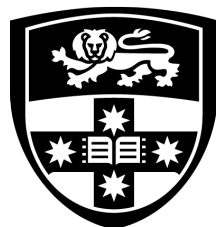
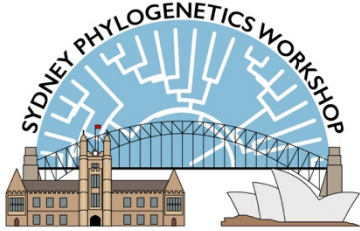


12th annual workshop

29–30 July 2021



THE UNIVERSITY OF
SYDNEY



Overview

Introduction

This free 2-day workshop will provide an introduction to phylogenetic analysis, including practical exercises based on the software *MEGA*, *IQ-TREE*, *BEAST 2*, and *ASTRAL*. It is primarily aimed at research students and postdoctoral researchers in the Asia-Pacific region, but other prospective attendees are welcome. Prior knowledge of basic phylogenetics is very helpful but not essential.

The workshop will comprise a series of lectures (delivered in Zoom webinar form) and 'take-home' practical exercises (notes provided). Day 1 will cover interpreting phylogenetic trees, molecular evolution, molecular data, sequence alignment, evolutionary models, phylogenetic methods, and phylogenetic analysis using *IQ-TREE*. The second day will provide an introduction to Bayesian phylogenetic analysis and will include models and priors, molecular clocks, estimating timescales, and phylogenomics.

Computing

The practical exercises will involve basic analyses of prepared data sets. Please download and install [MEGA](#) (version 7 or higher), [IQ-TREE](#) (version 2), [BEAST 2](#) (version 2.4.8 or higher), [Tracer](#), [FigTree](#), and [ASTRAL](#) prior to the workshop. Please note that the practical exercises will not be run as live sessions.

Resources

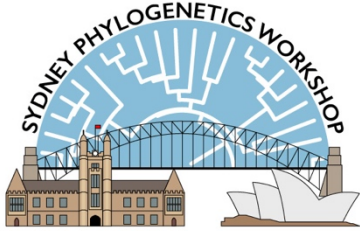
Workshop materials, including lecture slides and files for the practical exercises, will be available on [Github](#). Talk recordings and answers to the practical exercises will also be made available on Dropbox to all registered attendees of the workshop.

Further information

News about upcoming workshops can be found on our [website](#). Please contact Simon Ho (simon.ho@sydney.edu.au) if you have any questions or to register your interest for upcoming workshops.

Schedule

The Zoom webinar will commence at 11 am on Thursday 29 July (Sydney, GMT +10) each day and will run for approximately 5 hours (including short breaks). The timing of the workshop is most suitable for attendees in the Asia-Pacific region (e.g., it will commence at 9 am for attendees in Beijing and 1 pm for attendees in Auckland).



Speakers

Yasmin Asar, Simon Ho, Fred Jaya, and Mezzalina Vankan (University of Sydney)

The workshop is hosted by the Molecular Ecology, Evolution, and Phylogenetics research group at the University of Sydney. Several of the talks will be given by members of the group.

Yasmin 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.

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

Fred is a Research Assistant with a range of experience in computational biology, process automation, and pipeline development. Previously, he worked on various projects involving population genetics, biogeography, and epidemiology.

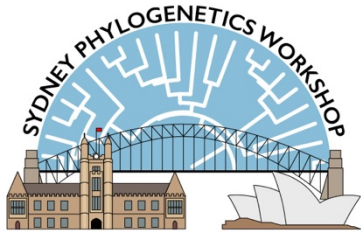
Mezzalina is an Honours student with interests in phylogenomics, phylogenetic signals in genome-scale data, and the evolution of Australian marsupials.

Minh Bui (Australian National University)

Minh leads the Computational Phylogenomics Lab, jointly affiliated with the Research School of Computer Science and Research School of Biology, Australian National University. His lab focuses on efficient bioinformatic methods, statistical models of molecular evolution, and algorithms and high-performance computing techniques for phylogenetics from ultra-large genomic data. Minh is the developer of the widely used phylogenetics software *IQ-TREE*.

David Duchêne (University of Copenhagen)

David is a Carlsberg Foundation research fellow at the University of Copenhagen. His research focuses on assessing and implementing models of molecular evolution on whole-genome data. His work examines the molecular (macro)evolution of a broad range of taxa. David also develops tools for improving modelling and inferences of the Tree of Life.



Workshop Programme

Thursday 29 July: Introduction to phylogenetic analysis

11.00 – 11.10	Welcome	Simon Ho
11.10 – 11.50	Lecture 1.1: Introduction to molecular phylogenetics	Yasmin Asar
12.00 – 12.45	Lecture 1.2: Evolutionary models	Simon Ho
13.00 – 13.45	Lecture 1.3: Phylogenetic data	Fred Jaya
14.00 – 14.45	Lecture 1.4: Phylogenetic methods	Simon Ho
15.00 – 15.45	Seminar: Phylogenetic analysis with <i>IQ-TREE</i>	Minh Bui
15.45 – 16.00	Additional time for questions	

Practical 1.1: Sequence alignment and phylogenetic analysis using *MEGA*

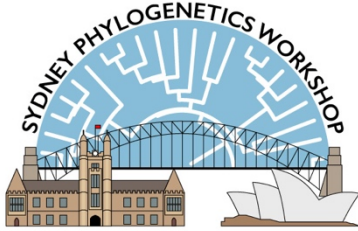
Practical 1.2: *IQ-TREE* workshop tutorial

Friday 30 July: Bayesian phylogenetics, molecular dating, and phylogenomics

11.00 – 11.45	Lecture 2.1: Bayesian phylogenetic analysis	Simon Ho
12.00 – 12.45	Lecture 2.2: MCMC sampling	Simon Ho
13.00 – 13.45	Lecture 2.3: Molecular dating	Simon Ho
14.00 – 14.30	Lecture 2.4: Calibrating the molecular clock	David Duchêne
14.45 – 15.15	Lecture 2.5: Phylogenomics	Mezzalina Vankan
15.15 – 16.00	Additional time for questions	

Practical 2.1: Bayesian analysis and molecular dating using *BEAST*

Practical 2.2: Phylogenomic analysis using *ASTRAL*



Useful 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.
- *Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10*
Suchard et al. (2018) *Virus Evol* 4: vey016.

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.