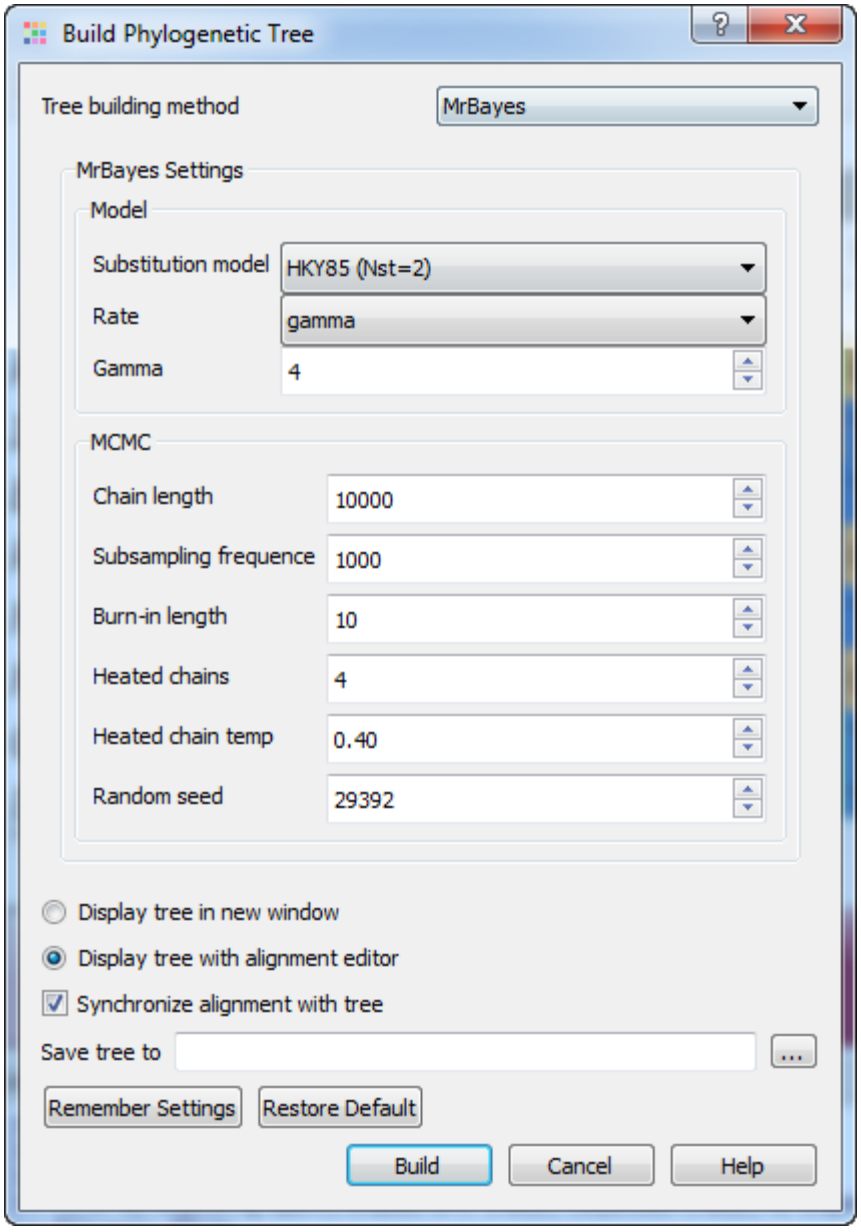
MrBayes

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



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

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

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 analisys:

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.