

# PhyML Maximum Likelihood

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

The dialog box is titled "Build Phylogenetic Tree" and contains the following settings:

- Tree building method:** PhyML Maximum Likelihood
- Substitution model:**
  - Substitution model: HKY85
  - Equilibrium frequencies: ☐ optimized ☒ empirical
  - Transition / transversion ratio: ☐ 0
  - Proportion of invariable sites: ☐ 0.00
  - Number of substitution rate categories: 4
  - Gamma shape parameter: ☐ 0
- Branch Support:**
  - ☒ Use fast likelihood-based method: aLRT
  - ☐ Perform bootstrap: 0
- Tree Searching:**
  - Make initial tree automatically (BioNJ):  ...
  - Type of tree improvement: NNI(fast)
  - ☐ Set number of random starting tree: 0
  - ☒ Optimise topology
  - ☒ Optimise branch lengths
- ☐ Display tree in new window
- ☒ Display tree with alignment editor
- ☒ Synchronize alignment with tree
- Save tree to:  ...
- Buttons: Remember Settings, Restore Default, Build, Cancel, Help

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.