


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

BUSTED without synonymous rate variation **found no evidence** (LRT, p-value = 0.262 \geq .05) of gene-wide episodic diversifying selection in the selected test branches of your phylogeny. Therefore, there is no evidence that any sites have experienced diversifying selection along the test branch(es). 

See [here](#) for more information about this method.
Please cite [PMID 25701167](#) if you use this result in a publication, presentation, or other scientific work.

Model fits

Model	<i>log L</i>	#. params	<i>AIC_c</i>	Branch set	ω_1	ω_2	ω_3	
Unconstrained model	-6396.1	52	12896.7	Test	0.00 (75.70%)	0.00 (23.57%)	1.89 (0.73%)	 ..
Constrained model	-6396.7	51	12895.9	Test	0.00 (25.78%)	0.00 (73.15%)	1.00 (1.07%)	 ..

This table reports a statistical summary of the models fit to the data. Here, **Unconstrained model** refers to the BUSTED alternative model for selection, and **Constrained model** refers to the BUSTED null model for selection.

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

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

BUSTED without synonymous rate variation **found evidence** (LRT, p-value = $0.019 \leq .05$) of gene-wide episodic diversifying selection in the selected test branches of your phylogeny. Therefore, there is evidence that at least one site on at least one test branch has experienced diversifying selection.

See [here](#) for more information about this method.
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Model fits i

Model	<i>log</i> L	#. params	AIC _c	Branch set	ω ₁	ω ₂	ω ₃	
Unconstrained model	-9287.4	181	18937.2	Test	0.07 (94.22%)	1.00 (0.58%)	9.07 (5.20%)	
Constrained model	-9290.6	180	18941.7	Test	0.00 (46.91%)	1.00 (4.87%)	1.00 (48.23%)	

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