

```
$hyphy ~/Development/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

```
$hyphy ~/Development/hyphy-analyses/FitMG94/FitMG94.bf --lrt Yes --alignment WestNileVirus_NS3.fas
```

Analysis Description

Fit an MG94xREV model with several selectable options frequency estimator and report the fit results including dN/dS ratios, and synonymous and non-synonymous branch lengths. v0.2 adds LRT test for dN/dS != 1

- __Requirements__: in-frame codon alignment and a phylogenetic tree
- __Written by__: Sergei L Kosakovsky Pond
- __Contact Information__: spond@temple.edu
- __Analysis Version__: 0.2

rooted: No

>code -> Universal

>Loaded a multiple sequence alignment with **19** sequences, **619** codons, and **1** partitions from `/Users/sergei/Dropbox/Talks/VEME-2021/data/WestNileVirus_NS3.fas`

>type -> global

>frequencies -> CF3x4

>lrt -> Yes

Obtaining branch lengths and nucleotide substitution biases under the nucleotide GTR model

>kill-zero-lengths -> Yes