

MrBayes

MrBayes is a freeware program for implementing [Bayesian](#) inference of phylogeny. Bayesian phylogenetic analysis proceeds by calculating the likelihood of the character data given an initially random [tree](#) topology, set of branch lengths and model of character evolution, and iteratively modifies each of these parameters in a Markov Chain Monte Carlo (MCMC) simulation. Moves that improve the likelihood of the data are always accepted, while those that do not are usually rejected (although some may occasionally be accepted within a certain threshold so as to avoid getting trapped in local optima). Following an initial trial period (known as 'burn in'), the likelihood scores will plane out and parameters will fluctuate between similar values, at which point trees are sampled at regular intervals to generate a *posterior distribution* of trees. Unlike the trees output by a cladistic analysis, which are based on a single optimality criterion (*i.e.*, [parsimony](#)), the posterior distribution of trees represents a set of phylogenetic hypotheses that explain the distribution of character states among the taxa under a range of plausible evolutionary assumptions. The posterior distribution of trees can be summarised by a consensus tree or "maximum clade credibility tree", while posterior probabilities for individual clades are calculated based on their frequency in the tree sample. The Bayesian approach has been found to be particularly effective when there is wide variance in the amount of evolution that has occurred in different regions of the [character data](#) or tree, since it explicitly incorporates these parameters (*i.e.*, branch lengths and substitution model) into the analysis.

See also: [Bayesian phylogenetics](#), [tools](#).

Reference

– *MrBayes: Bayesian Inference of Phylogeny*. Computer program. <http://mrbayes.sourceforge.net/>

JT