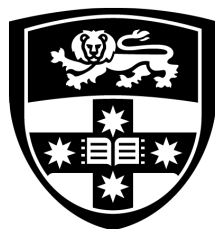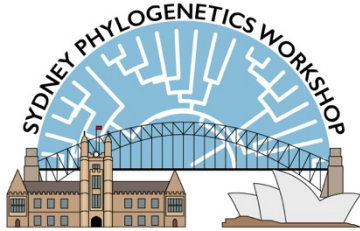**11ᵗʰ annual workshop**

28–29 January 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* and *BEAST 2*. It is primarily aimed at research students and postdoctoral researchers, but other prospective attendees are welcome. Prior knowledge of basic phylogenetics is helpful but not essential.

The workshop will comprise a series of lectures (delivered in Zoom webinar form) and 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 pathogen phylodynamics.

Computing

The practical exercises will involve basic analyses of prepared data sets. Please download and install *MEGA* (version 6 or higher), *BEAST 2* (version 2.4.8 or higher), *Tracer*, and *FigTree* prior to the workshop. Please note that the practical exercises will not be run as live sessions. Instead, we will provide a recorded video introduction and a recorded video 'walk-through' for each practical exercise, which can then be completed in your own time.

Resources

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

Further information

For news about upcoming workshops, including the Sydney Phylogenetics Workshop scheduled for July 2021, please visit 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 12 pm on Thursday 28 January (Sydney, GMT +11) each day and will run for approximately 4 hours (including short breaks). Local times are:

Auckland	14.00 – 18.00	Copenhagen	02.00 – 06.00
Sydney/Melbourne/Canberra	12.00 – 16.00	London	01.00 – 05.00
Adelaide	11.30 – 15.30	Rio de Janeiro	22.00* – 02.00
Brisbane	11.00 – 15.00	New York/Montreal	20.00* – 00.00
Darwin	10.30 – 14.30	Houston	19.00*–23.00*
Perth/Singapore/Beijing	09.00 – 13.00	Los Angeles	17.00*–21.00*
New Delhi/Colombo	06.30 – 10.30		

*previous day
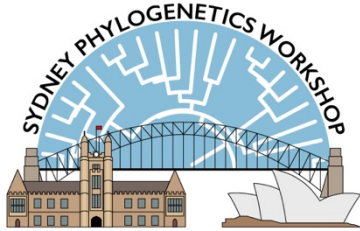
Speakers

Simon Ho and Fred Jaya (University of Sydney)

Simon is a Professor of Molecular Evolution at the University of Sydney, where he jointly leads the Molecular Ecology, Evolution, and Phylogenetics research group. He has research interests in molecular clocks, evolutionary rates, phylogenetic methods, genomic evolution, and molecular ecology. Simon recently edited the book *The Molecular Evolutionary Clock*, published by Springer in late 2020.

Fred is a Research Assistant in the Molecular Ecology, Evolution, and Phylogenetics research group at the University of Sydney. He has a range of experience in computational biology, process automation, and pipeline development. Previously, Fred worked on various projects involving population genetics, biogeography, and epidemiology.

### 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.

Barbara Brito-Rodriguez (University of Technology Sydney)

Barbara is a Chancellor's Postdoctoral Research Fellow at the University of Technology Sydney. She is interested in supporting the design of animal disease control measures and surveillance using the results of scientific studies. Her research areas are quantitative epidemiology, animal disease modelling, and molecular epidemiology (pathogen genetics) of infectious animal diseases.
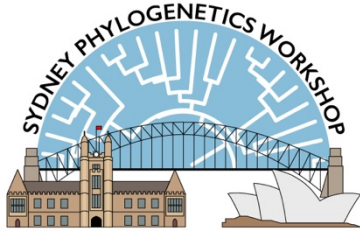
Workshop Programme

Thursday 28 January: Introduction to phylogenetic analysis

12.00 – 12.10	Welcome	Simon Ho
12.10 – 13.00	Lecture 1.1: Introduction to molecular phylogenetics	Simon Ho
13.15 – 14.00	Lecture 1.2: Evolutionary models	Simon Ho
14.00 – 14.30	Lecture 1.3: Phylogenetic data	Fred Jaya
14.45 – 15.30	Lecture 1.4: Phylogenetic methods	Simon Ho
15.30 – 16.00	Lecture 1.5: Phylogenetic analysis with IQ-TREE	Minh Bui

Practical 1: Sequence alignment and phylogenetic analysis using *MEGA*

Friday 29 January: Bayesian phylogenetics and molecular dating

12.00 – 13.00	Lecture 2.1: Bayesian phylogenetic analysis	Simon Ho
13.15 – 13.45	Lecture 2.2: Models and priors	David Duchêne
13.45 – 14.30	Lecture 2.3: Molecular dating	Simon Ho
14.45 – 15.15	Lecture 2.4: Calibrating the molecular clock	David Duchêne
15.15 – 15.45	Seminar: Phylodynamic analyses of viruses	Barbara Brito-Rodriguez
15.45 – 16.00	Questions	

Practical 2: Bayesian analysis and molecular dating using *BEAST*
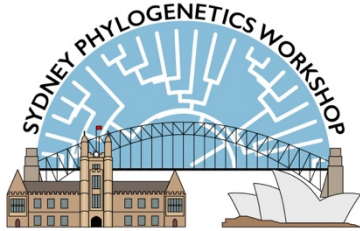
Useful Readings

Reference books

- *[Phylogenetics in the Genomic Era](#)*
  Scornavacca, Delsuc, & Galtier (eds) (2020) No commercial publisher | Open access.

- *The Molecular Evolutionary Clock: Theory and Practice*
  Ho (ed.) (2020) Springer.

- *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.

Molecular phylogenetics and Bayesian inference

- *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.