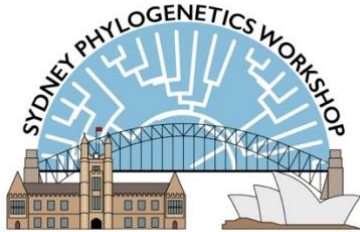


15th annual workshop

27–28 June 2024



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 *BEAST 2*. 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 at the University of Sydney. If you are travelling from outside Sydney, please organise your own travel and accommodation. Light catering, including morning tea, lunch, and afternoon tea, will be provided.

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

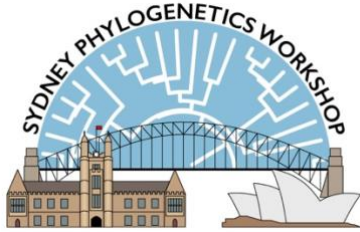
Workshop materials, including lecture slides and files for the practical exercises, will be available on [Github](#) prior to the start of the workshop. Answers to the practical exercises will also be made available on Dropbox to all attendees.

Registration

This is a free workshop but is limited to 55 attendees. Priority is given to applicants at early career stages (students and postdocs), applicants who will benefit the most from the workshop in the near future, and applicants from institutions in the Association of Pacific Rim Universities. Applications for the workshop closed on Friday 24 May.

Funding

The 2024 Sydney Phylogenetics Workshop is supported by the Association of Pacific Rim Universities.



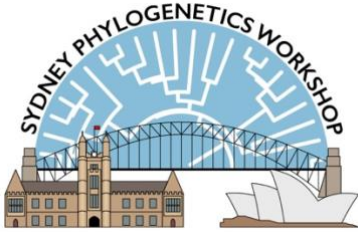
Workshop schedule

Thursday 27 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 (<i>MEGA</i>)
--- 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 (<i>MEGA</i> and <i>IQ-TREE</i>)

Friday 28 June

09.00 – 09.45	Lecture 2.1: Phylogenomics
09.45 – 11.00	Practical 2.1: Gene trees and species trees (<i>ASTRAL</i>)
--- 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 (<i>BEAST</i>)



Instructors

Maxim Adams, Simon Ho, Karen López, Toby Kovacs, Tony Rayos, and Younis Menkara

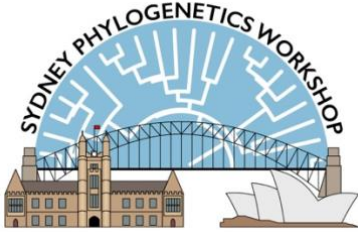
The workshop is hosted by the Molecular Ecology, Evolution, and Phylogenetics Lab at the University of Sydney.

Maxim Adams is a Research Assistant looking at the evolutionary origins of multiple sex chromosome systems in termites. He recently completed an Honours project on the biogeography, systematics and conservation genetics of Australian *Panesthia* cockroaches.

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 late 2020.

Karen López is a Postdoctoral Research Associate interested in the evolutionary causes of lineage diversification and morphological change, using molecular phylogenetic and phylogenomic hypotheses as a baseline. Karen works with several groups of organisms such as beetles, dragonflies, fairy shrimps, and angiosperms. Recently, she has been exploring the use of meta-analytical approaches to investigate the biotic or abiotic factors that affect rates of morphological evolution in various groups of organisms.

Additional support during the practical exercises will be provided by PhD students **Toby Kovacs, Tony Rayos, and Younis Menkara**.



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.