minimum of two years, subject to annual review, and can be started immediately.

The Guttman lab is a highly energetic and diverse group broadly focused on bacterial evolution in the context of host-microbe interactions. The lab aims to understand how bacterial pathogens adapt to changes in disease state or treatment over very short time scales in the CF lung; the evolution of host specificity and virulence and the emergence of new pathogens using the plant pathogen Pseudomonas syringae; and the role of microbial communities (microbiomes) in both human and plant health and disease. The Guttman lab is also closely associated with the Centre for the Analysis of Genome Evolution & Function (CAGEF), which is a genome centre with particular expertise in microbial and plant genomics and metagenomics. The genomic and bioinformatic resources afforded by CAGEF make the Guttman lab a particularly good place to work.

To apply, please send: 1) a cover letter outlining your previous experiences that make you suited for this position as well as your research and career goals; 2) a CV; and 3) contact information for three references: *david.guttman@utoronto.ca.*

More information about the Guttman laboratory can be found at guttman.csb.utoronto.ca, CAGEF at www.cagef.utoronto.ca, and the Department of Cell & Systems Biology at www.csb.utoronto.ca . The University of Toronto is the top university in Canada and ranked within the top 20 world-wide. It provides an outstanding scientific environment with a highly interactive community of researchers. The Guttman lab and University of Toronto are strongly committed to diversity and especially welcomes applications from racialized persons, persons of color, women, Indigenous / Aboriginal People, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas. Toronto is a diverse, vibrant, and cosmopolitan city; one of the most desirable in the world in which to work and live.

David S. Guttman Ph.D. Professor & Associate Chair for Research, Department of Cell & Systems Biology Director, Centre for the Analysis of Genome Evolution & Function University of Toronto Toronto, Ontario, Canada david.guttman@utoronto.ca

David Guttman <david.guttman@utoronto.ca>

UVienna PhD Postdoc EvolutionaryGenomics

Title: UVienna.PhD_Postdoc.EvolutionaryGenomics

Applications are invited for one Ph.D. and one postdoc position in the group of Qi Zhou in the Department of Molecular Evolution and Development at University of Vienna, Austria. Both are supported by the European Research Council (ERC) grant, and planned for two years for postdoc, and three years for Ph.D. with possible renewal. The successful applicants will use bioinformatic and experimental methods to study the evolution of Drosophila sex chromosomes. Most model species' sex chromosomes, e.g., those of human and D. melanogaster bear few traces of their evolution, because they are too ancient and have become too repetitive in sequence for investigation. A fundamental question concerns evolution biologist is what are the causes and consequences of Y chromosome degeneration? We will be using Drosophila species with recently born sex chromosome ('neo-sex') systems to address: How does the Y chromosome become epigenetically inert? How does this universal evolution process drive the adaptation of small RNA defence systems? And how does such a male-specific arms race between parasitic transposable elements and small RNAs fuel the changes of the female genome? The candidates are expected to be independent and highly motivated. Essential qualifications include demonstrated experience either in Drosophila genetics experiments (transgenics, CRISPR/Cas9 mutagenesis, in situ hybridisation) or bioinformatic studies (RNA-seq, ChIP-seq and corresponding NGS data analyses).

Successful applicants will receive very competitive salary and benefits (https://www.fwf.ac.at/en/research-funding/personnel-costs/), and enjoy the diverse and vibrant research environment of the Department and the University. The group members have frequent interactions with other neighbour labs of Drosophila neurobiology (Prof. Thomas Hummel) and developmental biology (Prof. Ulrich Technau), and have a chance to develop other collaborative research projects. The university is located in the city centre of Vienna, which houses numerous world's leading research institutes including Gregor Mendel Institute, Institute of Molecular Biotechnology and Institute of Science and Technology etc. The city now has gathered many great scientists in evolutionary biology (http://www.univie.ac.at/evolvienna/-?page_id=6), RNA biology (http://www.mfpl.ac.at/rna-biology/) and there is an encouraging plan to move the biology departments of the University near other institutes of Vienna Biocenter to form a new research cluster. Vienna has been voted as the world's most livable city for the eighth time, and is famous for its history and culture, and now also a modern and international lifestyle. Interested candidates please send her/his CV and contact information of three referees to Dr. Qi Zhou (qi.zhou@univie.ac.at). We will start reviewing the application immediately until the position is filled.

Qi Zhou <qi.zhou@univie.ac.at>

Yale PneumococcalEvolution

The Weinberger Lab at Yale School of Public Health (New Haven, CT) (https://medicine.yale.edu/lab/-weinberger/) is looking to hire a postdoctoral fellow for an NIH-funded study on the biological drivers of pneumococcal ecology and evolution, starting immediately. The goal of the project is to understand the biological and ecological drivers of changes in the bacterial population that have occurred following the introduction of pneumococcal vaccines. The ideal applicant will have strong experience in experimental microbiology/microbial ecology. Opportunities are available to shape the specifics and scope of the project. The research group is highly interdisciplinary and has individuals with expertise in microbiology, bioinformatics, mathematical modeling, and biostatistics. Experience with statistical programming (i.e., R) would be a plus. The candidate should be able to demonstrate evidence of strong written and oral communication skills and past productivity. The initial funding is for 2 years, with competitive pay. Please send a CV, 2 sample publications, and contact information for references to daniel.weinberger@yale.edu.

Assistant Professor Epidemiology of Microbial Diseases
Yale School of Public Health

Dan Weinberger <daniel.weinberger@yale.edu>

YaleU HIV phylogenetics

I have a one year computational phylogenetic postdoc position available in my lab. The postdoc will apply phylogenetic methods to identify potential transmission clusters on HIV phylogenies. These methods will include existing "phylodynamic" approaches, as well as new methods to be developed and implemented. Activities will include the use model-based approaches to identify transmission clusters based on HIV phylogeny structure, and longitudinal analysis of clusters through time as sequence data from new patients are added to the trees.

This position is supported by the newly funded NIH R01 award "Real Time Phylogeny and Contact Tracing to Disrupt HIV Transmission". This exciting collaboration, led by [Dr Rami Kantor](https://vivo.brown.edu/display/rkantor) and including colleagues from the Rhode Island Department of Health and other institutions, seeks to integrate real time phylogenetic and phylodynamic analyses of HIV sequence data into public health interventions to disrupt HIV transmission. Collaborators will acquire sequence data and generate phylogenetic trees that will serve as the starting point for the postdoc???s work. All patient data will be fully anonymized, and the postdoc will not work with any materials that are identifiable to patients.

Details

Please share this link to the ad: https://git.io/yale_postdoc_2018 Advisor: [Casey Dunn](http://dunnlab.org)

Location: [Department of Ecology and Evolutionary Biology](https://eeb.yale.edu), [Yale University](https://www.yale.edu), in New Haven, Connecticut, USA

Application due date: June 1, 2018 (or until filled)

Start date: September 1, 2018

Research skills sought

The successful candidate will have expertise and experience in the following areas: - Phylogenetic methods, including a solid grounding in phylogenetic models and phylogenetic comparative methods - Computational biology, including R and/or python, git, and common statistical methods

The following areas of expertise are desirable but not required: - Virus evolution - HIV biology - Epidemiology

Your application

Interested candidates should e-mail me at casey.dunn@yale.edu with the following items and information:

- CV - A brief description of why you are a good fit for the position - If available, a link to your GitHub profile, or other relevant accounts, with examples of code and analyses you have worked on in the past.

I will then request follow-up materials, including references, from the most suitable candidates. Applications will be considered until the position is filled, but please submit your application by the due date above to receive full consideration.

The candidate must have completed all requirements for a doctorate degree by the start date.

Workplace and lab environment

In the [Dunn Lab](http://dunnlab.org), we place a strong emphasis on open reproducible science and industry-standard tools (like Slack, Docker, and GitHub) for computational biology. See our [publications list](http://dunnlab.org/#publications) for links to preprints and git repositories associated with our papers. This builds on our work training biologists in general-purpose computational tools, including the book [Practical Computing for Biologists](http://practicalcomputing.org) that I co-authored. The postdoc who works on this computational project will benefit intellectually from interactions with others in the lab who are working on a variety of other phylogenetic projects, both theoretical and empirical. Many other labs in the [Yale Department of Ecology and Evolutionary Biology](https://eeb.yale.edu) also work on phylogenetic biology, providing a strong broader community.

Yale University is an Equal Opportunity/Affirmative Action Employer. Yale values diversity among its students, staff, and faculty and strongly welcomes applications from women, persons with disabilities, protected veterans and under-represented groups.

"Dunn, Casey" <casey.dunn@yale.edu>

WorkshopsCourses

Australia Scotland SpeciesDistributionModelling June

TWO Species Distribution Modelling (SDM) Courses in Australia and Scotland

SDM's are increasingly being used in evolutionary biology as part of the process in understanding how and why animals adapt top new niches.

1) Species distribution models using R (SDMR01) - Registration deadline approaching 21/05/2018!! https://www.prstatistics.com/course/species-distribution-models-using-r-sdmr01/ Delivered by Prof. Jane Elith, Dr. Gurutzeta Guillera and Jose Lahoz-Monfort from 12th - 15th June 2018 at Myuna Bay Sport and Recreation, Wangi Road, Myuna Bay, New South Wales 2264 Australia.

2) Species distribution/occupancy modelling using PRESENCE and R (OCCU01) https://www.prstatistics.com/course/species-distributionoccupancy-modelling-using-r-occu01/ Delivered by Dr Darryl MacKenzie form 25th - 29th June 2018 at PR statistics head office, 53 Morrison Street, Glasgow, Scotland, G5 8LB

1) Species distribution models using R (SDMR01) Course Overview: The aim of this four-day course is to work towards an understanding of, and practical ability to fit, species distribution models (SDMs). It will be useful if you plan to use SDMs, or if you just want to understand them better. We will focus on statistical models of species distributions - those that combine observed species records with environmental data. Using a mixture of lectures, computer exercises and case studies, participants will learn to: 1) identify relevant data, and prepare it for modelling; 2) fit models using several modelling methods (including Maxent, generalized linear models and their extensions, and boosted regression trees); 3) consider how to model species if detection is imperfect; 4) evaluate models and interpret them; 5) understand the range of practical issues that arise in typical applications of SDMs. Practical sessions will use the free statistical software, R - prior experience (even if some practice before you come) will be useful. Example data will be provided but participants may also bring their own data. Presenters include Jane Elith and Gurutzeta Guillera-Arroita, who are highly experienced in SDMs.

2) Species distribution/occupancy modelling using PRESENCE and R (OCCU01) Course Overview: The

presence or absence of a species across a set of landscape units is a fundamental concept widely used in ecology (e.g., species range or distribution, epidemiology, habitat modeling, resource selection probability functions, as a monitoring metric, metapopulation studies, biodiversity and species co-occurrence). An important sampling issue, however, is that a species may not always be detected when present at a landscape unit. This will result in "false absences" causing parameter estimates to be biased if unaccounted for, possibly leading to misleading results and conclusions, even with moderate levels of imperfect detection. This workshop will cover many of the latest methods for modeling patterns and dynamics of species occurrence in a landscape while accounting for the imperfect detection of the species. Including: - estimating level of occurrence at single point in time - identifying factors that influence species occurrence - creating species distribution maps - modelling changes in distribution over time - study design Participants will be introduced to available software through worked examples, and there will be special emphasis on aspects of study design. While primarily aimed at the beginner and intermediate level, more experienced researchers will also benefit from attending. The first four days will comprise of formal lectures and exercises, and the final morning will be an informal discussion/consulting session where participants can work on their own data, talk one-on-one with the instructor, etc.

If you have any questions please feel free to email oliverhooker@prstatistics.com

Oliver Hooker PhD. PR statistics

2018 publications -

Phenotypic and resource use partitioning amongst sympatric lacustrine brown trout, Salmo trutta. Biological Journal of the Linnean Society. DOI 10.1093/biolinnean/bly032

prstatistics.com facebook.com/prstatistics/ twitter.com/PRstatistics groups.google.com/d/forum/prstatistics-post-course-forum
prstatistics.com/organiser/oliver-hooker/

6 Hope Park Crescent Edinburgh EH8 9NA

+44 (0) 7966500340

Oliver Hooker <oliverhooker@prstatistics.com>

Barcelona EcoEvolutionOmics Jul8-13 LastCall

Course Announcement: Ecology through the omics lens. Last Call.

Dear colleagues, We still have few spots available for the 6th edition of the Ramon Margalef Summer Colloquia: 'Ecology through the omics lens' organized by the Marine Sciences Institute (ICM-CSIC) which will take place from July 8th - 13th in Barcelona, Spain.

Deadline for applications is extended until 10th of May!

Course Overview: The use of omics techniques has spread rapidly across the field of Ecology and Evolution during the last decade, but there is substantial work ahead to link the obtained results with the existent ecological theory. The course aims to move from "what" to "why" when using omics approaches to study the ecosystem, as well as to frame their omics-based research in a theoretical ecological fr amework. The course will cover different environments (marine, terrestrial, host associated) as well as organismal sizes (from microbes to plants and animals), thus becoming an excellent opportunity to bring together researchers with similar questions, but working in fields that seldom communicate between each other.

The Colloquium will be structured in 4 sessions. Each session consist of a combination of lectures, and group discussions. Take a look at the CONFIRMED SPEAKERS at: http://www.acoio.org/margalef-summer-colloquia/program/ or see below.

INTENDED AUDIENCE: Advanced doctoral students and early post-docs are encouraged to apply.

Deadline for applications is extended until 10th of May.

FELLOWSHIPS to students from developing countries are available. DISCOUNTS for ISME members, SCB members and BIB members.

For more information and registrations, go to: http://www.acoio.org/margalef-summer-colloquia or contact us to: margalefcolloquia[a]acoio.org

PRELIMINARY PROGRAM:

-Session 1: Populations, Community and Functional Ecology Silvia G. Acinas, Institut de Ciències del Mar (CSIC), Spain Marta Pascual, Universitat de Barcelona, Spain Jed Fuhrman, University of Southern California, USA

-Session 2: Ecosystem ecology Damien Eveillard, Université de Nantes, France Marta Goberna, Centre d'Investigacions sobre Desertificació (UV-CSIC), Spain TBC

- Session 3: Evolutionary Ecology and Co-evolution Naiara Rodríguez-Ezpeleta, AZTI, Spain Esther Garcés, Institut de Ciències del Mar (CSIC), Spain Purificación López-García, Ecologie, Systémati que et Evolution, Université Paris-Sud-CNRS, France Alex Mitchell, The European Bioinformatics Institute, UK

- Session 4: Quantitative and Theoretical Ecology Pedro Cermeño, Institut de Ciències del Mar (CSIC), Spain Santiago F. Elena, IBMCP (CSIC-UPV) & 2SysBio (CSIC-UV), Spain; The Santa Fe Institute, Santa Fe, USA TBC

- Wrap-up Session: Carles Pedrós-Alió, National Center for Biotechnology (CSIC), Spain Marta Estrada, Institut de Ciències del Mar (CSIC), Spain

Best regards,

Dr. Javier del Campo, Dr. Ramiro Logares and Dr. Celia Marrase Ramon Margalef Summer Colloquium 2018 Organizers

WEB: www.acoio.org/margalef-summer-colloquia FACEBOOK: www.facebook.com/MargalefSummerColloquia VÃDEO: www.youtube.com/watch?v=Mlyfgt1bN_E&feature=youtu.be margalefcolloquia@acoio.org

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Barcelona EvolutionaryNGS Jul2-6

Dear all,

here you can find information about the postgraduate course "INTRODUCTION TO NEXT-GENERATION SEQUENCING: APPLICATIONS IN ECOLOGY AND EVOLUTION" (3 ECTS credits) which whill take place in the Faculty of Biology (Universitat de Barcelona), Barcelona, from 2nd to 6th July. The Institut BotÃ nic de Barcelona (CSIC), the Universidad Rey Juan Carlos and the IRBio-Universitat de Barcelona participate in the course organisation, with the support of the Fundacion General CSIC.

The course is aimed at graduates, postgraduates and PhD students on Evolutionary Biology and related sciences, interested in knowing the new tools and the potential that is being developed with the new techniques of massive parallel sequencing. No specific training in bioinformatics is necessary although basic knowledge is desirable.

The main objective of this course is to show a battery of potential applications of the NGS by researchers who are currently working with this technological approach. As an introductory course, the main purpose is not looking for a complex or deep training in a specific technique, but to give a broad view of the available approaches.

The assistant to this course should end with the feeling of knowing the techniques and their applications, with the purpose of being able to assess which ones may be interesting for their research or on which to deepen in later stages.

The specific objectives are:

1. To present an updated information on the different NGS techniques and their applications, potential and complexity.

2. To provide basic training in the main software for each of the techniques, as well as in data processing, and give tips on how to expand knowledge. This includes from the quality analysis, edition and analysis of the files to the interpretation of results. We aim that, with this basic knowledge, the student can be trained later if he is interested in a specific aspect of the ones addressed (for example, attending specialized courses or self-taught).

3. To favour the contact between students interested in specific techniques with teachers and specialized personnel, for possible collaborations or training. Please visit our website to have more information about the course content: http://www.ibb.csic.es/en/formacio/col% C2%B7laboracions-en-docencia/curs-postgraduat/ Online enrolment: https://www.ub.edu/acad/npost/fitxes/3/201711079.php Enrolment deadline: 25/06/2018 LIMITED CAPACITY

S0nia Garcia Institut BotÃ nic de Barcelona (CSIC) Passeig del Migdia s/n | 08038 Barcelona | Tel. (0034) 932 890 611 | Fax (0034) 932 890 614 soniagarcia@ibb.csic.es | sphaeromeria@gmail.com | skype: sonia.garcia31

SÃ²nia Garcia <sphaeromeria@gmail.com>

Barcelona MacroevolutionOnPhylogenies Oct8-11

Dear colleagues,

Registration is open for the following course: “Using Geiger, Phytools, and other Computational Tools to Study Macroevolution on Phylogenies”

Dates: October 8th-11th, 2018, Barcelona (Spain).

Place: Capellades, Barcelona (Spain).

Instructors: Dr Liam Revell (University of Massachusetts Boston, USA) and Dr Luke Harmon (University of Idaho, USA).

PROGRAM

Monday, October 8th, 2018.

- Introduction to phylogenies and the comparative method.—[Lecture] - Introduction the basics of the R statistical computing environment.—[Exercise] - Introduction to reading, writing, manipulating, and visualizing phylogenies and comparative data in R.—[Exercise] - Models of phenotypic trait evolution on trees: Brownian motion.—[Lecture] - Simulating Brownian motion on trees using R.—[Exercise] - Introduction to the phylogenetic comparative method: Phylogenetic independent contrasts.—[Lecture] - Phylogenetic independent contrasts and exploring the properties of contrasts regression using simulation in R.—[Exercise] - Phylogenetic generalized least squares regression and phylogenetic generalized ANOVA.—[Exercise]

Tuesday, October 9th, 2018.

- Multivariate statistical methods with phylogenies: Phylogenetic principal components analysis, canonical correlation analysis, and other approaches.—[Lecture] - Phylogenetic PCA and phylogenetic CCA in R.—[Exercise] - Continuous character models of trait evolution on phylogenies.—[Lecture] - Fitting continuous character models to univariate trait data in R.—[Exercise] - Ancestral state reconstruction I: Continuous characters.—[Lecture] - Reconstructing ancestral states for continuous traits on phylogenies using R.—[Exercise]

Wednesday, October 10th, 2018.

- Ancestral state reconstruction II: Discrete characters.—[Lecture] - Reconstructing ancestral states for discrete traits on phylogenies using R.—[Exercise] - Exploring the limitations of ancestral state reconstruction for continuous and discrete characters on phylogenies using R.—[Exercise] - Testing for the influence of one discrete character on a second using Pagel’s (1994) method.—[Lecture] - Exploring the promise and limitations of the Pagel (1994) method using R.—[Exercise] - Analysing discrete character coevolution, and the evolution of discrete and continuous characters using the threshold model.—[Lecture]

Thursday, October 11th, 2018.

- Fitting models of discrete and continuous character evolution on trees using the threshold model.—[Exercise] - Multi-rate, multi-regime, and multivariate models of character evolution on phylogenies.—[Lecture] - Fitting multi-regime and multivariate models for continuous character evolution in -—[Exercise] - Visualizing trees and phylogenetic comparative data.—[Lecture] - Plotting phylogenies and comparative data using R.—[Exercise] - Wrap-up and optional additional exercise or lecture.

More information and registration (https://www.transmittingscience.org/courses/evolution/using-geiger-phytools-other-computational-tools-study-macroevolution- phylogenies/)

With best regards

Sole

Soledad De Esteban-Trivigno,PhD. Scientific—Director Transmitting Science (http://www.transmittingscience.org/)

Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.org>

Berlin IntroToR Jun18-22 LastCall

Getting started with R

Where: Berlin

When: 18-22 June 2018

Instructor: Dr. Alexandre Courtiol (Reearcher at the IZW, Berlin).

R is extremely powerful, free of charge and open source. Despite these benefits, many avoid R, or struggle with it, as writing computer code to do any operation – a requirement in R – is at first both difficult and intimidating.

This course aims at overcoming those challenges by providing solid basics in R. At the end of the course, participants should feel much more at ease writing a computer script in the R language which covers the entire spectrum of a statistical analysis: reading data, editing them, plotting them, and analysing them.

This course is aimed at scientists from quantitative sciences (e.g. biology, epidemiology, psychology...). It has been created with biologists in mind but it should accommodate scientists from other disciplines. No previous experience with R is required. Participants should have a basic familiarity with statistical terms and concepts.

For more information please visit our website

(https://www.physalia-courses.org/courses-workshops/-course13/)

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

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mobile: +49 15771084054

https://groups.google.com/forum/#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Berlin RADseq Jul2-6

Dear all,

we will run a RAD-seq data analysis Workshop based on Stacks 2.0 this July (2nd-6th) in Berlin, with Dr. Julian Catchen (University of Illinois, Urbana-Champaign; http://catchenlab.life.illinois.edu/) and Dr. Josie Paris (University of Sussex, UK).

In this course, we will introduce the different approaches for obtaining reduced representation genome sequencing data and will specially focus on the data analysis. We will cover all necessary steps to obtain genome variants from short read data that are informative for population genetics, phylogenetic and association studies.

This course is aimed at researchers and technical workers who are generating and/or analyzing reduced representation genome sequencing data (RAD-seq, ddRAD, 2bRAD, GBS,). Examples demonstrated in this course will involve primarily non-model organisms and examples of applications of this data type for different purposes will be covered. Attendees should have a background in biology. We will dedicate one session to some basic and advanced Linux concepts. Attendees should have also some familiarity with genomic data such as that arising from NGS sequencers.

Please visit our website to have more information about the course content: https://www.physalia-courses.org/-courses-workshops/course16/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Best regards,

Carlo

Carlo Pecoraro, Ph.D

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Berlin RADseq Jul2-6 LastCall

Dear all, last weeks to apply for our RAD-seq data analysis Workshop based on Stacks 2.0 this July (2nd-6th) in Berlin, with Dr. Julian Catchen (University of Illinois, Urbana-Champaign; (http://catchenlab.life.illinois.edu/)) and Dr. Josie Paris (University of Sussex, UK).

We have the last 4 places left and attendees are seated on a first-come, first-served basis.

In this course, we will introduce the different approaches for obtaining reduced representation genome sequencing data and will specially focus on the data analysis. We will cover all necessary steps to obtain genome variants from short read data that are informative for population genetics, phylogenetic and association studies.

This course is aimed at researchers and technical workers who are generating and/or analyzing reduced representation genome sequencing data (RAD-seq, ddRAD, 2bRAD, GBS,$B!D(B). Examples demonstrated in this course will involve primarily non-model organisms and examples of applications of this data type for different purposes will be covered. Attendees should have a background in biology. We will dedicate one session to some basic and advanced Linux concepts. Attendees should have also some familiarity with genomic data such as that arising from NGS sequencers.

Please visit our website to have more information about the course content: (https://www.physalia-courses.org/courses-workshops/course16/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

Best regards,

Carlo

Carlo Pecoraro, Ph.D

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Berlin Rcourses June

Dear all,

we will run two R courses this June!

1) Getting started with R (18-22 June 2018) with Dr. Alexandre Courtiol (Leibniz Institute for Zoo and Wildlife Research, Berlin (Germany)):

https://www.physalia-courses.org/courses-workshops/course13/ This course aims at overcoming those challenges by providing solid basics in R. At the end of the course, participants should feel much more at ease writing a computer script in the R language which covers the entire spectrum of a statistical analysis: reading data, editing them, plotting them, and analysing them. Because linear models are the dominant statistical tool in many fields, the part of the course focusing on analyses per se (see schedule) will focus on those, but principles seen during the class should greatly help those interested in other kind of analyses as well. The course will be presented over five days and will mix explanations and guided exercises. Students are free to practice with their own datasets during the course.

—-

2)Advanced R Programming (25-29 June 2018) with VP Nagraj (University of Virginia (USA))

https://www.physalia-courses.org/courses-workshops/course26/ The goal of this course is to provide training on how to start using R as a programming language: to write new functions, develop new tools or, at the very least, interact with data programmatically. While some examples may be drawn from bioinformatics, statistics and / or epidemiology, the material will not focus on data analysis techniques. As such, the course will generally be domain-agnostic. Researchers from a variety of disciplines are welcome. Those interested should have basicfamiliarity with R or another programming language.

—-

Best regards,

Carlo

"info@physalia-courses.org" <info@physalia-courses.org>

Berlin SpeciationGenomics Dec3-7

Course: Speciation Genomics

Berlin, 03-07 December 2018

Instructors:

Dr. Mark Ravinet (CEES, Univeristy of Oslo, Norway)

Dr. Joana I. Meier (University of Cambridge, UK)

Overview

This course will provide a thorough introduction to the growing field of speciation genomics. The course aims to take students from the initial steps required for handling raw sequencing data to demographic modelling and inference of genome-wide signatures of selection and introgression. Through a combination of lectures covering key theoretical and conceptual topics, alongside hands-on exercises, participants will learn the most important computational approaches used in speciation genomics. This will include a heavy emphasis on data visualization and intepretation. After completing of the course, the participants should be able to begin using NGS data to shed light on the genomic aspects of speciation in their study system of choice.

Format

This course is designed for researchers and graduate students with strong interests in applying novel high-throughput DNA sequencing technologies to study the population genomic basis of speciation. The course will mainly focus on the analysis of NGS data for study systems for which a reference genome is available. We will provide theoretical lectures and hands-on exercises drawing on examples of whole-genome resequenced and RAD-sequencing data. Participants will make use of the UNIX command line, R and Python throughout the course.

Assumed Background

The participants should have some basic background in evolution and genomics. No programming or scripting expertise is required. Previous experience in UNIX-based command line and R is an advantage but a standard introduction will be provided. All hands-on exercises will be run in a Linux environment on remote servers. Statistical analyses will be run in R using RStudio.

Learning Outcomes

Handling NGS data from raw reads to genetic variants Applying basic population genetic statistics Visualizing the genetic structure Inferring demographic history Identifying regions under divergent selection or barriers to gene flow Understanding the potential and limitations of different methods to detect regions under selection

—

Please visit our website to have more information about the course content: https://www.physalia-courses.org/courses-workshops/course37/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 15771084054 https://groups.google.com/forum/#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Berlin TrinityRNAseq Jun11-15 deadline

Dear all, the registration deadline for the Trinity Workshop (Berlin, 11-15 June 2018), with Brian Haas (Broad Institute, USA) and

Dr. Nicolas Delhomme (UmeÃ¥ Plant Science Center, Sweden), is soon approaching (May 11th).

We still have a few spots available. For more information about the Workshop, please visit our website: (https://www.physalia-courses.org/courses-workshops/course11/)

Should you have any questions, please do not hesitate to contact us.

Best regards,

Carlo

Carlo Pecoraro, Ph.D

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https://groups.google.com/forum/#!forum/physalia-courses info@physalia-courses.org

Buffalo NY AnthropologicalGenomics Aug1-3

Registration now is open for the 2018 Application of Genetics to Anthropological Research (AGAR) Bioinformatics Workshop. This year's workshop will provide students and scholars with experience in analyzing genomic data from installing and combining software to running variant call analyses, visualizing data, and testing for functional enrichment of significant regions. AGAR 2018 is partially funded by the National Science Foundation (Grant No. 1714867) and being organized by the American Association of Anthropological Genetics (AAAG) Education Committee. Workshop sessions are as follows:

Session 1: GNU Make and Version Control Introduction to installing and combining software for downstream analyses Session 2: GATK Basics of sequencing and BAM files: read depth, false-positive, false-negative, etc. Run variant calling pipeline starting with a BAM file and producing a VCF file

Session 3: VCF-tools Basics of VCF file Output data details: SNP density, Fst, Tajima's D, heterozygosity, etc.

Session 4: Data Visualization Basics of visualizing data: Tidy R, Tidyverse, Bioconductor, etc.

Session 5: Functional Genomics Investigate outliers and associated haplotypes for their impact on gene expression function, loss of function variants, GWAS variants, regulatory activity, etc.

Session 6: Statistical Considerations Basics of multiple testing correction methods and selection Optimize computing time by taking advantage of multiple processors

Session 7: Interval/Overlap Analyses Investigate if outliers in heterozygosity are enriched for particular genomic elements Basics on cross-species analyses and gene enrichment (GO, KEGG)

Dates: August 1-3, 2018

Location: University at Buffalo (SUNY), Buffalo, NY-COST

Thanks to NSF support, we will are able to offer registration at a highly reduced fee for students and postdocs:

Students: $100 Postdocs: $150 Faculty: $200

Lodging in dorms will be available at a cost of $100-$150 per night.

QUESTIONS Email Omer Gokcumen (omergokc@buffalo.edu) or Joanna Malukiewicz (jmalukie@gmail.com).

REGISTRATION Due to space limitations, individuals interested in participating in the AGAR workshop are required to apply. Attendees will be selected from the pool of applicants on the basis of the relevance of the material covered to the applicant's work. We anticipate that we will be able to accept the majority of applicants, but early career applicants will be given preference if there is insufficient space.

APPLICATIONS MUST BE RECEIVED NOT LATER THAN MAY 31, 2018. You will be notified on June 7 if you have been selected for a spot and will then have until June 30 to register for the workshop. Individuals requesting to be considered for financial aid will be notified if funds will be provided on June 7.

Registration Form Available Here: https://docs.google.com/forms/d/e/-1FAIpQLSdIBeTaR559KghGBPCKSJlW9yYMyIsbIgpcYii5HrtBEE5b-w/viewform Joanna Malukiewicz <jmalukie@gmail.com>

CatalinaIsland GenomicsWorkshops Aug10-26

Hi Colleagues,

We still have a few spots available in our summer genomics workshops on Catalina Island. This year we are including gene expression profiling with Tag-Seq, a cost-effective and accurate method that's been widely used in studies of corals, plants, and other non-model systems. And as usual, we are offering a workshop on SNP genotyping with 2bRAD, a similarly cost-effective method well-suited for non-model systems of interest for evolutionary biologists.

Our workshop includes the wet-lab procedures required to prepare sequencing libraries from biological samples and the computational procedures for converting raw DNA sequences into biological information.

The registration fee covers 1) Room and board (3 prepared meals a day, coffee & tea, and snacks) 2) Pilot data from your organism of interest 3) Training in each step of the process from nucleic acids in a tube to a spreadsheet describing gene expression or genotypes 4)

Participation in a group project to be written up in a joint publication

For more details, see our website at http://people.oregonstate.edu/˜meyere/workshops.html For questions about registration or logistics contact Demian Willette (demian.willette@lmu.edu). For specific questions about 2bRAD, contact Eli Meyer (eli.meyer@oregonstate.edu). For specific questions about Tag-Seq, contact Carly Kenkel (ckenkel@usc.edu). To reserve your spot, please confirm your participation no later than June 15 and pay registration fee no later than July 15th, 2018.

Thanks, hope to see some of you on Catalina this summer!

-Eli Meyer, Demian Willette, & Carly Kenkel

“meyere@oregonstate.edu” <meyere@oregonstate.edu>

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cE3c-Portugal Biology 2018-2019

Subject: Portugal-cE3c-Advanced Courses 2018/2019

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing 19 Advanced Courses during the scholar year 2018/2019@ Lisbon, Portugal

The detailed program of the Advanced Courses organized by cE3c for the academic year 2018/2019 is already available. They are 19 in total, of which 4 are new.

These courses are aimed for students enrolled in Doctoral Programmes in the Biology area. They can also be attended by post-graduate students of other Doctoral Programmes or Masters in Biology, or others with basic biology formation (such as BSc in Biology or related areas). In particular, attending these courses is free for students currently in the 1st year of the Doctoral Programmes in:

- Biology (FCUL),
- Biodiversity, Genetics and Evolution - BIODIV (ULisboa and UPorto), and
- Biology and Ecology of Global Changes - BEAG (ULisboa and UAveiro).

The courses have in general an intensive format, with one week of duration, being recognized for the 1st year of the Doctoral Programmes of PhD students of the Faculty of Sciences of the University of Lisbon (FCUL; 5-6 ECTs). Some have a shorter format (see details in each course’s programme).

We detail below the list of courses, corresponding teachers and calendars. More details (including programmes, prices and procedures for applications) can be found at:

http://ce3c.ciencias.ulisboa.pt/training/?cat Advanced Courses cE3c 2018/2019

October 15th to October 19th 2018 - Entomological Collections, Insect Systematics and Evolution (Luís Filipe Lopes et al.). Deadline for applications September 15th 2018.

October 22nd to October 26th 2018 - Bioinformatics analysis of biological sequences (Teresa Nogueira & Rita Ponce). Deadline for applications September 28th 2018.

November 5th to November 9th 2018 - Natural History Collections and Biodiversity (Maria Judite Alves et al.). Deadline for applications October 12th 2018.

November 12th to November 16th 2018 - Production of Science Communication Activities (Cristina Luís & Patricia Garcia Pereira). Deadline for applications October 12th 2018.

January 7th to January 11th 2019 - Scientific Writing and Communication (Gabor Lövei). Deadline for applications November 30th 2018.

January 14th to January 18th 2019 - Hands on Functional Diversity: from Ecological Indicators to Ecosystem Services (Laura Concostrina-Zubiri, Paula Matos, Alice Nunes et al.). Deadline for applications December 14th 2018.

January 21st to January 24th 2019 - Island Biogeography (Ana Margarida Santos et al.). Deadline for applications December 14th 2018.

January 28th to February 1st 2019 - Soil ecology and ecosystem services (Teresa Dias & Cristina Cruz). Deadline for applications: December 28th 2018.

February 4th to February 8th 2019 - Until death do us apart: living in a symbiotic world (Silvana Munzi, Cristina Cruz, Luis Carvalho, et al.). Deadline for applications December 14th 2018.

February 4th to February 8th 2019 - Practical course on Phylogenetics (Octávio Paulo). Deadline for applications: January 11th 2019.

February 11 th to February 15 th 2019 - Introduction to R for ecology and evolutionary biology (Vitor Sousa & Inês Fragata). Deadline for applications: January 11th 2019.

February 19th to February 22nd 2019 - Urban Ecology: the green within the city (Ana Catarina Luz, Pedro Pinho, Cristina Branquinho, et al.). Deadline for applications January 18th 2019.

March 18th to March 20th 2019 - Science and the Media (Marta Daniela Santos). Deadline for applications February 15th 2019.

May 13 th to May 17 th 2019 - Nature-Based Design Frameworks (Gil Penha-Lopes & Hugo Oliveira). Deadline for applications April 19th 2018.

June 3rd to June 7 th 2019 - Practical course on Phylogeography (Octávio Paulo). Deadline for applications May 10th 2019.

June 17 th to June 21st 2019 - Applied Methods in Community Ecology and Functional Ecology (Paulo Borges & François Rigal). Deadline for applications April 26th 2019.

June 24th to June 28 th 2019 - Measuring Biodiversity: How to get data, assess its quality and measure different aspects of diversity (Joaquín Hortal). Deadline for applications: May 31st 2019.

July 8th to July 12th 2019 - Stable isotopes in Ecology and Environment: a tool to integrate scales and complexity (Cristina Máguas). Deadline for applications June 1st 2019.

July 15th to July 19th 2019 - Lichens as a Tool for Interpretation of Environmental Changes and Management (Silvana Munzi, Pedro Pinho, Paula Matos et al.). Deadline for applications June 7th 2019.

Margarida Matos

Executive Committee of Centre for Ecology, Evolution and Environmental Changes

Faculdade de Ciências da Universidade de Lisboa

Margarida Matos, PhD Associate Professor

Researcher ID: K-2365-2012

ORCID ID: 0000-0001-6998-5133

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cE3c Portugal MeasuringBiodiversity Jun25-29

Subject: Portugal-cE3c-Course Measuring Biodiversity-June 25th-29th 2018

cE3c 'V Centre for Ecology, Evolution and Environmental Changes is organizing the Advanced Course Measuring Biodiversity by Joaquin Hortal - June 25th-29th 2018@ Lisbon, Portugal

Measuring Biodiversity: How to get data, assess its quality and measure different aspects of diversity

OBJECTIVES: This five-days intensive course offers an overview of the different ways to measure biodiversity, and provides tips for the stratification of primary biodiversity data and the construction of variables that describe its various facets. It also includes an in-depth review of the different types of data used to measure biodiversity and their problems and limitations.

See the PROGRAMME at: http://ce3c.ciencias.ulisboa.pt/training/?cat Course INSTRUCTOR: Joaquin Hortal (Senior Research Scientist, Museo Nacional de Ciencias Naturales 'V CSIC, Madrid, Spain)(http://jhortal.com/)

INTENDED AUDIENCE This five days intensive course will be open to a maximum number of 20 participants, being directed to PhD or MSc students in Ecology, Geography or related areas, and postdocs and other professionals working in related topics. The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL, UP) and Biology and Ecology of Global Changes (BEAG UL, UA). For information of fees for other participants see the programme details.

Deadline for applications: June 1st, 2018

For additional details about the course and to know how to register, go to: http://ce3c.ciencias.ulisboa.pt/training/?cat For more information about the course, please contact: jhortal@mncn.csic.es

Margarida Matos <mmmatos@fc.ul.pt>

CornellU ProgrammingPhylogeneticMethods Sep20-15

Announcement: Arbor Short-Course and Hackathon for Phylogenetic Comparative Methods

Short Course; 20-22 Sept 2018

Hackathon; 22-25 Sept 2018

Location: Cornell University, Ithaca NY

Empiricists: Are you sick of fighting with hard-to-use software to carry out phylogenetic comparative analyses? Do you seek a better way to complete analyses that lets you focus more on your data and less on buggy, hard-to-use code?

Programmers: Do you want to implement your methods in an easy-to-use, web-based framework? Would you like to expand your user base by implementing your methods on open-source web pages? Would you like to interact with a network of programmers developing modules to bring new functions to your comparative methods?

If you are either of the above, we announce an NSF-funded Short Course and Hackathon covering version 2.0 of Arbor, our software for comparative methods.

We will hold the *Short Course/Workshop* for end users from Sept 20-22 2018. Attendees will learn how to use Arbor to carry out ancestral state reconstructions, test linear models, and many other comparative analyses using a simple drag-and-drop interface implemented over the web. The workshop will also include a series of lectures on the basics of phylogenetic comparative methods, as well as a chance for users to discuss their work in a creative and supportive environment.

We will hold a *Hackathon* for programmers on 22-25 Sept 2018. Attendees will learn how Arbor can enable them implement their own comparative method(s) over the web, instantaneously building their userbase and enabling integration with other software through workflow development. We will cover how to build and host Arbor instances, implement new workflows combining methods for data manipulation, analysis, and visualization, and deploy these workflows on custom Arbor app pages providing an easy-to-use interface for users of all abilities.

Both the workshop and the hackathon have funds available to support travel and lodging for attendees. Apply by filling out this Google Doc application < https://docs.google.com/forms/d/e/1FAIpQLSef_eYz_0nnSn242O5jPR39dp4r-UA6hYBf8A3eb9L0aNaZ1g/viewform?c=0&w=1 > form by *July 15 2018*.

Questions?

Luke Harmon: lukeh@uidaho.edu

Chelsea Specht: cdspecht@cornell.edu

Bob Thacker: robert.thacker@stonybrook.edu

Chelsea Specht <cdspecht@cornell.edu>

Madrid StatisticalPhylogenetics Aug2-12

MADPHYLO: Madrid Workshop in Statistical Phylogenetics

Where: Real Jardin Botanico (CSIC), Madrid, Spain

When: 2nd-12th August 2018

www.madphylo.com Course overview:

Darwin founded the field of evolutionary biology on the concept that all organisms are related to one another through an unknown evolutionary tree. Phylogenetic or evolutionary inference has become an essential tool in many disciplines across the life sciences, from molecular epidemiology to paleontology. In this workshop, the participants will learn the theoretical and technical basis of stochastic modeling in evolutionary biology and phylogenetics. The workshop will also provide full training in the open software RevBayes, an R-like interactive environment based on graphical model concepts for the modeling of complex evolutionary problems. At the end of the workshop, the student will have an understanding of the assumptions behind state-of-the-art methods used in modern phylogenetic analysis, as well as being able to build up new models from existing functions in RevBayes.

Instructors:

The lecturers are prominent analytical systematists and evolutionary biologists, who are behind the development of many of the methodological and computing tools routinely used in modern phylogenetic inference and evolutionary biology: Prof. John Huelsenbeck (University of California, Berkeley), Prof. Brian Moore (University of California, Davis), Prof. Sebastian Hoehna (University Ludwig-Maximilians, Munich). The Workshop is organized and directed by Dr. Isabel Sanmartin (Real Jardin Botanico, CSIC, Madrid), who will also lecture.

Workshop details:

The course will be taught from August 2, 2018 to August 12, 2018. Lectures and practicals will be tightly linked, meaning that you will learn the theory and also how to apply the theory on the same day. Students are encouraged to bring their own laptops. The tuition for the course is deliberately low, at only 250 Euros. However, this tuition does not include room and board during the course. You will be required to find a place to stay if you are from outside of Madrid.

More details and how to register can be found on the website: https://www.madphylo.com Email isanmartin@rjb.csic.es or johnh@berkeley.edu for any questions.

Isabel Sanmartin, PhD Real Jardin Botanico, CSIC Plaza de Murillo 2 28014 Madrid, SPAIN Phone: +34 914203017 Fax: +34 914200157 email: isanmartin@rjb.csic.es

Isabel Sanmartin <isanmartin@rjb.csic.es>

MaxPlanck Ploen TalkingEvolution Sep26-28

REGISTRATION DEADLINE EXTEND TO MAY 7th 2018!!

Register now for the workshop 'Talking Evolution - On Principles and Advances in Evolutionary Thinking'!

https://workshops.evolbio.mpg.de/event/8/ This workshop will take place from September 26th-September 28th 2018 at the Max Plank Institute for Evolutionary Biology in Plön, Germany.

It aims to clarify, update and expand on traditional evolutionary thinking by providing a platform for discussion. Critics have argued evolutionary studies to be very gene-centric and dismissive of other mechanisms contributing to evolutionary change. In particular, they call for a wider recognition of topics such as:

- Niche construction theory - Extra-genetic inheritance - Developmental bias - Phenotypic plasticity

While the importance of these fields is backed by empirical evidence, wider recognition is trailing behind. We would like to change that. If this interests you, please join us and let's talk evolution

Keynote talks will be given by: - Paul M. Brakefield (Trinity College, UK) - Luis-Miguel Chevin (CEFE, France) - Troy Day (Queen's University, Canada) - Ilkka Kronholm (University of Jyväskylä, Finland) - Kevin Laland (University of St. Andrews, UK) - Sonia E. Sultan (Wesleyan University, USA)

All the accepted participants will be able to present their research either in the form of a talk or a poster.

Scientific Organizers: Noémie Erin, Alice Feurtey, Dominik W. Schmid, Vandana R. Venkateswaran

Workshop coordination: Maren Lehmann

"erin@evolbio.mpg.de" <erin@evolbio.mpg.de>

Montana PopGenomicsDataAnalysis Sep9-15

Population Genomics Data Analysis Course and Workshop: "ConGen-2018"

Theme: Applications of Next Gen Sequencing Data to Understand Population Structure, Adaptive Evolution, and Environmental Influences on Genomic Variation.

Instructors include: Fred Allendorf, Eric Anderson, Paul Hohenlohe, Tiago Antao, Brian Hand, Marty Kardos, Brenna Forester, MacKenzie Gavery, Tabatha Graves, Joanna Kelley, Gordon Luikart, Mike Miller, Kristein Reugg, Robin Waples, and more TBA.

When: September 9-15, 2018,

Where: Flathead Lake Biological Station, Polson, Montana

For details on ConGen-2018: see http://www.umt.edu/-sell/cps/congen2018/ Travel support: The first 25 students or postdocs accepted to participate will receive a $400-$600 travel support scholarship (depending on travel distance and cost)

ConGen 2013 dinner by the lake ConGen 2018 view from Biostation

Course Objective: To provide training in conceptual and practical aspects of data analysis for understanding the population and evolutionary genomics of natural and managed populations. Emphasis will be on next generation sequence data analysis (RADs, whole genome sequence analyses, RNAseq) and interpretation of output from recent novel statistical approaches and software programs. The course include discussions among early career researchers (student participants) and >12 leaders in population genomics (instructors) to help develop our next generation of conservation and evolutionary geneticists.

Who should apply: Advanced Undergrads, M.S. & Ph.D. students, post-docs, faculty, agency researchers, and population biologists having taken at least one semester university-level course in population genetics and a course in population ecology. Participation will be limited to ˜30 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own NGS data to analyze.

Past courses: see Andrews & Luikart 2014, http://onlinelibrary.wiley.com/doi/10.1111/mec.12686/abstract and Benestan et al. 2016: http://onlinelibrary.wiley.com/doi/10.1111/mec.13647/full; gordon.luikart@mso.umt.edu

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OakSpring PlantSystematics Sep18-27 Deadline

Oak Spring eFLOWER Summer School Oak Spring Garden Foundation, Upperville, Virginia, USA; 18-27 September 2018

Only one week left to apply!

UPDATE: The Society of Systematic Biologists (SSB) is now officially sponsoring the Summer School and will provide financial support to help recover the air travel costs of participants from more distant geographic locations!

Full information available here: http://eflower.myspecies.info/ oakspringsummerschool

We invite applications for the Oak Spring eFLOWER Summer School to be held at the Oak Spring Garden Foundation in Upperville, Virginia (USA) from 18 to 27 September 2018. The goal of the Summer School is to deliver high-quality training in the modern comparative methods used to study plant macroevolution. While the methods are general and applicable to any group of organisms, all of our empirical datasets will be drawn from our recent work on flowering plants. A unique feature of this School will be that the students themselves will participate in the creation of the datasets (floral traits and fossil calibrations) in our collaborative database PROTEUS, thereby gaining hands-on experience of the problems and questions associated with compiling data and building real-life datasets for comparative analyses. In doing so, we hope to further promote the rapidly evolving field of macroevolution among graduate students in plant sciences, while also conveying our experience in building high-quality datasets.

Topics addressed in the Summer School will include: divergence time estimation using molecular dating methods (relaxed clock methods, fossil calibration), ancestral state reconstruction and correlation of morphological traits (using maximum likelihood and Bayesian methods), and diversification rates and state-dependent diversification. All of these approaches start with phylogenetic trees obtained from molecular or genomic data and thus prior understanding of and experience with phylogenetic reconstruction based on such data is an essential prerequisite for participants, because this topic will not be taught in the Summer School. We also plan to include an outreach component in the form of a short video made by the participants during the course, explaining in simple terms what they have learned and why these methods are important to understand plant evolution.

The Oak Spring eFLOWER Summer School is free (no registration fee), including food and accommodation on site. All participants will also receive up to US$ 1000 on a reimbursement basis for their economy flights to Dulles Airport (IAD), Washington D.C. In addition, the Society of Systematic Biologists (SSB) will further reimburse up to US$ 500 on air travel costs of up to eight participants from more distant locations. Participants are entirely responsible for arranging their own travel insurance and visas. The School is ideally suited to graduate students (enrolled in a master's or PhD program) who already have some botanical and phylogenetic background, but who lack training in current macroevolutionary methods. International applicants are welcome (but fluency in English is a requirement of the course) and we will attempt to achieve a good balance in terms of gender and origin in the final Summer School group selected.

To apply, please send a one-page letter of motivation and a CV, as a single PDF file with your name, to herve.sauquet@gmail.com. Deadline for applications: 1st June, 2018. Decisions will be made by 18th June. Please include the names and contact details of two referees (e.g., current or previous supervisor), but no letter of support (we will contact referees if necessary). Applications that do not meet these requirements may be automatically rejected. The total number of participants will be limited to 15.

Organizers: Hervé Sauquet (Royal Botanic Gardens and Domain Trust, Australia) Susana Magallón (Universidad Nacional Autónoma de México, Mexico) Jürg Schönenberger (University of Vienna, Austria) Peter Crane (Oak Spring Garden Foundation, USA)

Confirmed Guest Lecturers: Else Marie Friis (Swedish Museum of Natural History, Sweden) Laura Lagomarsino (Louisiana State University, USA) Stacey Smith (University of Colorado-Boulder, USA)

Links to learn more: Oak Spring Garden Foundation < https://www.osgf.org/ > Society of Systematic Biologists < http://www.systbio.org/ > eFLOWER project < http://www.eflower.org/ > First eFLOWER Summer School < http://eflower.myspecies.info/node/45 >

– Dr. Hervé Sauquet

Systematic Botanist, Royal Botanic Gardens and Domain Trust Mrs Macquaries Rd Sydney, NSW 2000, Australia E-mail: herve.sauquet@rbgsyd.nsw.gov.au or herve.sauquet@gmail.com

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Ploen StructuredPopModels Sep5-7

Ploen.EvolStructuredPopulatons.Sep5-7

***** DEADLINE EXTENDED *****

Dear Colleagues,

we are happy to announce the workshop “Evolutionary Models of Structured Populations: Integrating Methods” taking place in Ploen on September 5 - 7th, 2018.

Speakers are: Annette Baudisch (University of Southern Denmark), Oana Carja (University of Pennsylvania), Hal Caswell (University of Amsterdam), Nicole Creanza (Vanderbilt University), Florence Debarre (Centre Interdisciplinaire de Recherche en Biologie), Andre M. de Roos (University of Amsterdam) and Bartlomiej Waclaw (University of Edinburgh).

Registration and abstract submission is NOW EXTENDED UNTIL MAY 11:

https://workshops.evolbio.mpg.de/event/7/registrations/7/ Prior to the start of the workshop, Hal Caswell will give a tutorial about sensitivity analysis of demographic models for ecology and evolution in the morning of the first day (Sept 5th). The tutorial is meant mostly for junior scientists and researchers new to demographic modelling; some math background is assumed.

This tutorial is limited to 20 participants.

We hope to see you at the workshop! Please spread the word to potentially interested colleagues.

Best wishes, Laura Hindersin & Stefano Giaimo

Stefano Giaimo <giaimo@evolbio.mpg.de>

QuebecCity eDNAmetabarcoding Nov19-23

Workshop: eDNA Metbarcoding

When: 19-23 November 2018

Where: Institut de Biologie Intégrative et des Systèmes (IBIS), Laval University, Québec City (Québec), Canada

Instructors:

Dr. Vasco Elbrecht (University of Guelph, Canada)

Eric Normandeau (Laval University, Canada)

Website: (https://www.physalia-courses.org/courses-workshops/course40/)

Course Overview Obtaining environmental DNA (eDNA) from water, soil, air, gut content or other sample types holds great promises for biodiversity research and assessment. Targeted species specific markers, and broader, more inclusive metabarcoding approaches using universal primer sets can detect invasive and rare rare species, or the range of taxa present in ecosystems from trace amounts of DNA. eDNA can capture sample diversity using non-invasive or minimally invasive methods/techniques. However, due to the low quantity of DNA present in samples, these approaches often require specialized laboratory protocols, careful sample handling to prevent contamination, as well as specialized bioinformatic processing due to high levels of noise and the presence of non-target taxa.

After completing the workshop, students should be in a position to (1) understand the potential and capabilities of eDNA barcoding and metabarcoding, (2) run complete analyses of eDNA metabarcoding pipelines and obtain diversity inventories and ecologically interpretable data from raw next-generation sequence data and (3) design their own eDNA projects, including bioinformatic data analysis and planning of laboratory work. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically to participants.

While this course will focus on eDNA metabarcoding, however targeted single species detection and other alternatives will also be explored, as they can sometimes be suitable metabarcoding alternatives.

Targeted audience & ASSUMED BACKGROUND This workshop is mainly aimed at researchers and technical workers with a background in ecology, biodiversity or community biology who want to use molecular tools for biodiversity research, and researchers in other areas of bioinformatics who want to learn ecological applications for biodiversity-assessment. In general, it is suitable for every researcher who wants to join the growing eDNA community. This workshop will review mostly techniques and software useful for eukaryotic single species detection and eDNA metabarcoding. Other workshops focused on procedures currently used in bulk sample and microbial metabarcoding will be available from Physalia-courses. A survey will be provided 2 weeks ahead of the workshop, where participants can mention topics or aspects they are particularity interested in.

No programming or scripting experience is necessary, but some previous expertise using the Linux console and/or R will be most welcome. All examples will be run either in Linux or Mac environments. Please make sure to have linux installed if you bring a Windows based laptop. Among the software and tools we will be using is R or Rstudio (+ the JAMP & PrimerMiner package), FastQC, Usearch, Vsearch, Cutadapt, and mBRAVE.net. No prior knowledge of these software packages is required.

TEACHING FORMAT The workshop is delivered over 5 days (see the detailed curriculum below). The lectures are interactive with active discussion where asking questions is strongly encouraged. A key aspect of this course are practical sessions in primer development, bioinformatic analysis of high throughput sequence data, and data visualization as well as a project planning exercise to apply what you learned in this course.

Session content: (https://www.physalia-courses.org/courses-workshops/course39/curriculum39/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

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https://groups.google.com/forum/#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

QuebecCity PopulationGenomics Nov12-16

Workshop: Introductory Population Genomics

When: 12-16 November 2018

Where: Institut de Biologie Intégrative et des SystÂÂmes (IBIS), Laval University, Québec City (Québec), Canada

Instructors:

Dr. Martin Taylor[ ](https://www.physalia-courses.org/instructors/t9/) (University of East Anglia, UK)

Dr. Lewis Spurgin (University of East Anglia, UK)

Website: (https://www.physalia-courses.org/courses-workshops/course39/)

Course Overview Next generation sequencing has revolutionized evolutionary biology allowing unprecedented resolution and insight into evolutionary questions that appeared intractable only a few years ago. The course will cover the basics of population genomic analysis from SNP data onwards and will cover the key analyses that may be required to successfully analyze a population genetic data set. The course will NOT cover steps prior to generation of a .vcf file or SNP data set such as NGS data demultiplexing, clustering and SNP calling (This is covered in detail in the Introduction to RADseq course). This course will introduce Linux and the command line environment, basic perl and python usage, file conversions and manipulation, population structure and differentiation in R, outlier analysis, landscape / seascape genomics and introgression. Having completed the course, students should have a good understanding of the software and methods available for population genomic analysis and be competent in population genomic analysis.

Targeted audience & ASSUMED BACKGROUND This workshop is aimed at postgraduate students and early career researchers who are interested in using population genomic tools in their research. No previous experience of bioinformatics is required, but an underpinning in evolutionary biology and basic population genetics concepts such as Hardy Weinberg Equilibrium and FST are desirable. The course will use a range of software including the Linux operating system and R.

TEACHING FORMAT The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of a combination of lectures and practical exercises, with breaks at the organisers'Â discretion. There will also be time for students to discuss their own problems and data.

Session content: (https://www.physalia-courses.org/-courses-workshops/course9/curriculumpg/)

Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Carlo Pecoraro, Ph.D

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Switzerland MicrobialBiodiversity Jun17-18

Antarctic microbial genomic tools Hands-on Training Workshop @ POLAR 2018

17-18 June 2018 room C157 WSL Institute for Snow and Avalanche Research SLF Flüelastrasse 11 Davos Dorf Swisserland

A hands-on workshop with invited instructors with expertise in genome standards, biological diversity databases, microbial diversity and (meta)genome sequence analyses will include information on preparing internationally accepted environmental context data and submissions of data sets to sequence repositories (e.g. EMBL, NCBI) will be the focus of Day 1.

Data processing pipelines for next generation sequencing analysis of microbial diversity data (focused on 16S and 18S rRNA) as well as discussions of meta 'omic data analysis, statistics and modeling tools for both amplicon and 'omic data will be demonstrated and discussed on Day 2. Time will be allocated to practical hands on learning to facilitate an interactive learning environment.

Participants are encouraged to bring a computer, projects to register and any associated data if they wish to work on their own data. Example data sets will be available. A small workshop participation fee of $100 per person will be required. Participants will also have to have registered and paid for the Open Science Conference and the satellite meetings (30 CHF) (more details see http://www.polar2018.org).

Confirmed speakers / instructors:

- Alison Murray, Professor, Division of Earth and Ecosystem Sciences, Desert Research Institute, Reno, NV, U.S.A. - Thomas Pommier, Ecological Microbiology, Université Claude Bernard Lyon, France - Craig Herbold, Department of Microbiology and Ecosystem Science, Division of Microbial Ecology, University of Vienna, Austria - Damien Eveillard, Computational Biology, Université of Nantes, France - Ivaylo Kostadinov, Department of Life Sciences & Chemistry Jacobs Unversity, Bremen - Pier Buttigieg, Biosciences - Deep-sea Ecology and Technology, Alfred Wegner Institute

Space is limited. Registrations will be confirmed with payment. Interested participants need to contact Alison Murray (mars.biodiversity@gmail.com).

Anton Van de Putte <antonarctica@gmail.com>

UExeter MicrobialID Aug28-31

Cornwall(UK). RESOLVING_MICROBIAL_COMMUNITIES_AT_STRAIN-LEVEL_RESOLUTION.28-31Aug.

Workshop: resolving microbial communities at strain-level resolution

When: 28-31 August 2018

Where: University of Exeter Cornwall Campus, Penryn, Cornwall, U.K.

Website: https://metagmicros.weebly.com/ Background The vast majority of biodiversity on Earth is contained in microbial communities. Metagenomics involves the high-throughput sequencing of random DNA fragments isolated from microbial communities, followed by assembly into longer fragments and assignment of gene functions and taxonomic identities. Novel computational developments are allowing us to increasingly resolve strain- and species level differences from metagenomic data. Rather than viewing communities as 'bags of genes', this approach enables us to gain deeper insights into the composition and functioning of microbial communities. Metagenome-assembled genomes(MAGs) can be operationally defined by binning metagenomic assemblies according to nucleotide composition and depth of coverage across multiple samples. However, it remains unclear to what extent these operationally defined MAGs correspond to different theoretical concepts of species, the natural units of evolution and ecology.

Workshop The main focus of the workshop will be genome-resolved metagenomics, and the opportunities and pitfalls it brings into microbiology. We will cover reconstructing microbial genomes from metagenomes, screening the quality of metagenome-assembled genomes (MAGs), studying their environmental heterogeneity through single-nucleotide variants (SNVs), deconvoluting sub-population genomes using SNV patterns, pangenomics, phylogenomics and visualization strategies to investigate fundamental questions of microbiology.

Instructors:

Chris Quince (University of Warwick)

Murat Eren (University of Chicago)

Tom Delmont (University of Chicago)

Nicolas Tromas (University of Montreal/University of Exeter)

Speakers:

Rachel Whitaker (University of Illinois)

Jesse Shapiro (University of Montreal)

Michiel Vos (University of Exeter)

Audience We aim to deliver a hand-on approach to metagenomics analyses and combine this with lectures and group discussions. The number of attendees is limited to 40-60 participants. We strive to stimulate participation by early-career researchers and to have an equal gender ratio. Please follow the link on the website to register an expression of interest and to send an email expressing how this workshop could benefit your work and what your current position (e.g. PhD student, lecturer) is. At the start of June, you will be notified of the success of your application and sent a link with payment details and accommodation options.

The meeting is sponsored by MRC CLIMB (https://www.climb.ac.uk/).

Nicolas Tromas (tromas.nicolas@gmail.com) and Michiel Vos (m.vos@exeter.ac.uk)

"Vos, Michiel" <M.Vos@exeter.ac.uk>

UGothenburg PopulationGenomicsBioinformatics Nov5-9

Dear all,

Please find below the preliminary schedule and general aims of the course, "An introduction to bioinformatic tools for population genomic data analysis", offered November 5-9 2018 at the Tjärnö Marine Laboratory on the island of Tjärnö outside of Strömstad on the Swedish West Coast (http://loven.gu.se/english/about_the_loven_centre/tjarno).

There is no course fee. Accommodation and meals for students are provided by the Centre for Marine Evolutionary Biology. Students will need to provide their own means of transportation to and from the course, however.

The course will be open to a maximum of 18 students, as large parts of the course will consist of hands-on exercises. The aim is a broad mix of students both from the University of Gothenburg and from the outside, mainly PhD students but postdocs are also welcome to apply.

Knowledge of general molecular biology and genetics is necessary, as is some previous experience with commandline interfaces. Previous experience working on a remote server will also be beneficial. No previous bioinformatics skills are needed, however.

For more information and registration, please visit the course web site at: https://sites.google.com/view/bioinformaticpipelines2018 Deadline for registration is September 15th 2018.

Please note that ALL students must bring their own computers.

Best wishes,

Pierre De Wit

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An introduction to bioinformatic tools for population genomic data analysis, 2.5 higher education credits Third

Cycle

Faculty of Science; Department of Marine Sciences

The Centre for Marine Evolutionary Biology

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1. Course content

This course aims at detailed understanding and hands-on experience of using state of the art bioinformatics pipelines for one“s own biological research questions. An important aspect of the course is to show how genomic data can be applied to address and answer research questions in the fields of genetics, ecology, population biology, biodiversity monitoring and conservation. The students will be trained in the latest bioinformatic methods to analyze high throughput sequencing data, which is present in many research projects. The course will cover basic computing tools required to run command line applications, processing high throughput sequencing data of whole genome / exome / restriction site digested (RAD) DNA for population genomic studies.

The first part of the course introduces general computing tools for beginners such as the UNIX command line environment, bash commands, data formatting using regular expressions and basic scripting in the unix shell with a series of examples and exercises using a remote server. The course introduces bioinformatics software for analysis of RAD-data, and downstream population genetic analysis of genotype data. The course also introduces basic and advanced concepts of population genomics data analysis such as genome/transcriptome assembly, alignment/mapping, differential Gene expression, functional enrichment tests, SNP genotyping, PCA, outlier tests. The course corresponds to 1 week of full time studies and and is composed of lectures, demonstrations and computer labs.

2. Outcomes

1. Knowledge and understanding 1a. Demonstrate advanced knowledge of experimental strategies, applications and bioinformatic tools for population genomics. 1b. Demonstrate advanced knowledge of the potential of genomics approaches to answer ecosystem-wide questions, in particular for

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UK BioinformaticsForDNAandRNAsequenceAnalysis 29Oct-2Nov

Introduction to bioinformatics for DNA and RNA sequence analysis (IBDR01)

https://www.prinformatics.com/course/introduction-to-bioinformatics-for -dna-and-rna-sequence-analysis-ibdr01/

This course will be deliver by Dr Malachi Griffith and Dr Obi Griffith (from Washington University) and will take place in Glasgow City Centre form 28th October - 2nd November 2018

Course Overview:

Analysis of high throughput genome and transcriptome data is major component of many research projects ranging from large-scale precision medicine efforts to focused investigations in model systems. This analysis involves the identification of specific genome or transcriptome features that predispose individuals to disease, predict response to therapies, influence diagnosis/prognosis, or provide mechanistic insights into disease models. During this course (IBDR01), students will perform an example end-to-end bioinformatics analysis of genome (WGS and Exome) and transcriptome (RNA-seq) data. Students will start with raw sequence data for a hypothetical case, learn to install and use the tools needed to analyze this data on the cloud, and visualize and interpret results. After completing the course, students should be in a position to (1) understand raw sequence data formats, (2) perform bioinformatics analyses on the cloud, (3) run complete analysis pipelines for alignment, variant calling, annotation, and RNA-seq (transcriptome analysis approaches will be a major component of the workshop), (4) visualize and interpret whole genome, exome and RNA-seq results, (5) leverage the identification of passenger variants for immunotherapy applications, and (6) begin to place these results in a clinical context by use of variant knowledgebases. The data, tools, and analysis will be most directly relevant to human genomics and bioinformatics research. However, many of the skills and concepts covered will be applicable to other human diseases and model organisms. Furthermore, many analysis concepts covered during the workshop will be broadly applicable to other “big data” research problems. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically to participants.

Intended Audience

This workshop is primarily aimed at researchers and technical workers with a background in biology who want to learn fundamental bioinformatics skills for genomics with a particular emphasis on biomedical research applications. The course is essentially a crash course in bioinformatics for next generation sequence data analysis. It would also be useful for students with a computational background who seek an introduction to genomics technology and analysis approaches. In general, it is suitable for anyone working with genome or transcriptome (RNA-seq) data in the context of disease research. Attendees are encouraged to bring their own data or project outlines for discussion. Some time during the course will be dedicated to consultation with a team of instructors from the McDonnell Genome Institute.

Monday 29th - Classes from 09:30 to 17:30

Session 1. Introduction to genomics and bioinformatics. In this session, students will be introduced to key concepts of genomics and their application to genomics research and precision medicine in cancer. An introduction to next-generation sequencing platforms and related bioinformatics approaches will also be provided. Core concepts and tools introduced: fundamentals of genome and transcriptome analysis, next-generation sequencing, precision/personalized medicine approaches (using cancer as an exemplar disease).

Session 2. Introduction to genomics data, file formats, QC, and cloud analysis. In this session, students will be introduced to a hypothetical patient case and related samples to be analyzed throughout the course. Students will be provided with an introduction to the whole genome, exome, transcriptome and other data sets we have generated for this test case. Information on where to get the raw data and how to access it (and other test data) will be provided. Using this data as an example, the students will learn fundamentals of next generation sequence (NGS) data formats. The students will also be introduced to accessory files needed for analysis including reference genomes, reference transcriptomes, and annotation files. Tools for QC analysis of raw data will be demonstrated. Since most analysis will be performed on the cloud, each student will learn how to launch and log into their own cloud compute environment. Students will learn how to install bioinformatics tools and learn to use some of the most broadly useful tool kits for NGS data. Core concepts and tools introduced: file formats (Fasta, FastQ, SAM/BAM/CRAM, VCF, GTF), bedtools, Picard, samtools, fastQC, cloud computing (AWS, EC2).

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UK EukaryoticMetabarcoding Jul23-27

This is a final call for the upcoming course "Eukaryotic metabarcoding"

https://www.prinformatics.com/course/eukaryotic-metabarcoding-eukb01/ The deadline for registration is July 13th and we still have a few places left.

This course will be delivered by Dr. Owen Wangensteen and will take place in Glasgow form the 23rd - 27th July

Course Overview:

Metabarcoding techniques are a set of novel genetic tools for assessing biodiversity of natural communities. Their potential applications include (but are not limited to) accurate water quality, soil diversity assessment, trophic analyses of digestive contents, early detection of non-indigenous species, studies of global ecological patterns and biomonitoring of anthropogenic impacts. This course will give an overview of metabarcoding procedures with an emphasis on practical problem-solving and hands-on work using analysis pipelines on real datasets. After completing the course, students should be in a position to (1) understand the potential and capabilities of metabarcoding, (2) run complete analyses of metabarcoding pipelines and obtain diversity inventories and ecologically interpretable data from raw next-generation sequence data and (3) design their own metabarcoding projects, using bespoke primer sets and custom reference databases. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically to participants.

Email oliverhooker@PRinformatics.com

Check out our sister sites,

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www.PRinformatics.com (Bioinformatics and data science) www.PSstatsistics.com (Behaviour and cognition)

Up-coming courses

1. May 21^st - 25^th 2018

INTRODUCTION TO PYTHON FOR BIOLOGISTS (IPYB05)

Glasgow, Scotland, Dr. Martin Jones

http://www.prinformatics.com/course/introduction-to-python-for-biologis ts-ipyb05/

2. May 21^st - 25^th 2018

INTRODUCTION TO REMOTE SENISNG AND GIS FOR ECOLOGICAL APPLICATIONS (IRMS01)

Glasgow, Scotland, Prof. Duccio Rocchini, Dr. Luca Delucchi

www.prinformatics.com/course/introduction-to-remote-sensing-and-gis-for -ecological-applications-irms01/

3. May 28^th - 31^st 2018

STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR (SIMM04)

Canada (QUEBEC) Dr. Andrew Parnell, Dr. Andrew Jackson

www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm04 /

4. May 28^th - June 1^st 2018

ADVANCED PYTHON FOR BIOLOGISTS (APYB02)

Glasgow, Scotland, Dr. Martin Jones

www.prinformatics.com/course/advanced-python-biologists-apyb02/ 5. June 12^th - 15^th 2018

SPECIES DISTRIBUTION MODELLING (DBMR01)

Myuna Bay sport and recreation, Australia, Prof. Jane Elith, Dr. Gurutzeta Guillera

www.prstatistics.com/course/species-distribution-models-using-r-sdmr01/ 6. June 25^th - 29^th 2018

SPECIES DISTRIBUTION/OCCUPANCY MODELLING USING R (OCCU01)

Glasgow, Scotland, Dr. Darryl McKenzie (PROTEUS)

www.prstatistics.com/course/species-distributionoccupancy-modelling-usi ng-r-occu01/

7. July 2^nd - 5^th 2018

SOCIAL NETWORK ANALYSIS FOR BEHAVIOURAL SCIENTISTS USING R (SNAR01)

Glasgow, Scotland, Prof. James Curley

http://www.psstatistics.com/course/social-network-analysis-for-behavior al-scientists-snar01/

8. July 8^th - 12^th 2018

MODEL BASE MULTIVARIATE ANALYSIS OF ABUNDANCE DATA USING R (MBMV02)

Glasgow, Scotland, Prof. David Warton

www.prstatistics.com/course/model-base-multivariate-analysis-of-abundan ce-data-using-r-mbmv02/

9. July 23^rd - 27^th 2018

EUKARYOTIC METABARCODING (EUKB01)

Glasgow, Scotland, Dr. Owen Wangensteen

http://www.prinformatics.com/course/eukaryotic-metabarcoding-eukb01/ 10. September 24^th - 28^th

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UK FunctionalEcology Nov26-30

Functional ecology from organism to ecosystem: theory and computation (FEER01)

This course will be delivered by Dr. Francesco de Bello, Dr. Lars Götzenberger and Dr. Carlos Carmona and will take places in Glasgow city centre from 26th - 30th November 2018.

Course Overview: The course will describe different aspects and methods in the field of functional ecology, combining theoretical lessons with hands-on real data. Lectures will provide the theoretical and mathematical basis for different applications of functional traits at organismal, community and ecosystem levels, with examples across different trophic levels. This will serve as a basis for exploring the practical tools to connect the effect of land-use and climate change on biodiversity to the effect of biodiversity on to multiple ecosystem functions and ecological services. An overview of existing computational methods, including recent developments authored by the lecturers, will be provided during the course and the students will learn how to apply them using functions and scripts run in R. Students are welcome to apply these tools to their own data, or use the data provided, to be analysed during the course while benefiting from advise by the lecturers. As such, compared to other courses given by the lectures, this is a slightly a more advanced and data oriented course which concentrates on detailed and practical aspects in functional traits related applications, especially computational ones. The aim of the course is to provide participants with a handy synthesis of existing concepts, tools and trends in functional ecology and guide them to apply these tools to their own field of interest. As the field of functional ecology is rapidly expanding, participants will be ready to exploit the potential of the main trait approaches.

Monday 26th - Classes from 09:30 to 17:30 - People's traits game - Introduction to functional ecology and key definitions - Environmental filtering and related community metrics - Overview on functional trait community metrics - Practical with 'community weighted mean' and solution to potential biases

Tuesday 27th - Classes from 09:30 to 17:30 - Species level analyses - Missing values and trait databases - Functional diversity indices (alpha, beta and gamma diversity) - Practical with functional diversity indices

Wednesday 28th - Classes from 09:30 to 17:30 - Trait evolution and the relevance of phylogenetic distance between species - Phylogenetic corrections - Combining functional and trait information - Practical on phylogeny and traits

Thursday 29th - Classes from 09:30 to 17:30 - Community assembly: theory - Community assembly: from species to community level analyses - Null-models - Practical on community assembly

Friday 30th - Classes from 09:30 to 16:00 - Effects of traits on ecosystem processes and services - The trait sampling game - Intraspecific trait variability: biological relevance and quantification - Practical on intraspecific trait variability

Email oliverhooker@prstatistics.com

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1. May 21st - 25th 2018 INTRODUCTION TO PYTHON FOR BIOLOGISTS (IPYB05) Glasgow, Scotland, Dr. Martin Jones http://www.prinformatics.com/course/introduction-to-python-for-biologists-ipyb05/ 2. May 21st - 25th 2018 INTRODUCTION TO REMOTE SENISNG AND GIS FOR ECOLOGICAL APPLICATIONS (IRMS01) Glasgow, Scotland, Prof. Duccio Rocchini, Dr. Luca Delucchi www.prinformatics.com/course/introduction-to-remote-sensing-and-gis-for-ecological-applications-irms01/ 3. May 28th - 31st 2018 STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR (SIMM04) Canada (QUEBEC) Dr. Andrew Parnell, Dr. Andrew Jackson www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm04/ 4. May 28th - June 1st 2018 ADVANCED PYTHON FOR BIOLOGISTS (APYB02) Glasgow, Scotland, Dr. Martin Jones www.prinformatics.com/course/advanced-python-biologists-apyb02/ 5. June 12th - 15th 2018 SPECIES DISTRIBUTION MODELLING (DBMR01) Myuna Bay sport and recreation, Australia, Prof. Jane Elith, Dr. Gurutzeta Guillera www.prstatistics.com/course/species-distribution-models-using-r-sdmr01/ 6. June 25th - 29th 2018

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UK ModellingEvolution Nov19-23

Structural Equation Modelling for Ecologists and Evolutionary Biologists (SEMR02)

https://www.prstatistics.com/course/structural-equation-modelling-for-ecologists-and-evolutionary-biologists-semr02/ This course will be delivered by Jon Lefcheck author of the piecwise package and wiltake place in lasgow City Centre for the 19th - 23 November 2018

Course Overview: The course is a primer on structural equation modelling (SEM) and confirmatory path analysis, with an emphasis on practical skills and applications to real-world data. Structural equation modelling is a rapidly growing technique in ecology and evolution that unites multiple hypotheses in a single causal network. It provides an intuitive graphical representation of relationships among variables, underpinned by well-described mathematical estimation procedures. Several advances in SEM over the past few years have expanded its utility for typical ecological datasets, which include count data, missing observations, and nested or hierarchical designs.

We will cover the basic philosophy behind SEM, provide approachable mathematical explanations of the techniques, and cover recent extensions to mixed effects models and non-normal distributions. Along the way, we will work through many examples from the primary literature using the open-source statistical software R (www.r-project.org). We will draw on two popular R packages for conducting SEM, including lavaan and piecewiseSEM. Participants are encouraged to bring their own data, as there will be opportunities throughout the course to plan, analyze, and receive feedback on structural equation models.

Email oliverhooker@prstatistics.com

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Vancouver StatisticalGenomicsProgramming Jul30

If you are statistical genomicist or work in evolution and are planning to attend the Joint Statistical Meetings in Vancouver, then there is a short course that may be of interest to you. Drs Ken Lange, Eric Sobel, Hua Zhou and I (UCLA Biomath, Human Genetics and Biostatistics Faculty) will be teaching a Julia Language Statistical Computing course with application to Genomics on Monday 7/30.

The course is suitable for students as well as for statistical genomicists. Programming experience in Julia is NOT required. Below is a short description. If anyone has a question they can email me (Janet Sinsheimer - janets@mednet.ucla.edu). Early registration for JSM ends 5/31 and early registration for the short course ends 6/29.

Thanks, Janet

Joint Statistical Meetings Course CE-18C Mon, 7/30/2018, 8:30 AM - 5:00 PM Julia Meets Mendel: Algorithms and Software for Modern Genomic Data Analysis (ADDED FEE) - Professional Development Continuing Education Course ASA Instructor(s): Kenneth Lange, UCLA, Janet Sinsheimer, UCLA, Eric Sobel, UCLA, Hua Zhou, UCLA Challenges in statistical genomics and precision medicine are enormous. Datasets are becoming bigger and more varied, demanding complex data structures and integration across multiple biological scales. Analysis pipelines juggle many programs, implemented in different languages, running on different platforms, and requiring different I/O formats. This heterogeneity erects barriers to communication, data exchange, data visualization, biological insight and replication of results. Statisticians spend inordinate time coding/debugging low-level languages instead of creating better methods and interpreting results. The benefits of parallel and distributed computing are largely ignored.

The time is ripe for better statistical genomic computing approaches. This short course reviews current statistical genomics problems and introduces efficient computational methods to (1) enable interactive and reproducible analyses with visualization of results, (2) allow integration of varied genetic data, (3) embrace parallel, distributed and cloud computing, (4) scale to big data, and (5) facilitate communication between statisticians and their biomedical collaborators. We present statistical genomic examples and offer participants hands on coding exercises in Julia as part of the OpenMendel project (https://openmendel.github.io). Julia is a new open source programming language with a more flexible design and superior speed over R and Python. R and Matlab users quickly adapt to Julia.

Janet Sinsheimer PhD Professor Human Genetics, Biomathematics David Geffen School of Medicine at UCLA Professor Biostatistics Fielding School of Public Health, UCLA

"Sinsheimer, Janet" <JanetS@mednet.ucla.edu>

Yokohama CulturalEvolution Jul17

Title: workshop "the (co-)evolution of genes, languages, and music from data analyses to theoretical models"

Date: Tues 17 July

Place: Kihara Institute for Biological Research, Yokohama City University (Yokohama, Japan)

It aims to clarify the evolution of languages/music and similarities/differences from biological evolution through quantitative datasets. We provide three sessions presenting 1. dispersals of language (and music) relating to migration histories from genetics side, 2. linguistic and musicological studies, and 3. theoretical modelings of cultural and linguistic evolution. Then, we will have a discussion about what we can learn about the evolution of languages and music through the different types of the datasets in the final session.

Speakers in each field: Genetics: Hiromi Matsumae (Tokai University), Chiara Barbieri (University of Zurich), Linguistics: Koji Kawahara (Nagoya University of Foreign Studies), Musicology: Patrick E. Savage (Keio University), Theoretical modeling: Takashi Hashimoto (JAIST), Yasuo Ihara (University of Tokyo)

Discussants: Hiroki Oota (Kitasato University), Kentaro Shimizu (University of Zurich/Yokohama City University), others.

For questions about the workshop, please contact organizers, Hiromi Matsumae & Kentaro Shimizu.

More details will be updated soon. website: https://sites.google.com/view/wgly2018 – Hiromi Matsumae, Ph.D Assistant Professor, Department of Molecular Life Science, Tokai University School of Medicine Simokasuya 143, Ishehara, Kanagawa, 259-1193, Japan E-mail: matsumae.hiromi.g@tokai.ac.jp

"hiromi.matsumae@gmail.com"
<hiromi.matsumae@gmail.com>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly 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.