

# Sydney Phylogenetics Workshop

Monday 17 – Wednesday 19 July, 2017



## Overview

This free 3-day workshop will provide an introduction to phylogenetic analysis, including practical exercises based on the software *MEGA* and *BEAST*. It is suitable for graduate students and postdoctoral researchers. Prior knowledge of basic phylogenetics is helpful but not essential.

The workshop will comprise a series of lectures and practical exercises. The first day will cover interpreting phylogenetic trees, molecular data, sequence alignment, evolutionary models, and phylogenetic methods. The second day will provide an introduction to Bayesian phylogenetic analysis and will include Bayesian statistics, priors, and molecular dating. The third day will cover more advanced topics, including phylogenomics and demographic analysis.

## Instructors

The workshop will be run by members of the **Molecular Ecology, Evolution, and Phylogenetics Laboratory** in the School of Life and Environmental Sciences, University of Sydney. The lead organisers are Prof. Simon Ho and Dr David Duchêne. The teaching team includes A/Prof. Nate Lo, Dr Mark de Bruyn, Andrew Ritchie, Zoe Patterson Ross, and Nik Mather.

## Venue

The workshop will be held in Seminar Room 022 of the New Law Building Annex at the University of Sydney (this is the red building in the map at the end of this programme). This room can be found two floors below ground level.

Lunch will not be provided, but the building has a café and coffee outlet on the ground floor. Vending machines are located immediately outside the workshop room. A list of good nearby cafés and restaurants will be provided.

## Computing

The practical exercises will involve basic analyses of prepared data sets. You will need to bring your own laptop. Please download and install *MEGA* (version 6 or 7), *BEAST* 1.8.X, *Tracer*, and *FigTree* prior to the workshop.

## Registration

The workshop is free to attend, but there will be a limit of 40 participants. For enquiries, please contact Simon Ho ([simon.ho@sydney.edu.au](mailto:simon.ho@sydney.edu.au)).

## Workshop Programme

### Monday 17 July: Introduction to phylogenetic analysis

09.15 – 09.30	Arrival and set-up	
09.30 – 09.40	Welcome	Simon Ho
09.40 – 10.30	Lecture 1.1: Introduction to molecular phylogenetics	Nate Lo
10.30 – 11.00	Practical 1a: Sequence alignment in <i>MEGA</i>	Nate Lo
	--- Break ---	
11.15 – 12.00	Lecture 1.2: Evolutionary models	Simon Ho
12.00 – 12.30	Lecture 1.3: Phylogenetic data	Mark de Bruyn
	--- Lunch break ---	
13.15 – 14.00	Lecture 1.4: Phylogenetic methods	Simon Ho
14.00 – 17.00	Practical 1b: Model selection and phylogenetics in <i>MEGA</i>	Zoe Patterson Ross & Nik Mather

### Tuesday 18 July: Bayesian phylogenetics and molecular dating

09.30 – 10.30	Lecture 2.1: Bayesian phylogenetic analysis	Simon Ho
10.30 – 11.00	Lecture 2.2: Models and priors	David Duchêne
	--- Break ---	
11.15 – 12.30	Practical 2a: Bayesian analysis using <i>BEAST</i>	David Duchêne
	--- Lunch break ---	
13.15 – 14.00	Lecture 2.3: Molecular dating	Simon Ho
14.00 – 14.30	Lecture 2.4: Calibrating the molecular clock	David Duchêne
14.30 – 17.00	Practical 2b: Molecular dating using <i>BEAST</i>	David Duchêne

### Wednesday 19 July: Phylogenomics and populations

09.30 – 10.00	Lecture 3.1: Phylogenomics	Simon Ho
10.00 – 10.30	Lecture 3.2: Analysing populations	Simon Ho
10.30 – 11.00	Lecture 3.3: Tip-dating analysis	David Duchêne
	--- Break ---	
11.15 – 12.30	Practical 3: Population analysis using <i>BEAST</i>	Andrew Ritchie
	--- Lunch break ---	
13.15 – 15.00	Free time for consultation and discussion	

## Useful Readings

### Reference books

- *An Introduction to Molecular Evolution and Phylogenetics*  
Bromham (2016) Oxford University Press.
- *Molecular Evolution: A Statistical Approach*  
Yang (2014) Oxford University Press.
- *The Phylogenetic Handbook*  
Lemey, Salemi, & Vandamme (2009) Cambridge University Press.
- *Bayesian Phylogenetics: Methods, Algorithms, and Applications*  
Chen, Kuo, & Lewis (2014) Chapman & Hall / CRC.

### Molecular phylogenetics and Bayesian inference

- *Molecular phylogenetics: principles and practice*  
Yang & Rannala (2012) *Nat Rev Genet* 13: 303–314.
- State-of-the-art methodologies dictate new standards for phylogenetic analysis  
Anisimova et al. (2013) *BMC Evol Biol*, 13: 161.
- *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 et al. (2012) *Mol Biol Evol* 29:1969-1973.

### Molecular dating

- *A practical guide to molecular dating*  
Sauquet (2013) *C R Palevol*, 12: 355–367.
- *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.
- *Inferences from tip-calibrated phylogenies: a review and a practical guide*  
Rieux & Balloux (2016) *Mol Ecol*, 25: 1911–1924.

