

Introduction to Pathogen Phylogenetic Analysis

Monday 21 – Tuesday 22 November, 2016

Overview

This workshop will provide an introduction to phylogenetic analyses of infectious pathogens. It will cover basic concepts in phylogenetic analysis and practical sessions using popular software packages and empirical data. The workshop will be run by Dr Sebastián Duchêne and Jane Hawkey from the Centre for Systems Genomics of the University of Melbourne.

The workshop will consist of two modules. The first module will provide a basic framework to analyse molecular data and interpret phylogenetic trees and other parameters. The second module involves Bayesian methods and phylogenetic epidemiology. Some familiarity with molecular evolution and experience using the command line is useful but not essential. Participants are encouraged to bring data sets and questions to discuss potential analyses using phylogenetic methods.

Computing

The practical sessions will consist of analyses of publically available data sets. We will use various software packages freely available online, and which can be installed in Windows, Mac, and UNIX platforms. Please bring a laptop and install the following packages before attending the workshop:

- *MEGA* (megasoftware.net)
- *PhyML* (<http://www.atgc-montpellier.fr/phyml/>)
- *BEAST 2* (<http://beast2.org>)
- *Tracer* (tree.bio.ed.ac.uk/software/tracer/),
- *FigTree* (tree.bio.ed.ac.uk/software/figtree/)
- *TempEst* (tree.bio.ed.ac.uk/software/tempest/)
- R (<https://www.r-project.org>)
- Rstudio 1.0 (www.rstudio.com)

Venue

West room, University House @The Woodward (<http://unihouse.org.au>)
University of Melbourne
185 Pelham St, Carlton, 3052

Useful references

- *An Introduction to Molecular Evolution and Phylogenetics* Bromham (2016) Oxford University Press.
- *Molecular Evolution: A Statistical Approach* Yang (2014) Oxford University Press.
- *Estimating evolutionary timescales using the molecular clock* Ho & Duchene (2014) *Mol Ecol* 23: 5947–5965.
- *Molecular phylogenetics: principles and practice* Yang & Rannala (2012) *Nat. Rev. Genet.* 13: 303-314.

Programme

Day 1 - Monday 21 November

09:15 – 09:30 Arrival

09:30 – 10:30 Lecture 1.1: Introduction to molecular phylogenetics

10:30 – 11:00 Practical 1a: Sequence alignment in *MEGA*

-- Coffee break --

11:30 – 12:30 Lecture 1.2: Substitution models

-- Lunch --

13:30 – 14:30 Lecture 1.3: Phylogenetic methods

14:30 – 15:00 Practical 1b: Model selection in *MEGA*

15:00 – 15:15 Practical 1c: Maximum likelihood analysis in *PhyML*

15:15 – 15:30 Questions and discussion

-- Coffee break --

15:45 – 16:00 Lecture 1.4: The molecular clock

16:00 – 16:30 Practical 1d: Assessing temporal structure in *TempEst*

16:30 – 17:00 Questions and discussion

Day 2 - Tuesday 22 November

09:15 – 09:30 Arrival

09:30 – 10:30 Lecture 2.1: Bayesian phylogenetics

10:30 – 11:00 Lecture 2.2: Priors

-- Coffee break --

11:30 – 12:00 Practical 2: Markov Chain Monte Carlo

12:00 – 12:30 Lecture 2.3: Demographic priors and model selection

-- Lunch --

13:30 – 14:30 Practical 3: Molecular dating using *BEAST*

14:30 – 14:45 Questions and discussion

14:45 – 15:15 Lecture 2.4: Infectious disease phylodynamics

-- Coffee break --

15:30 – 16:15 Practical 4: Molecular epidemiology in *BEAST*

16:15 – 17:00 Phylogenetics clinic and open questions

