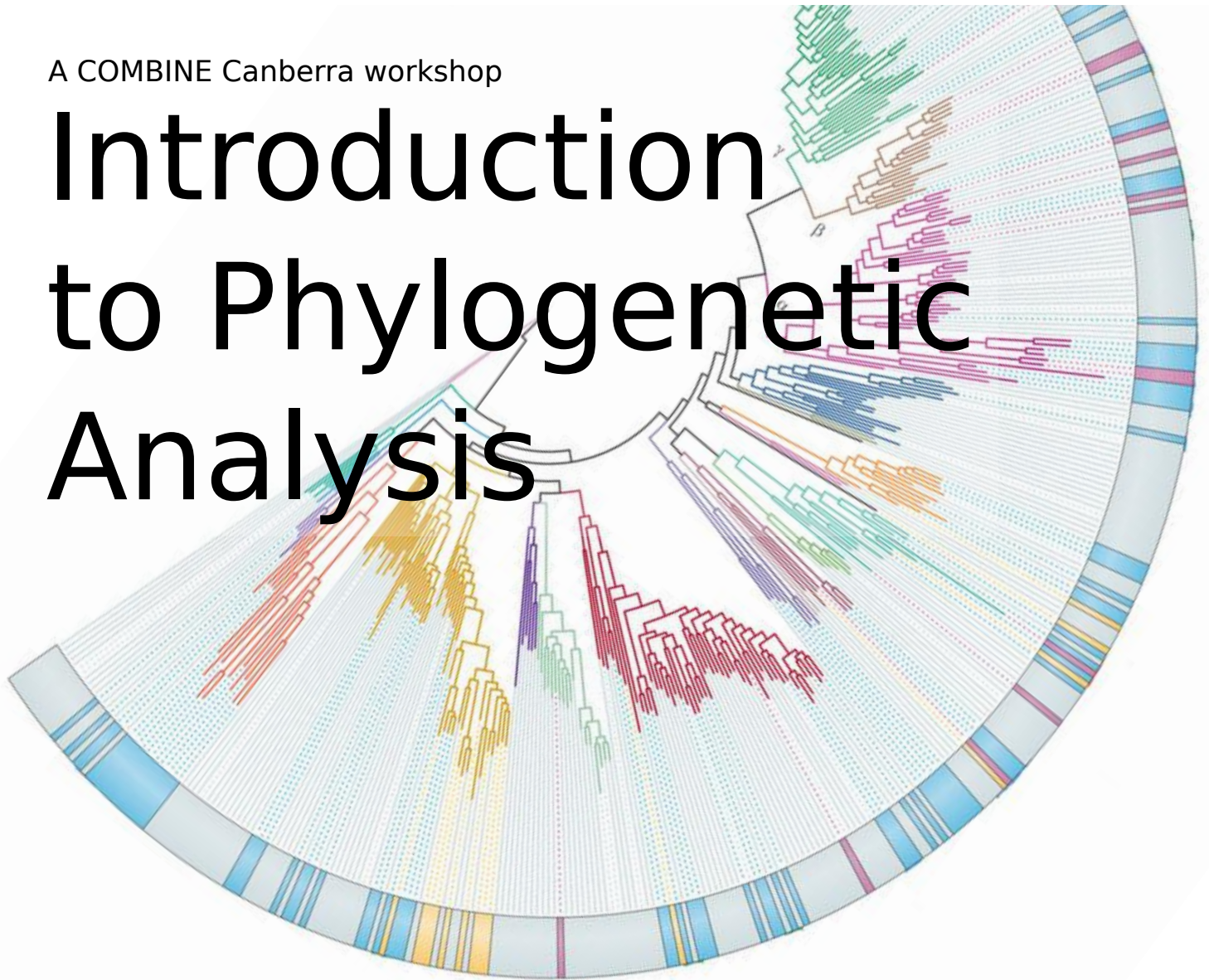


A COMBINE Canberra workshop

Introduction to Phylogenetic Analysis



29-30th January 2015

The Australian National University, Canberra

A **free** two-day workshop providing an introduction to phylogenetic analysis, including sequence alignment, evolutionary models, phylogenetic methods, Bayesian analysis, and demographic reconstruction.

Featuring: Presentations by Assoc. Prof Simon Ho (USyd), and including practical exercises with the software **MEGA** and **BEAST**.

**General registrations close
Wednesday 28th January
2015.**

Venue: Sciences Teaching
Building 136 Linnaeus Way,
The Australian National University,
Canberra.

**For further information and
registration visit**

> www.bit.ly/ANU_Phylo

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COMBINE 

Introduction to Phylogenetic Analysis

Thursday 29 – Friday 30 January, 2015

Overview

This workshop will provide an introduction to phylogenetic analysis, including practical exercises based on the software *MEGA* and *BEAST*. It is suitable for graduate students, postdoctoral researchers, and academics at all levels of experience. Prior knowledge of basic phylogenetics is helpful but not strictly necessary.

The workshop will be run by Associate Professor Simon Ho, Sebastián Duchêne, and David Duchêne. Simon and Sebastián are from the *Molecular Ecology, Evolution, & Phylogenetics* (MEEP) lab in the School of Biological Sciences, University of Sydney. David is a PhD student from the Research School of Biology at the Australian National University.

All lectures and practical classes will be held in the Sciences Teaching Building 136, Linnaeus Way at the Australian National University.

Programme

The workshop will comprise a series of lectures and practical exercises. The first day will cover interpreting phylogenetic trees, sequence alignment, evolutionary models, and phylogenetic methods. The second day will focus on Bayesian phylogenetic analysis and will include molecular clocks, estimating timescales, coalescent theory, and demographic reconstruction.

The practical exercises will involve basic analyses of a prepared data sets. We will be using free software that can be installed on PC, Mac, and UNIX platforms.

Workshop Programme

Thursday 29 January: Introduction to phylogenetic analysis

09.30 – 09.45	Welcome	
09.45 – 10.30	Lecture 1: Introduction to phylogenetic analysis	Simon Ho
10.30 – 11.00	Practical 1a: Sequence alignment in <i>MEGA</i>	
	--- Morning tea ---	
11.30 – 12.00	Lecture 2: Evolutionary Models	Sebastián Duchêne
12.00 – 13.00	Practical 1b: Model selection in <i>MEGA</i>	
	--- Lunch break ---	
14.00 – 15.00	Lecture 3: Phylogenetic Methods	Simon Ho
15.00 – 17.00	Practical 1c: Phylogenetic analysis in <i>MEGA</i>	

Friday 30 January: Bayesian phylogenetic analysis

09.30 – 10.15	Lecture 4: Bayesian phylogenetic analysis	Simon Ho
10.15 – 11.00	Lecture 5: Rates and timescales	Sebastián Duchêne
	--- Morning tea ---	
11.30 – 13.00	Practical 2: Molecular-clock analysis in <i>BEAST</i>	
	--- Lunch break ---	
14.00 – 15.00	Lecture 6: Analysing populations	Simon Ho
15.00 – 17.00	Practical 3: Inferring population history in <i>BEAST</i>	

Useful References

Reference books

- *Bayesian Phylogenetics: Methods, Algorithms, and Applications*
Chen, Kuo, & Lewis (2014) Chapman & Hall / CRC.
- *Molecular Evolution: A Statistical Approach*
Yang (2014) Oxford University Press.
- *The Phylogenetic Handbook*
Lemey, Salemi, & Vandamme (2009) Cambridge University Press.
- *Reading the Story in DNA*
Bromham (2008) Oxford University Press.
- *Inferring Phylogenies*
Felsenstein (2003) Sinauer Associates.

Molecular clocks and calibrations

- *Estimating evolutionary timescales using the molecular clock*
Ho & Duchêne (2014) *Mol Ecol* 23: 5947–5965.
- *The changing face of the molecular evolutionary clock*
Ho (2014) *Trends Ecol Evol* 29: 496–503.
- *Accounting for calibration uncertainty in phylogenetic estimation of evolutionary divergence times*
Ho & Phillips (2009) *Syst Biol* 58: 367–380.

Demographic reconstruction

- *Skyline-plot methods for estimating demographic history from nucleotide sequences*
Ho & Shapiro (2011) *Mol Ecol Res* 11: 423–434.
- *Bayesian inference of population size from multiple loci*
Heled & Drummond (2008) *BMC Evol Biol* 8: 289.
- *Bayesian coalescent inference of past population dynamics from molecular sequences*
Drummond, Rambaut, Shapiro, & Pybus (2005) *Mol Biol Evol* 22: 1185–1192.

Gene trees and species trees

- *Statistical binning enables an accurate coalescent-based estimation of the avian tree*
Mirarab, Bayzid, Boussau, & Warnow (2014) *Science*, 346: 1337.
- *Bayesian inference of species trees from multilocus data*
Heled & Drummond (2010) *Mol Biol Evol* 27: 570–580.
- *Gene tree discordance, phylogenetic inference and the multispecies coalescent*
Degnan & Rosenberg (2009) *Trends Ecol Evol* 24: 332–340.