

Scottish Phylogeny Discussion Group

University of Glasgow, 30th March 2012



Programme

— Scottish
— Phylogeny
— Discussion
— Group



CEGG

The discussion group will be held in the Gilbert Scott conference rooms, 253 and 356. These are situated within the historic main building of the University, just off the West Quadrangle (see maps at end of programme).

1 PM, Room 253

Buffet lunch and registration.

2 PM, Room 356

Introduction to the Scottish Phylogeny Discussion Group.

Dr Chris Quince, University of Glasgow

2:10 PM, Room 356

Biodiversity Informatics: An Emerging Computational Science.

Dr. Alexandros Stamatakis, Heidelberg Institute for Theoretical Studies

Abstract:

Biodiversity informatics and phyloinformatics in particular are currently facing a paradigm shift toward becoming a 'real' computational science. Molecular sequencing technologies are developing at a rapid pace, providing the biological sciences with enormous amounts of new data. Due to the necessity to process (and store) huge amounts of data, we expect the field to undergo an analogous transition that physics or computational fluid dynamics underwent 20 to 30 years ago. For instance, we are already facing such data analysis challenges in the 1000 insect transcriptome sequencing project (www.1kite.org). Such evolutionary studies require software that scales far beyond a multi-core node, that can be checkpointed and restarted with low overhead, and that can accommodate the memory requirements of whole-genome datasets under likelihood-based models. As an example of the efforts to turn biodiversity informatics into a computational science, I will describe RAxML-Light, a dedicated tool for large-scale phylogenetic inference on supercomputers under maximum likelihood. RAxML-Light implements a light-weight checkpointing mechanism, deploys 128-bit (SSE3) and 256-bit (AVX) vector intrinsics, offers two orthogonal memory saving techniques, and provides a fine-grain production-level MPI (Message Passing Interface) parallelization of the likelihood function. To demonstrate scalability and robustness of the code, we inferred a phylogeny on a simulated DNA alignment (1481 taxa, 20,000,000 bp) using 672 cores. This alignment required one TeraByte of RAM to compute the likelihood score on a single tree.

Web: www.exelixis-lab.org

3:00 PM, Room 356

Calculating likelihoods under the coalescent.

Mr Konrad Lohse, University of Edinburgh

3:20 PM, Room 356

Defining ecotypes on phylogenetic trees from microbiomics data.

Dr Chris Quince

3:40 PM, Room 253

Tea/Coffee.

4:00 PM, Room 356

The population genetics of the human influenza virus.

Dr Trevor Bedford

4:20 PM, Room 356

Using placements to learn about microbial ecology.

Dr Erick Matsen – by video conference

4:50-5:30 PM, Room 253

Drinks and general discussion.

The meeting will be followed by dinner at a restaurant in Glasgow. Dinner is open to anyone registered for the meeting, but **requires separate booking in advance**. If you would like dinner, please tell Chris Quince (christopher.quince@glasgow.ac.uk) before 26th March. Dinner will be charged at cost.

Speakers

Trevor Bedford

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Erick Matsen

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Organizer

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Further Information

The Scottish Phylogeny Discussion Group is funded by a grant from the Scottish Bioinformatics Forum and by the Centre for Evolution, Genes and Genomics at the University of St Andrews. For information on the Scottish Phylogeny Discussion Group and its activities, please see:

<http://biology.st-andrews.ac.uk/cegg/spdg>



