

Viral phylodynamics using BEAST2

International Bioinformatics Conference on Virus Evolution and Molecular Epidemiology

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The training session will consist of a one hour lecture followed by a one hour tutorial. During the lecture we will review some basic concepts of Bayesian phylogenetic inference, and I will introduce the main components of a BEAST model. In the tutorial session we will perform a basic analysis on viral genomes in BEAST 2. The focus of the tutorial will be on setting model components, in particular choosing suitable priors, and inspecting and interpreting the output. If time allows we will also examine different types of tree priors and learn how to do post-processing in R.

Required Software

You are required to bring your own laptop to the workshop. The software below **must** be installed prior to arrival.

- **BEAST 2:** BEAST 2 is a cross-platform program for Bayesian phylogenetic analysis of molecular sequences. We will be using BEAST v2.4.6 for the workshop (<http://beast2.org/>).
- **FigTree:** FigTree is a graphical viewer of phylogenetic trees, specifically designed to display summarized and annotated trees produced by BEAST. (<http://tree.bio.ed.ac.uk/software/figtree/>).
- **Tracer:** Tracer is a program for analysing the trace files generated by Bayesian MCMC runs. It can be used to check mixing, ESS, parameter correlations, etc. (<http://tree.bio.ed.ac.uk/software/tracer/>).
- **Java 8 JDK:** This Java SE Development Kit is required for BEAST 2 (<http://www.oracle.com/technetwork/java/javase/downloads/jdk8-downloads-2133151.html>).
- **R (optional):** R is a free software environment that provides a wide variety of statistical (linear and nonlinear modelling, classical statistical tests, time-series analysis, classification, clustering) and graphical techniques, and is highly extensible (<https://www.r-project.org/>).
- **RStudio (optional):** RStudio IDE is a user interface for R (<https://www.rstudio.com/>).

Pre-workshop recommended reading

Statistics and mathematics primers

I am aware that not all of the workshop participants have a mathematical background and may have difficulty understanding some of the theory. The two links below can help to refresh the basic concepts, but are by no means meant to be comprehensive resources.

- Seeing Theory (<http://students.brown.edu/seeing-theory/index.html>): This website gives a very brief, but pretty and easy to understand introduction to many of the fundamental concepts in statistics.
- Ziheng Yang's statistics primer (<http://abacus.gene.ucl.ac.uk/PPS/PrimerProbabilityStatistics.pdf>): Gives a more in-depth introduction to the topic.

Further reading

The books below are not all focused on BEAST or even Bayesian phylogenetics. However, each of the books contains at least one background chapter on the theory of molecular evolution, as well as more in-depth chapters on the models implemented in BEAST and BEAST 2. Most of the books also contain at least some discussion of Bayesian inference.

- [Bayesian Evolutionary Analysis with BEAST](#), *Alexei J. Drummond, Remco R. Bouckaert*
- [Molecular Evolution: A Statistical Approach](#), *Ziheng Yang*
- [The Phylogenetic Handbook](#), *Philippe Lemey, Marco Salemi, Anne-Mieke Vandamme*
- [Molecular Evolution: A Phylogenetic Approach](#), *Roderick D.M. Page, Edward C. Holmes*
- [Inferring Phylogenies](#), *Joseph Felsenstein*