Gene-wide selection analysis using a branch-site method (BUSTED), WNV NS3

```
hyphy busted --srv No --alignment
data/WestNileVirus_NS3.fna --
starting-points 5
```

Produces
WestNileVirus_NS3.fna.BUSTED.json file

View in http://vision.hyphy.org/BUSTED

Based on the likelihood ratio test, there **is no** evidence of *episodic diversifying selection* in this dataset (p=0.2691).

BUSTED analysis (v4.0) was performed on the alignment from /Users/sergei/Dropbox/Talks/VEME-current/data/WestNileVirus_NS3.fas using HyPhy v2.5.40. This analysis **did not include** site-to-site synonymous rate variation.

Suggested citation: Gene-wide identification of episodic selection, Mol Biol Evol. 32(5):1365–71, Synonymous Site-to-Site Substitution Rate Variation Dramatically Inflates False Positive Rates of Selection Analyses: Ignore at Your Own Peril, Mol Biol Evol. 37(8):2430–2439

Evidence ratio threshold | 10 | Update

19 sequences in the alignment	**619** codon sites in the alignment	**1** partitions
33 median branches/partition used for testing	**3 classes** non-synonymous rate variation	**None** synonymous rate variation
0.27 p-value for episodic diversitying selection	**0** Sites with ER≥10 for positive selection	**N/A:N/A** Multiple hit rates (2H:3H)

Alignment-wide results

Model	Log (L)	AIC-c	Params.	Rate distribution	Rate plot
Unconstrained model	−6396.17	12896.8	52	Tested ω 0.003895 (98.862%) 0.004316 (0.40762%) 1.859 (0.73075%) Mean = **0.01745**, CoV = **9.054**	
Constrained model	−6396.79	12896.0	51	Tested ω 0.003674 (0.10704%) 0.003690 (98.824%) 1.000 (1.0691%) Mean = **0.01434**, CoV = **7.145**	

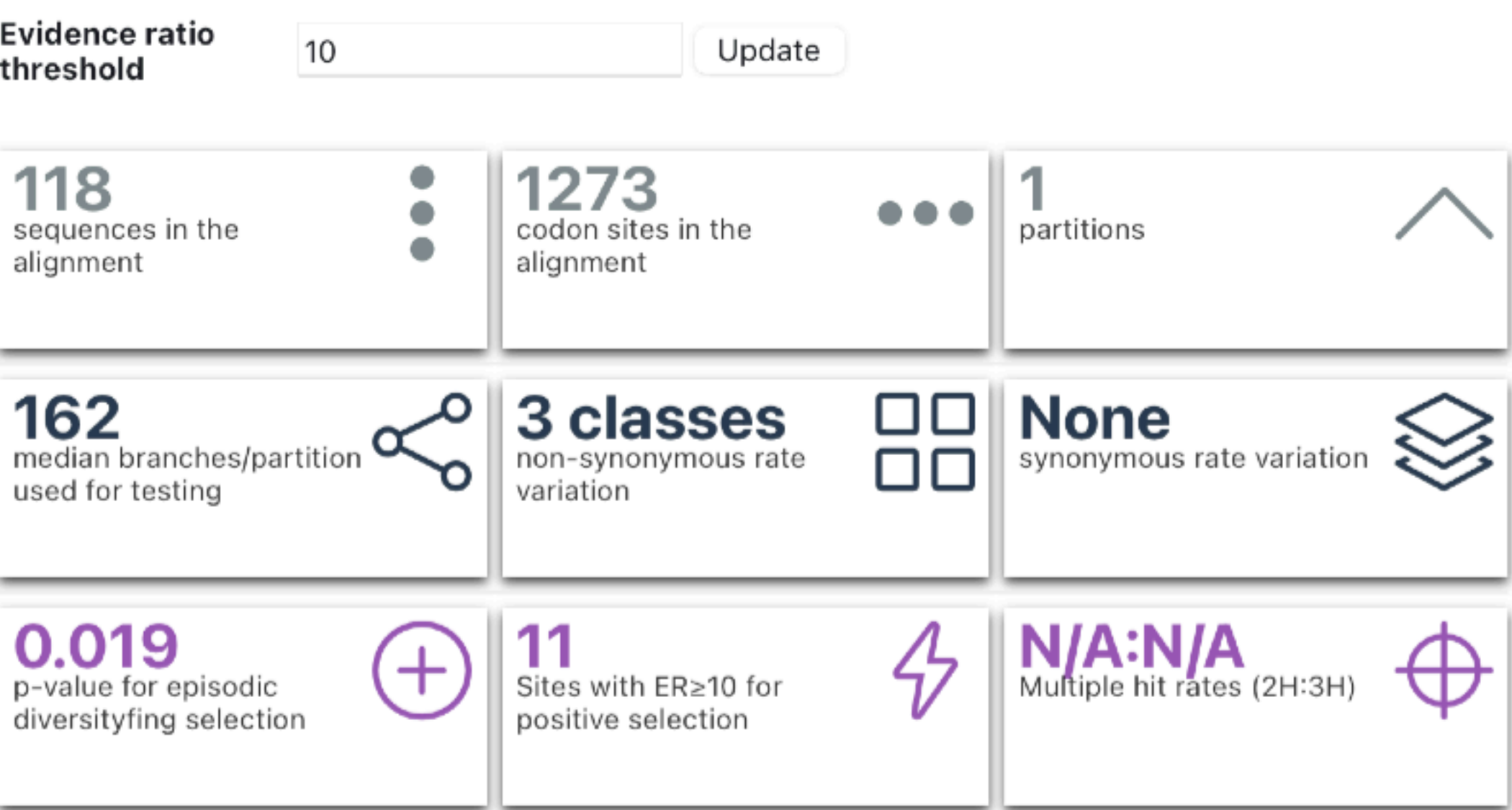# Gene-wide selection analysis using a branch-site method (BUSTED), SARS-CoV-2 spike

```
hyphy busted --srv No --alignment
data/spike.fas --tree data/
spike.tree --starting-points 5
```

Produces *spike.fas.BUSTED.json* file
View in http://vision.hyphy.org/BUSTED

Based on the likelihood ratio test, there **is** evidence of *episodic diversifying selection* in this dataset (p=0.01901).

BUSTED analysis (v4.0) was performed on the alignment from
/Users/sergei/Dropbox/Talks/VEME-current/data/spike.fas using HyPhy v2.5.40.
This analysis **did not include** site-to-site synonymous rate variation.

Suggested citation: *Gene-wide identification of episodic selection, Mol Biol Evol. 32(5):1365–71, Synonymous Site-to-Site Substitution Rate Variation Dramatically Inflates False Positive Rates of Selection Analyses: Ignore at Your Own Peril, Mol Biol Evol. 37(8):2430–2439*

Evidence ratio threshold [10] [Update]

118 sequences in the alignment	**1273** codon sites in the alignment	**1** partitions
162 median branches/partition used for testing	**3 classes** non-synonymous rate variation	**None** synonymous rate variation
0.019 p-value for episodic diversityfing selection	**11** Sites with ER≥10 for positive selection	**N/A:N/A** Multiple hit rates (2H:3H)

Alignment-wide results

Model	Log (L)	AIC-c	Params.	Rate distribution	Rate plot
Unconstrained model	−9287.35	18937.1	181	**Tested ω** 0.000 (0.45262%) 0.2561 (97.532%) 14.88 (2.0156%) Mean = **0.5497**, CoV = **3.740**	
Constrained model	−9290.62	18941.7	180	**Tested ω** 0.000 (46.919%) 1.000 (2.2974%) 1.000 (50.784%) Mean = **0.5308**, CoV = **0.9402**	