

# MrBayes

The *Building Phylogenetic Tree* dialog for the *MrBayes* method has the following view:

The screenshot shows a software dialog box titled "Build Phylogenetic Tree". At the top, there is a "Tree building method" dropdown menu set to "MrBayes". Below this is a section titled "MrBayes Settings". Inside this section, there is a "Model" subsection with three settings: "Substitution model" set to "HKY85 (Nst=2)", "Rate" set to "gamma", and "Gamma" set to "4". Below the "Model" subsection is an "MCMC" subsection with six settings: "Chain length" (10000), "Subsampling frequency" (1000), "Burn-in length" (10), "Heated chains" (4), "Heated chain temp" (0.40), and "Random seed" (29392). Below the "MCMC" subsection are three radio buttons: "Display tree in new window" (unselected), "Display tree with alignment editor" (selected), and a checked checkbox "Synchronize alignment with tree". Below these is a "Save tree to" text field with a browse button "...". At the bottom of the dialog are four buttons: "Remember Settings", "Restore Default", "Build", "Cancel", and "Help".

There are two steps to a phylogenetic analysis using *MrBayes*:

1. Set the evolutionary model.
2. Run the Markov chain Monte Carlo (MCMC) analysis.

The evolutionary model is defined by the following parameters:

*Substitution model* — specifies the general structure of a DNA substitution model. This parameter is available for the nucleotide sequences. It corresponds to the Nst setting of MrBayes. You may select one of the following:

- JC69 (Nst=1)
- HKY85 (Nst=2)
- GTR (Nst=6)

*Rate matrix (fixed)* — specifies the fixed-rate amino-acid model. This parameter is available for amino-acid sequences. The following models are available:

- poisson
- jones
- dayhoff

- mtrev
- mtmam
- wag
- rtrev
- cprev
- vt
- blosum
- equaline

The following parameters are common for nucleotide and amino-acid sequences:

*Rate* — sets the model for among-site rate variation. Select one of the following:

- equal — no rate variation across sites.
- gamma — gamma-distributed rates across sites. The rate at a site is drawn from a gamma distribution. The gamma distribution has a single parameter that describes how much rates vary.
- propinv — a proportion of the sites are invariable.
- invgamma — a proportion of the sites are invariable while the rate for the remaining sites are drawn from a gamma distribution.

*Gamma* — sets the number of rate categories for the gamma distribution.

You can select the following parameters for the MCMC analysis:

*Chain length* — sets the number of cycles for the MCMC algorithm. This should be a big number as you want the chain to first reach stationarity, and then remain there for enough time to take lots of samples.

*Subsampling frequency* — specifies how often the Markov chain is sampled. You can sample the chain every cycle, but this results in very large output files.

*Burn-in length* — determines the number of samples that will be discarded when convergence diagnostics are calculated.

*Heated chains* — number of chains will be used in Metropolis coupling. Set 1 to use usual MCMC analysis.

*Heated chain temp* — the temperature parameter for heating the chains. The higher the temperature, the more likely the heated chains are to move between isolated peaks in the posterior distribution.

*Random seed* — a seed for the random number generator.

*Display tree in new window* - displays tree in new window.

*Display tree with alignment editor* - displays tree with alignment editor.

*Synchronize alignment with tree* - synchronize alignment and tree.

*Save tree to* — file to save the built tree.

Press the *Build* button to run the analysis with the parameters selected and build a consensus tree.