

Introduction to Phylogenetic Analysis

8–9 September, 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 Rob Lanfear (Macquarie University) and Simon Ho (University of Sydney), with assistance from Charles Foster and Jun Tong (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

8 September: Introduction to phylogenetic analysis (Rob Lanfear)

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| 09.00 – 09.10 | Welcome |
| 09.10 – 10.00 | Lecture 1: Introduction to phylogenetic analysis |
| 10.00 – 10.30 | Lecture 2: Alignment |
| 10.30 – 11.00 | Practical: Automated sequence alignment |
| <i>--- Morning tea ---</i> | |
| 11.15 – 12.00 | Practical: Manual refining the alignment |
| 12.00 – 13.00 | Lecture 3: Phylogenetic methods |
| <i>--- Lunch break ---</i> | |
| 14.00 – 16.00 | Practical: Phylogenetic analysis |

9 September: Bayesian phylogenetic analysis (Simon Ho)

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| 09.30 – 10.15 | Lecture 4: Bayesian phylogenetic analysis |
| 10.15 – 11.00 | Lecture 5: Rates and timescales |
| <i>--- Morning tea ---</i> | |
| 11.15 – 13.00 | Practical 2: Molecular-clock analysis |
| <i>--- Lunch break ---</i> | |
| 14.00 – 14.30 | Lecture 6: Analysing populations |
| 14.30 – 16.00 | Practical 3: Inferring population history |

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*
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.



CAMPUS MAP

