

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 diversifying 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), WNV NS3

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

Produces *HIV-sets.fas.BUSTED.json* file
View in <http://vision.hyphy.org/BUSTED> or <https://observablehq.com/@spond/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 diversifying 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	

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 *HIV-sets.fas.BUSTED.json* file
View in <http://vision.hyphy.org/BUSTED> or <https://observablehq.com/@spond/busted>