



\$hyphy ~/hyphy-analyses/FitMG94/FitMG94.bf --help

Available analysis command line options

Use --option VALUE syntax to invoke

If a [required] option is not provided on the command line, the analysis will prompt for its value

[conditionally required] options may or not be required based on the values of other options

rooted

Accept rooted trees

default value: No

code

Which genetic code should be used

default value: Universal

alignment [required]

An in-frame codon alignment in one of the formats supported by HyPhy

tree [conditionally required]

A phylogenetic tree

applies to: Please select a tree file for the data:

type

Model type: global (single dN/dS for all branches) or local (separate dN/dS)

default value: terms.global [computed at run time]

applies to: Model Type

frequencies

Equilibrium frequency estimator

default value: CF3x4

lrt

Perform LRT to test which for dN/dS == 1 (global model only)

default value: No

output

Write the resulting JSON to this file (default is to save to the same path as the alignment file + 'MG94.json')

default value: fitter.codon_data_info[terms.json.json] [computed at run time]

save-fit

Save MG94 model fit to this file (default is not to save)

default value: /dev/null