

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

Available analysis command line options

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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 ~/hyphy-analyses/FitMG94/FitMG94.bf --lrt Yes --alignment data/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
```

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- __Written by__: Sergei L Kosakovsky Pond
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- __Contact Information__: spond@temple.edu
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- __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
```