

# Applied Bayesian Phylogenetics

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There are several software packages to perform Bayesian phylogenetics.

## MrBayes

MrBayes is a program for Bayesian inference and model choice across a wide range of phylogenetic and evolutionary models. MrBayes uses Markov chain Monte Carlo (MCMC) methods to estimate the posterior distribution of model parameters. Has mostly been replaced by RevBayes, but is still useful for some analyses.

<http://nbisweden.github.io/MrBayes/>

## RevBayes

A fuller featured successor to MrBayes. RevBayes provides an interactive environment for statistical computation in phylogenetics. It is primarily intended for modeling, simulation, and Bayesian inference in evolutionary biology, particularly phylogenetics.

<https://revbayes.github.io/>

## BEAST2

BEAST 2 is a cross-platform program for Bayesian phylogenetic analysis of molecular sequences. It estimates rooted, time-measured phylogenies using strict or relaxed molecular clock models. It can be used as a method of reconstructing phylogenies but is also a framework for testing evolutionary hypotheses without conditioning on a single tree topology. BEAST 2 uses Markov chain Monte Carlo (MCMC) to average over tree space, so that each tree is weighted proportional to its posterior probability. BEAST 2 includes a graphical user-interface for setting up standard analyses and a suite of programs for analysing the results.

<http://www.beast2.org/> Well developed set of tutorials at

<https://taming-the-beast.org/>

Introductory BEAST 2 tutorial

https:

[//taming-the-beast.org/tutorials/Introduction-to-BEAST2/](https://taming-the-beast.org/tutorials/Introduction-to-BEAST2/)