```
$hyphy ~/Development/hyphy-analyses/FitMG94/FitMG94.bf --help

Available analysis command line options
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Use --option VALUE syntax to invoke
If a [reqired] 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 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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- __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