

# Introduction to Phylogenetic Analysis

**Monday 18 – Tuesday 19 July, 2016**

**School of Life and Environmental Sciences**



## Overview

This free workshop will provide an introduction to phylogenetic analysis, including practical exercises based on the software *MEGA*, *MrBayes*, and *BEAST*. It is suitable for graduate students and postdoctoral researchers. Prior knowledge of basic phylogenetics is helpful but not essential. The workshop will be run by Prof. Simon Ho, A/Prof. Nathan Lo, Dr David Duchêne, and Andrew Ritchie from the School of Life and Environmental 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 models and priors, molecular clocks, and estimating timescales.

## Computing

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. The workshop venue is equipped with dual-boot Mac computers. You are welcome to use your own laptop, but please install *MEGA* 6 or 7, *MrBayes* 3.2, *BEAST* 1.8, *Tracer*, and *FigTree* prior to the workshop.

## Venue

All components of the workshop, including the lectures and practical exercises, will be held in the Robert Brown Computing Laboratory in the Macleay Building A12, University of Sydney. This building is shown in red in the map at the end of this programme.

Tea, coffee, biscuits, and fruit will be provided during the morning tea break, and will be available throughout the practical sessions. However, please do not consume food or drink inside the computing laboratory.

Lunch will not be provided, but we can recommend the Courtyard Café (sandwiches, salads, pasta) in the nearby Holme Building. There are also some good options within a 10-minute walk towards Broadway (Eat Falafel, Vietnamese Rolls) and on Glebe Point Rd.

## Workshop Programme

### Monday 18 July: Introduction to phylogenetic analysis

09.15 – 09.30	Arrival	
09.30 – 09.40	Welcome	Simon Ho
09.40 – 10.30	Lecture 1.1: Introduction to molecular phylogenetics	Nathan Lo
10.30 – 11.00	Practical 1a: Sequence alignment in <i>MEGA</i>	
	--- Morning tea ---	
11.20 – 12.00	Lecture 1.2: Evolutionary models	David Duchêne
12.00 – 12.45	Practical 1b: Model selection in <i>MEGA</i>	
	--- Lunch break ---	
13.30 – 14.30	Lecture 1.3: Phylogenetic methods	Simon Ho
14.30 – 17.00	Practical 1c: Phylogenetic analysis in <i>MEGA</i>	

### Tuesday 19 July: Bayesian phylogenetic analysis

09.15 – 09.30	Arrival	
09.30 – 10.30	Lecture 2.1: Bayesian phylogenetic analysis	Simon Ho
10.30 – 11.00	Lecture 2.2: Models and priors	David Duchêne
	--- Morning tea ---	
11.20 – 12.45	Practical 2: Bayesian analysis using <i>MrBayes</i>	
	--- Lunch break ---	
13.30 – 14.30	Lecture 2.3: Rates and timescales	Simon Ho
14.30 – 17.00	Practical 3: Molecular dating using <i>BEAST</i>	

## Useful References

### Reference books

- *An Introduction to Molecular Evolution and Phylogenetics*  
Bromham (2016) Oxford University Press.
- *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.
- *Inferring Phylogenies*  
Felsenstein (2003) Sinauer Associates.

### 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.
- *MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space*  
Ronquist *et al.* (2012) *Syst Biol* 61: 539–542.

### Molecular clocks and calibrations

- *Bayesian molecular clock dating of species divergences in the genomics era*  
dos Reis, Donoghue, & Yang (2016) *Nat Rev Genet* 17: 71–80.
- *Estimating evolutionary timescales using the molecular clock*  
Ho & Duchêne (2014) *Mol Ecol* 23: 5947–5965.
- *Accounting for calibration uncertainty in phylogenetic estimation of evolutionary divergence times*  
Ho & Phillips (2009) *Syst Biol* 58: 367–380.

CAMPERDOWN AND DARLINGTON CAMPUS MAP

