

Introduction to Phylogenomics

Tuesday 1 December, 2026

Overview

This half-day workshop will provide an introduction to phylogenomics. It will comprise a series of lectures and practical exercises that will cover the interpretation of phylogenetic trees, data types, evolutionary models, maximum likelihood, gene trees vs species trees, and phylogenomic analysis. The workshop will include short practical exercises based on the software *MEGA*, *IQ-TREE*, and *ASTER*. Prior knowledge of basic phylogenetics, or at least familiarity with molecular data and interpreting phylogenetic trees, is very helpful.

Instructors

The workshop will be run by Simon Ho and Manuela Cascini from the Molecular Ecology, Evolution, and Phylogenomics Laboratory in the School of Life and Environmental Sciences, University of Sydney.

Venue

The workshop will be held at the University of Wollongong, in association with the AES×SASB Conference.

Resources and computing

Workshop materials, including lecture slides and files for the practical exercises, will be available on [Github](#) prior to the start of the workshop.

The practical exercises will involve basic analyses of prepared data sets. Please bring your own laptop to the workshop, with the following software installed: [MEGA 12](#), [IQ-TREE 3](#), [ASTER](#), and [FigTree](#).

Schedule

13.00 – 13.10	Introduction to the workshop
13.10 – 14.00	Lecture 1: Molecular phylogenetics
14.00 – 15.00	Practical exercise 1: Phylogenetic analysis using <i>MEGA</i>
	--- Afternoon tea ---
15.15 – 16.00	Lecture 2: Phylogenomics
16.00 – 17.00	Practical exercise 2: Phylogenomic analysis using <i>IQ-TREE</i> and <i>ASTER</i>