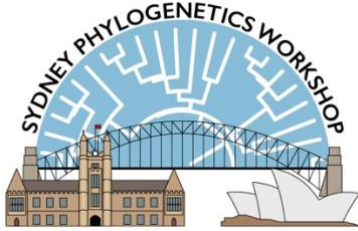# 14th annual workshop

27–28 July 2023

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*, and *BEAST 2*. It is primarily 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, phylogenetic methods, and phylogenomics. Day 2 will provide an introduction to phylogenetic analysis using *IQ-TREE*, Bayesian phylogenetic analysis, and estimating timescales.

Venue

The workshop will be held in the Refectory in the Main Building, located on the main Camperdown campus of the University of Sydney. Please be aware that the university has more than one "Refectory"! If you are travelling from outside Sydney, please organise your own accommodation. Light catering will be provided during the workshop.

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*, *IQ-TREE* (version 2), *BEAST 2* (version 2.4.8 or higher), *Tracer*, and *FigTree*.

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 workshop has space for 40 attendees, with 20 places reserved for students and postdocs and 15 places for members of the Genetics Society of Australasia. Registration has closed.

Funding

The 2023 Sydney Phylogenetics Workshop is supported by the Genetics Society of Australasia.
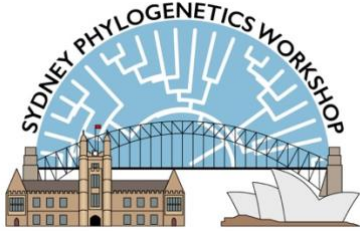
Instructors

Yasmin Asar, Simon Ho, Karen Lopez, Toby Kovacs, and Maxim Adams (University of Sydney)

The workshop is hosted by the Molecular Ecology, Evolution, and Phylogenetics Lab at the University of Sydney.
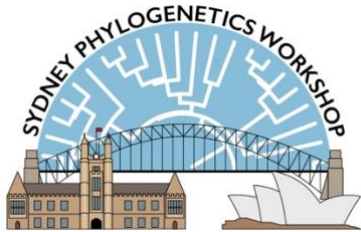
Yasmin Asar is a PhD student working on evolutionary simulations and joint analyses of molecular and morphological data, with a focus on the evolution of flowering plants. She is jointly supervised by Simon Ho and Hervé Sauquet (Royal Botanic Gardens, Sydney).

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

Additional support during the practical exercises will be provided by **Karen Lopez** (postdoctoral research associate) and **Toby Kovacs** (PhD student) from the Molecular Ecology, Evolution, and Phylogenetics Lab.

Fred Jaya (Australian National University)

Fred Jaya is a PhD student under the supervision of Rob Lanfear and Minh Bui at the Australian National University. He was recently a Research Assistant in the Molecular Ecology, Evolution, and Phylogenetics Lab at the University of Sydney. He has a range of experience in computational biology, process automation, and pipeline development. Fred has worked on various projects involving population genetics, biogeography, epidemiology, and genomics.

Workshop Programme

Thursday 27 July

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	Yasmin Asar
10.30 – 11.00	Practical 1.1a: Sequence alignment in *MEGA*	
	--- Break ---	
11.15 – 12.00	Lecture 1.2: Evolutionary models	Simon Ho
12.00 – 12.30	Lecture 1.3: Phylogenetic data	Fred Jaya
	--- Lunch break ---	
13.15 – 14.00	Lecture 1.4: Phylogenetic methods	Simon Ho
14.00 – 14.30	Lecture 1.5: Phylogenomics	Simon Ho
14.30 – 17.00	Practical 1.1b: Model selection and phylogenetics in *MEGA*	
	Optional Practical 1.2: Phylogenomic analysis using *ASTRAL*	

Friday 28 July

09.15 – 09.30	Arrival	
09.30 – 10.30	Lecture 2.1: Phylogenetic analysis with *IQ-TREE*	Fred Jaya
10.30 – 11.00	Practical 2.1: *IQ-TREE* workshop tutorial	
	--- Break ---	
11.15 – 12.30	Practical 2.1: *IQ-TREE* workshop tutorial (continued)	
	--- Lunch break ---	
13.15 – 14.15	Lecture 2.2: Bayesian phylogenetics	Simon Ho
14.20 – 15.00	Lecture 2.3: Molecular dating	Simon Ho
15.00 – 17.00	Practical 2.2: Bayesian analysis and molecular dating in *BEAST*	
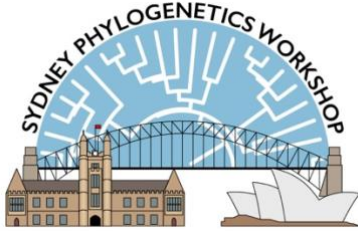
Recommended Readings

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.