

Introduction to Phylogenetic Analysis



Thursday 10 July, 2014



Overview

This workshop will provide an introduction to the principles and practice of molecular phylogenetic analysis. The workshop is suitable for beginners and will comprise a series of lectures and practical exercises. Using two popular packages for phylogenetic analysis, *MEGA* and *BEAST*, participants will learn how to select models, infer phylogenies, and estimate timescales from DNA sequence data.

The workshop will be held in a computing lab in the **Charles Perkins Centre** at the University of Sydney. It will be run by A/Prof Simon Ho (simon.ho@sydney.edu.au), with assistance from Daej Arab. The workshop will involve a series of lectures and practicals. The practical exercises will involve basic analyses of a prepared data sets using desktop PCs. We will be using free phylogenetic software that can be installed on PC, Mac, and UNIX platforms.

Programme

09.00 – 09.15	Arrival and set-up
09.15 – 09.30	Introduction to the workshop
09.30 – 10.00	Lecture: Principles of phylogenetic analysis
10.00 – 10.15	Practical: Sequence alignment
	<i>Tea break</i>
10.30 – 11.15	Lecture: Phylogenetic methods and models
11.15 – 12.30	Practical: Maximum parsimony & maximum likelihood
	<i>Lunch break</i>
13.30 – 14.30	Lecture: Bayesian phylogenetic analysis
14.30 – 16.30	Practical: Bayesian analysis and molecular clocks

Useful references

Introductory books on phylogenetics

- *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

- *Molecular-clock models for estimating evolutionary rates and timescales*
Ho & Duchêne (2014) *Mol Ecol* submitted (email to request preprint).
- *The changing face of the molecular clock*
Ho (2014) *Trends Ecol Evol* revision submitted (email to request preprint).
- *Accounting for calibration uncertainty in phylogenetic estimation of evolutionary divergence times*
Ho & Phillips (2009) *Syst Biol* 58: 367-380.