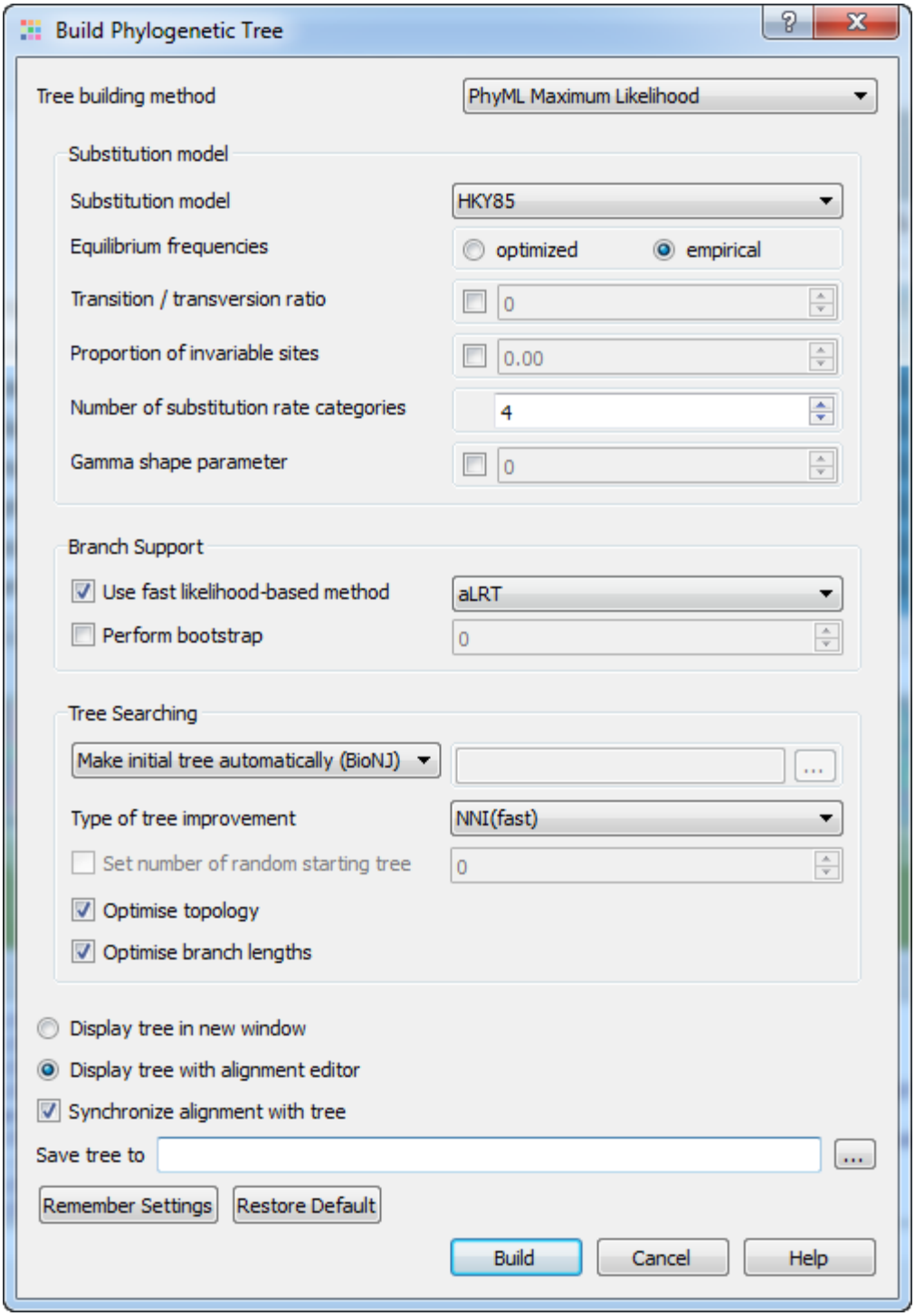
PhyML Maximum Likelihood

The *Building Phylogenetic Tree* dialog for the *PhyML Maximum Likelihood* method has the following view:



There following parameters are available:

Substitution model parameters - selection of the Markov model of substitution:

Substitution model - model of substitution.

Equilibrium frequencies - equilibrium frequencies.

Transition/transversion ratio - fix or estimate the transition/transversion ratio in the maximum likelihood framework.

Proportion of invariable sites - the proportion of invariable sites, i.e., the expected frequency of sites that do not evolve, can be fixed or estimated.

Number of substitution rate categories - number of substitution rate categories.

Gamma shape parameter - the shape of the gamma distribution determines the range of rate variation across sites.

Branch support parameters - selection of the method that is used to measure branch support:

Use fast likelihood method - use fast likelihood method.

Perform bootstrap - the support of the data for each internal branch of the phylogeny can be estimated using non-parametric bootstrap.

Tree searching parameters - selection of the tree topology searching algorithm:

Make initial tree automatically - initial tree automatically.

Type of tree improvement - type of tree improvement.

Set number of random starting tree - number of random starting tree.

Optimize topology - the tree topology is optimised in order to maximise the likelihood.

Optimize branch lengths - optimize branch lengths.

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.