Introduction to Phylogenetic Analysis

Thursday 1 – Friday 2 October, 2015

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 essential.

The workshop will be run by Associate Professor Simon Ho and Dr Sebastián Duchêne from the School of Biological Sciences, University of Sydney.

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. We will be using free software that can be installed on PC, Mac, and UNIX platforms.

Workshop Programme

Thursday 1 October: Introduction to phylogenetic analysis

09.00 – 09.10	Welcome	
09.10 – 10.00	Lecture 1: Introduction to phylogenetic analysis	Simon Ho
10.00 – 10.30	Practical 1a: Sequence alignment in *MEGA*	
10.30 – 11.00	Lecture 2: Evolutionary Models	Sebastián Duchêne
	--- Morning tea ---	
11.15 – 12.00	Practical 1b: Model selection in *MEGA*	
12.00 – 13.00	Lecture 3: Phylogenetic methods	Simon Ho
	--- Lunch break ---	
14.00 – 16.00	Practical 1c: Phylogenetic analysis in *MEGA*	

16.15   *Seminar: Evolutionary insights from molecular clocks*
Simon Ho

Friday 2 October: Bayesian phylogenetic analysis

09.15 – 10.15	Lecture 4: Bayesian phylogenetic analysis	Simon Ho
10.15 – 11.00	Lecture 5: Rates and timescales	Sebastián Duchêne
	--- Morning tea ---	
11.15 – 13.00	Practical 2: Molecular-clock analysis in *BEAST*	
	--- Lunch break ---	
14.00 – 14.45	Lecture 6: Analysing populations	Simon Ho
14.45 – 16.30	Practical 3: Inferring population history in *BEAST*	

Useful References

Reference books

- *Bayesian Phylogenetics: Methods, Algorithms, and Applications*
Chen, Kuo, & Lewis (2014) Chapman & Hall / CRC.

- *Molecular Evolution: A Statistical Approach*
Yang (2014) Oxford University Press.

- *The Phylogenetic Handbook*
Lemey, Salemi, & Vandamme (2009) Cambridge University Press.

- *Reading the Story in DNA (new version coming out soon)*
Bromham (2008) Oxford University Press.

- *Inferring Phylogenies*
Felsenstein (2003) Sinauer Associates.

Molecular clocks and calibrations

- *Estimating evolutionary timescales using the molecular clock*
Ho & Duchêne (2014) *Mol Ecol* 23: 5947–5965.

- *The changing face of the molecular evolutionary clock*
Ho (2014) *Trends Ecol Evol* 29: 496–503.

- *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.