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Prior Distributions on Phylogenetic Trees

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Abstract

In Bayesian inference of phylogenetics the MCMC simulation method is used to estimate the support of phylogenetic trees. MCMC simulation is very useful for estimating the support of the most probable trees, but gives little information about the great majority of the possible trees. Bayesian inference has the ability to incorporate previous knowledge into a new analysis, specified in terms of a prior distribution. In this thesis I investigate four different methods for evaluating the result of an MCMC simulation in order to estimate the support of all possible trees, thus enabling the result to be used as a prior distribution. Two of the methods, the WIB and the BM method produced reasonable results, whereas the other two, the WAB and the SCM method did not produce reasonable results. I will discuss suggestions on how these methods could be improved in the future.

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