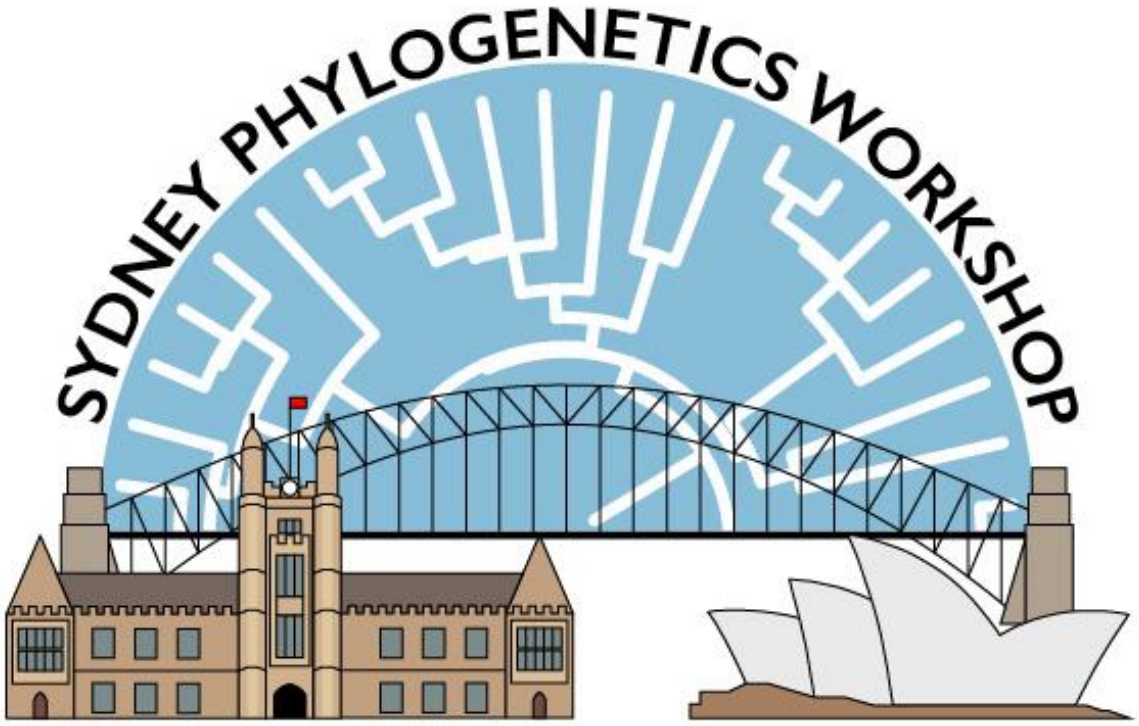
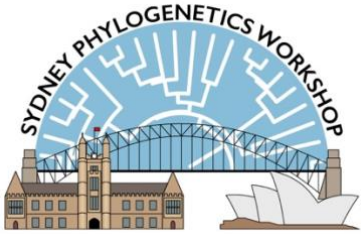


17th annual workshop

25–26 June 2026

DRAFT PROGRAMME

THE UNIVERSITY OF SYDNEY



Overview

Introduction

This 2-day workshop will provide an introduction to phylogenetic analysis, including practical exercises based on the software *MEGA*, *IQ-TREE*, *ASTRAL*, and *BEAST2*. It is aimed at early career researchers (students and postdocs), but other attendees are welcome. Prior knowledge of basic phylogenetics, or at least familiarity with molecular data and interpreting phylogenetic trees, is very helpful.

The workshop will comprise a series of lectures and practical exercises. Day 1 will deal with interpreting phylogenetic trees, molecular evolution, phylogenetic data, sequence alignment, evolutionary models, and phylogenetic methods. Day 2 will provide an introduction to phylogenomics, Bayesian phylogenetic analysis, and estimating timescales.

Venue

The workshop will be held on the main Camperdown campus of the University of Sydney. If you are travelling from outside Sydney, please organise your own travel and accommodation. Light catering will be provided, including morning tea and lunch. Tea and coffee will be available throughout the day.

Online attendance

Attendees can join the workshop online via Zoom. Online participants will be able to view all of the lectures and can complete the practical exercises on their own computers. Although the workshop instructors will not be able to supervise the practical exercises for online attendees, we will attempt to answer any questions posted in the Zoom chat.

Computing

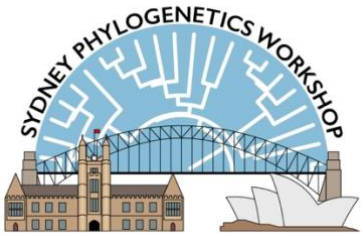
The practical exercises will involve basic analyses of prepared data sets. Please bring your own laptop computer for these exercises. We strongly recommend installing the following software prior to the start of the workshop: *MEGA* v12, *IQ-TREE* v2.4.0, *ASTRAL-III* v5.7.8, *BEAST2* v2.7.7, *Tracer* v1.7.2, and *FigTree* v1.4.4. Please note that these are not necessarily the very latest versions of the software.

Resources

Workshop materials, including lecture slides and files for the practical exercises, will be available on Github prior to the start of the workshop. Answers to the practical exercises will also be made available on Dropbox to all attendees.

Registration

This is a free workshop but is limited to 30 in-person attendees and 80 online attendees. Priority is given to applicants who are: at early career stages (students and postdocs); likely to derive the most benefit in the near future; and from the Asia-Pacific region. Applications for the workshop will close on Friday 29 May.



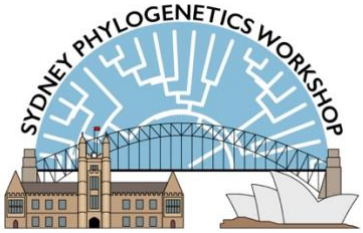
Workshop schedule

Thursday 25 June

09.00 – 09.30	Arrival and set-up
09.30 – 09.40	Welcome
09.40 – 10.30	Lecture 1.1: Introduction to molecular phylogenetics
10.30 – 11.00	Practical 1.1: Sequence alignment (*MEGA*)
	--- Break ---
11.15 – 12.00	Lecture 1.2: Evolutionary models
12.00 – 12.30	Lecture 1.3: Phylogenetic data
	--- Lunch break ---
13.15 – 14.00	Lecture 1.4: Phylogenetic methods
14.00 – 17.00	Practical 1.2: Model selection and phylogenetic analysis (*MEGA* and *IQ-TREE*)

Friday 26 June

09.00 – 09.45	Lecture 2.1: Phylogenomics
09.45 – 11.00	Practical 2.1: Gene trees and species trees (*ASTRAL*)
	--- Break ---
11.15 – 12.30	Lecture 2.2: Bayesian phylogenetics I
	--- Lunch break ---
13.15 – 13.45	Lecture 2.3: Bayesian phylogenetics II
13.45 – 14.30	Lecture 2.4: Molecular dating
14.30 – 17.00	Practical 2.2: Bayesian phylogenetics and molecular dating (*BEAST*)



Instructors

The workshop is organised and hosted by the Molecular Ecology, Evolution, and Phylogenomics Lab at the University of Sydney. Members of the research group will deliver the lectures and supervise the practical exercises.

Simon Ho is a Professor of Molecular Evolution with research interests in molecular clocks, evolutionary rates, phylogenomics, genomic evolution, and molecular ecology. He edited the book *The Molecular Evolutionary Clock*, published by Springer in 2020.

Manuela Cascini is a postdoctoral researcher with interests in phylogenomics, molecular evolution, and conservation genomics. She is integrating genomic, morphological, and bioinformatic approaches to investigate evolutionary rates across different parts of the tree of life.

Younis Menkara is a PhD student interested in the evolution, systematics, and taxonomy of marine fishes. He has expertise in genomic analysis, morphological study, and working with museum specimens.

Eilish McMaster is a PhD student working on population genomics of Australian flowering plants, particularly threatened species. She has expertise in population genetics and genomics.

Saphira Bloom-Quinn is a PhD student working on the phylogenomics of mosses. She has expertise in phylogenetic analysis, bryology, and herbarium collections.

Maxim Adams is a PhD student working on the evolution, ecology, and conservation of island species, focusing on the invertebrates of the Pacific Ocean. He has expertise in genomics, molecular evolution, and molecular ecology.

Recommended readings

Reference books

- *Phylogenetics in the Genomic Era*
  Scornavacca, Delsuc, & Galtier (eds) (2020) No commercial publisher | Open access
- *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
- *The Molecular Evolutionary Clock: Theory and Practice*
  Ho (ed.) (2020) Springer

Molecular phylogenetics and Bayesian inference

- *Phylogenetic tree building in the genomic age*
  Kapli et al. (2020) *Nat Rev Genet* 21: 428–444
- *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

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.
- *Bayesian molecular dating: opening up the black box*
  Bromham et al. (2018) *Biol Rev* 93: 1165–1191.

Phylogenomics

- *Estimating phylogenetic trees from genome-scale data*
  Liu et al. (2015) *Ann N Y Acad Sci*, 1360: 36–53.