

Bayesian phylogenetic inference for big data.

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Phylogenetics studies the evolutionary relationships between different organisms, and its main goal is the inference of the tree of life. Bayesian phylogenetic inference through Markov chain Monte Carlo (MCMC) has been widely used since their introduction in the 1990s. The downside of MCMC is that the parameter space of trees is typically of very high dimension. Thus, a single step of MCMC will hold most of the parameters fixed, resulting in highly dependent samples. We present a novel method to obtain independent samples of trees. This methodology is an alternative to MCMC and it shows some potential of being computationally tractable for large trees and data sets.