# Advanced Phylogenetic Analysis

## Monday 16 – Wednesday 18 November, 2015


Australian National University

### Overview

This workshop will cover advanced topics in phylogenetic analysis. It is suitable for graduate students, postdoctoral researchers, and academics with experience in phylogenetics. All participants are assumed to have knowledge of the principles and practice of phylogenetics, including the Bayesian framework.

The workshop is organised by **COMBINE**, a student-run Australian organisation for researchers in computational biology, bioinformatics, and related fields. It will be presented by Associate Professor Simon Ho and Dr Sebastián Duchêne, with assistance from Dr Luana Lins, David Duchêne, Jun Tong, and Charles Foster. All of the instructors are members or affiliates of the *Molecular Ecology, Evolution, and Phylogenetics (MEEP)* Laboratory at the University of Sydney.

All lectures and practical classes will be held on Level 3 of the Sciences Teaching Building (136) at the Australian National University, Canberra. Catering will be provided throughout the workshop.

### Programme

The workshop will comprise a series of lectures and practical exercises. The first day will cover likelihood methods, model selection, and data selection. The second day will cover Bayesian phylogenetics, priors, and Bayesian model selection. The third day will have a focus on molecular dating, including clock models, calibrations, and tip-dating.

The practical exercises will involve analyses of a prepared data sets using *RAxML*, *PartitionFinder*, *BEAST*, *MrBayes*, and *MCMCtree*. These are freely available and can be installed on PC, Mac, and UNIX platforms.

COMBINE

For Australian students and early career researchers in bioinformatics and computational biology

# Workshop Programme

## Mon 16 Nov: Likelihood-based phylogenetics

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|---|---|---|
| 09.15 – 09.25 | Arrival and set-up | |
| 09.25 – 09.30 | Welcome | SH |
| 09.30 – 10.15 | **Lecture 1.1**: Statistical phylogenetics | SH |
| 10.15 – 11.00 | **Lecture 1.2**: Evolutionary models | SD |
| | *--- Tea break ---* | |
| 11.20 – 13.00 | **Practical**: Model selection using *PartitionFinder* | SH / SD |
| | *--- Lunch break ---* | |
| 14.00 – 14.40 | **Lecture 1.3**: Maximum likelihood | SH |
| 14.40 – 15.00 | **Lecture 1.4**: Topology tests | LL |
| 15.00 – 17.00 | **Practical**: Likelihood analysis using *RAxML* | SH / SD |

## Tue 17 Nov: Bayesian phylogenetics and model selection

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|---|---|---|
| 09.30 – 10.30 | **Lecture 2.1**: Bayesian phylogenetic analysis | SH |
| 10.30 – 11.00 | **Lecture 2.2**: Models and priors | DD |
| | *--- Tea break ---* | |
| 11.20 – 12.00 | **Practical**: Bayesian analysis using *MrBayes* | SH / DD |
| | *--- Lunch break ---* | |
| 13.00 – 14.00 | *Seminar: Molecular evolutionary clocks in the genomic era* | SH |
| 14.00 – 14.30 | **Lecture 2.3**: Bayesian model selection | DD |
| 14.30 – 17.00 | **Practical**: Models and priors in *MrBayes* | SH / DD |

## Wed 18 Nov: Molecular dating

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|---|---|---|
| 09.30 – 10.00 | **Lecture 3.1**: Molecular dating | SH |
| 10.00 – 10.30 | **Lecture 3.2**: Models of rate variation | SD |
| 10.30 – 11.00 | **Lecture 3.3**: Calibrating the molecular clock | JT |
| | *--- Tea break ---* | |
| 11.20 – 13.00 | **Practical**: Molecular dating using *BEAST* | SH / JT |
| | *--- Lunch break ---* | |
| 14.00 – 14.30 | **Lecture 3.4**: Tip-dating analysis | SD |
| 14.30 – 16.00 | **Practical**: Genome-scale dating using *MCMCtree* | CF |

Presenters: Simon Ho (SH), Sebastian Duchêne (SD), David Duchêne (DD), Luana Lins (LL), Jun Tong (JT), and Charles Foster (CF)

# Useful References

## General reference books and papers

- **An Introduction to Molecular Evolution and Phylogenetics**
  Bromham (Jan 2016) Oxford University Press.
- **Molecular Evolution: A Statistical Approach**
  Yang (2014) Oxford University Press.
- **The Phylogenetic Handbook**
  Lemey, Salemi, & Vandamme (2009) Cambridge University Press.
- **Inferring Phylogenies**
  Felsenstein (2004) Sinauer Associates.
- **Molecular phylogenetics: principles and practice**
  Yang & Rannala (2012) *Nat Rev Genet*, 13: 303–314.

## Bayesian phylogenetics and model selection

- **Bayesian Phylogenetics: Methods, Algorithms, and Applications**
  Chen, Kuo, & Lewis (2014) Chapman & Hall / CRC.
- **Assessing absolute model performance in phylogenomics**
  Duchêne, Duchêne, & Ho (in review).
- **Model selection in phylogenetics**
  Sullivan & Joyce (2005) *Ann Rev Ecol Evol Syst*, 36: 445–466.

## Molecular dating

- **A practical guide to molecular dating**
  Sauquet (2013) *C R Palevol*, 12: 355–367.
- **Estimating evolutionary timescales using the molecular clock**
  Ho & Duchêne (2014) *Mol Ecol*, 23: 5947–5965.
- **Biogeographic calibrations for the molecular clock**
  Ho *et al*. (2015) *Biol Lett*, 11: 20150194.
- **Accounting for calibration uncertainty in phylogenetic estimation of evolutionary divergence times**
  Ho & Phillips (2009) *Syst Biol*, 58: 367–380.
- **Dating tips for divergence-time estimation**
  O'Reilly, dos Reis, & Donoghue (2015) *Trends Genet*, 31: 637–650.