

Introduction to Phylogenetic Analysis

Monday 21 – Tuesday 22 July, 2014

School of Biological Sciences



Overview

This workshop will provide an introduction to phylogenetic analysis, including practical exercises based on the software *MEGA* and *BEAST*. It is suitable for graduate students, postdoctoral researchers, and academics at all levels of experience. Prior knowledge of basic phylogenetics is helpful but not strictly necessary.

The workshop will be run by A/Prof Simon Ho, A/Prof Nate Lo, Sebastian Duchene, and Charles Foster from the *Molecular Ecology, Evolution, & Phylogenetics* (MEEP) lab in the School of Biological Sciences, University of Sydney. If you have questions about the workshop, please contact Simon (simon.ho@sydney.edu.au). All lectures and practicals will take place in Dry Lab 2 in the Charles Perkins Centre at the University of Sydney. Please refer to the map at the end of this programme.

Programme

The workshop will comprise a series of lectures and practical exercises. The first day will cover interpreting phylogenetic trees, sequence alignment, evolutionary models, and phylogenetic methods. The second day will focus on Bayesian phylogenetic analysis and will include molecular clocks, estimating timescales, coalescent theory, and demographic reconstruction.

The practical exercises will involve basic analyses of a prepared data sets using desktop PCs. Participants are welcome to bring their own laptops, provided that you have installed the software that will be used in the practical sessions. We will be using free software that can be installed on PC, Mac, and UNIX platforms.

Programme

Monday 21 July: Introduction to phylogenetic analysis

09.30 – 09.45	Welcome	Simon Ho
09.45 – 10.30	Lecture: Introduction to phylogenetic analysis	Nathan Lo
10.30 – 11.00	Practical: Sequence alignment in <i>MEGA</i>	
--- Morning tea ---		
11.15 – 11.45	Lecture: Evolutionary Models	Sebastián Duchêne
11.45 – 12.15	Practical: Model selection in <i>MEGA</i>	
--- Lunch break ---		
13.30 – 14.30	Lecture: Phylogenetic Methods	Simon Ho
14.30 – 16.30	Practical: Phylogenetic analysis in <i>MEGA</i>	

Tuesday 22 July: Bayesian phylogenetic analysis

09.30 – 10.15	Lecture: Bayesian phylogenetic analysis	Simon Ho
10.15 – 11.00	Lecture: Rates and timescales	Sebastián Duchêne
--- Morning tea ---		
11.15 – 12.30	Practical: Molecular-clock analysis in <i>BEAST</i>	
--- Lunch break ---		
13.30 – 14.30	Lecture: Analysing populations	Simon Ho
14.30 – 16.30	Practical: Inferring population history in <i>BEAST</i>	

Useful References

Introductory books

- *The Phylogenetic Handbook*
Lemey, Salemi, & Vandamme (2009) Cambridge University Press.
- *Reading the Story in DNA*
Bromham (2008) Oxford University Press.
- *Inferring Phylogenies*
Felsenstein (2003) Sinauer Associates.
- *Molecular Evolution: A Phylogenetic Approach*
Page & Holmes (1998) Wiley-Blackwell.

Bayesian phylogenetic analysis

- *Bayesian inference of phylogeny: a non-technical primer*
Archibald, Mort, & Crawford (2003) *Taxon* 52: 187-191.
- *Bayesian phylogenetics with BEAUti and the BEAST 1.7*
Drummond, Suchard, Xie, & Rambaut (2012) *Mol Biol Evol* 29:1969-1973.
- *BEAST: Bayesian evolutionary analysis by sampling trees*
Drummond & Rambaut (2007) *BMC Evol Biol* 7: 214.

Molecular clocks and calibrations

- *Estimating evolutionary timescales using the molecular clock*
Ho & Duchêne (2014) *Mol Ecol* submitted.
- *The changing face of the molecular evolutionary clock*
Ho (2014) *Trends Ecol Evol* in press.
- *Accounting for calibration uncertainty in phylogenetic estimation of evolutionary divergence times*
Ho & Phillips (2009) *Syst Biol* 58: 367-380.

Demographic reconstruction

- *Skyline-plot methods for estimating demographic history from nucleotide sequences*
Ho & Shapiro (2011) *Mol Ecol Res* 11: 423-434.
- *Bayesian inference of population size from multiple loci*
Heled & Drummond (2008) *BMC Evol Biol* 8: 289.
- *Bayesian coalescent inference of past population dynamics from molecular sequences*
Drummond, Rambaut, Shapiro, & Pybus (2005) *Mol Biol Evol* 22: 1185-1192.

Gene trees and species trees

- *Gene tree discordance, phylogenetic inference and the multispecies coalescent*
Degnan & Rosenberg (2009) *Trends Ecol Evol* 24: 332-340.

Workshop Location

The workshop will be held in the Dry Lab 2 in the Charles Perkins Centre, University of Sydney. From the main entrance to the building, the lab is behind the reception desk and to the right.



Places to eat

On campus

- Taste Baguette (Charles Perkins Centre)
- Various food outlets (Manning Building)
- Courtyard Café (Holme Building)

Near campus

- Lots of restaurants and cafes along Missenden Rd and King St, Newtown

MOLECULAR ECOLOGY, EVOLUTION, & PHYLOGENETICS LABORATORY



Art by Ainsley Seago

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