

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 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	

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Murrell et al | Mol. Biol. Evol | 32(5) | 1365–1371

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

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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 threshold10Update

118sequences in the alignment

1273codon sites in the alignment

1partitions

162median branches/partition used for testing

3 classesnon-synonymous rate variation

None synonymous rate variation

0.019p-value for episodic diversifying selection

11Sites with ER≥10 for positive selection

N/A:N/AMultiple 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	