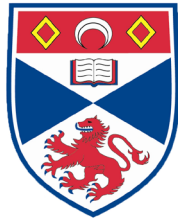


# Scottish Phylogeny Discussion Group

University of St Andrews, 16 June 2011



University  
of  
St Andrews

## Programme

— Scottish  
— Phylogeny  
— Discussion  
— Group



CEGG

All events are in Dyers Brae House. For venue information, see [http://biology.st-andrews.ac.uk/cegg/docs/SPDG\\_info\\_June2011.pdf](http://biology.st-andrews.ac.uk/cegg/docs/SPDG_info_June2011.pdf).

1 PM, Seminar Room

Buffet lunch and registration.

2 PM, Lecture Theatre

Introduction to the Scottish Phylogeny Discussion Group.

**Daniel Barker, University of St Andrews**

2:10 PM, Lecture Theatre

Detecting incomplete lineage sorting and gene duplication in non-binary species trees.

**Dannie Durand, Carnegie Mellon University**

Sequence data have proved a powerful source of evidence for inferring species trees. However, gene duplication and loss, horizontal gene transfer, and incomplete lineage sorting can all result in an incongruent gene tree that disagrees with the species tree. Duplication, loss and transfer can be inferred using phylogenetic reconciliation, an approach based on formal comparison of gene and species tree topologies. However, reconciliation algorithms typically do not consider incomplete lineage sorting. While the assumption that incomplete lineage sorting does not occur may be justified in well resolved species trees with long branches, it is imperative to consider incomplete lineage sorting when the species tree is unresolved.

We present parsimony algorithms for reconciling a resolved gene tree with an unresolved species tree that take incomplete lineage sorting into account and can distinguish incomplete lineage sorting from other events that cause gene tree incongruence. I will discuss the application of our methods to resolve polytomies in species trees and to test the hypothesis that incomplete lineage sorting is a rare event in well resolved species lineages. Analyses of gene trees from five well-studied taxonomic groups will be presented as a practical demonstration of this approach. Our algorithms have been implemented in Notung [<http://www.cs.cmu.edu/~durand/Notung>], a freely available software tool.

3:15 PM, Lecture Theatre

Brachiopod phylogeny: current work.

**Bernie Cohen, University of Glasgow**

An amateur assessment of where deep metazoan phylogeny appears to be going and (if there's time) new ideas about shells and shell ribs.

3:35 PM, Seminar Room  
Tea/Coffee.

4 PM, Lecture Theatre

Automating phylogenomic analysis – some initial thoughts.

**Frank Wright, Biomathematics and Statistics Scotland**

4:20 PM, Lecture Theatre

iPhy: an Integrated Phylogenetics Workbench.

**Martin Jones, University of Edinburgh**

4:40 PM, Lecture Theatre

Population structure of bottlenose dolphins (*Tursiops truncatus*) in UK waters.

**Valentina Islas, University of St Andrews**

5:00 PM, Lecture Theatre

*Campylobacter*. Using phylogeny to understand the biology of a human zoonotic gastro-intestinal bacterial pathogen.

**Ken Forbes, University of Aberdeen**

5:20–5:30 PM

Meeting ends.

The meeting will be followed by dinner at a restaurant in St Andrews. Dinner is open to anyone registered for the meeting, but **requires separate booking in advance**. If you would like dinner, please tell Daniel Barker ([db60@st-andrews.ac.uk](mailto:db60@st-andrews.ac.uk)) before 13 June. Dinner will be charged at cost.

## Speakers

Bernie Cohen

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Dannie Durand

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## Organizer

Daniel Barker

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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>