13ᵗʰ annual workshop
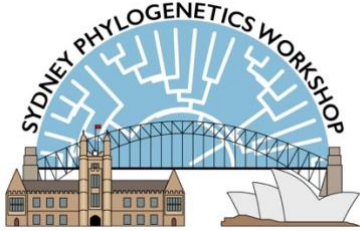
27–29 July 2022

Overview

Introduction

This 3-day online 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 early career researchers (research students and postdoctoral researchers) in the Asia-Pacific region, but other attendees are welcome. Prior knowledge of basic phylogenetics is very helpful but not essential.

The workshop will comprise a series of lectures and supervised practical exercises, all delivered via Zoom. Day 1 will cover interpreting phylogenetic trees, molecular evolution, molecular data, sequence alignment, evolutionary models, and phylogenetic methods. Day 2 will cover maximum-likelihood analysis using *IQ-TREE* and introductory Bayesian phylogenetics. Day 3 will cover molecular clocks, estimating timescales, and phylogenomics.

Computing

The workshop will be delivered via Zoom webinar (lectures) and Zoom meetings (practical exercises). Please install Zoom on your computer prior to the workshop.

The practical exercises will involve basic analyses of prepared data sets. Please download and install *MEGA*, *IQ-TREE* (version 2), *BEAST 2* (version 2.4.8 or higher), *Tracer*, *FigTree*, and *ASTRAL* prior to the workshop.

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.

Registration

The workshop has space for 100 registered attendees. The first 60 places were offered on first-come-first served basis, with the remaining 40 places offered to research students on the waiting list or from partner institutions in the Association of Pacific Rim Universities.

Schedule

The workshop will commence at 11 am on Wednesday 27 July (Sydney, GMT +10) and will run for approximately 5 to 6 hours each day (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).
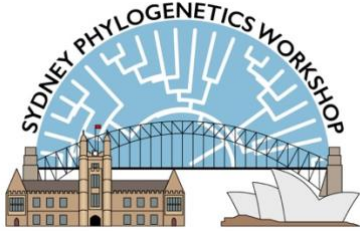
Instructors

Yasmin Asar, Simon Ho, Toby Kovacs, and Nate Lo (University of Sydney)

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

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 recently edited the book *The Molecular Evolutionary Clock*, published by Springer in late 2020.

Additional support during the practical exercises will be provided by **Toby Kovacs** (PhD student) and **Nate Lo** (Professor of Evolutionary Biology).

Fred Jaya, Minh Bui, Nhan Trong Ly, and Caitlyn Cherryh (Australian National University)

Fred Jaya is a PhD student under the supervision of Rob Lanfear 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.

Minh Bui 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*.

Additional support during the practical exercises will be provided by **Nhan Trong Ly** (PhD student) and **Caitlyn Cherryh** (PhD student).
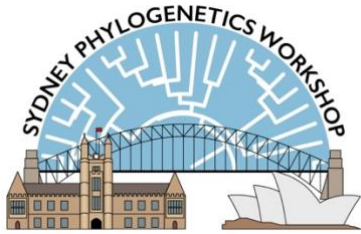
Workshop Programme

Wednesday 27 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 – 17.00	Practical 1.1: Sequence alignment and phylogenetic analysis using *MEGA*	

Thursday 28 July: Maximum-likelihood and Bayesian analysis

11.00 – 12.00	Lecture 2.1: Phylogenetic analysis with *IQ-TREE*	Minh Bui
12.15 – 14.15	Practical 2.1: *IQ-TREE* workshop tutorial	
14.30 – 15.15	Lecture 2.2: Bayesian phylogenetics 1	Simon Ho
15.30 – 16.00	Lecture 2.3: Bayesian phylogenetics 2	Simon Ho

Friday 29 July: Molecular dating and phylogenomics

11.00 – 12.00	Lecture 3.1: Molecular dating	Simon Ho
12.15 – 14.15	Practical 3.1: Bayesian analysis and molecular dating using *BEAST*	
14.30 – 15.15	Lecture 3.2: Phylogenomics	Simon Ho
15.15 – 16.00	Additional time for questions	
Post-workshop	Practical 3.2: Phylogenomic analysis using *ASTRAL*	
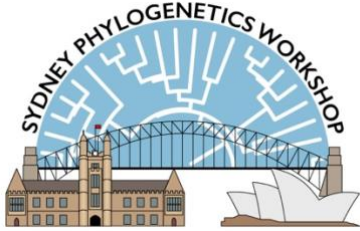
Useful Readings

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

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.