

# 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.  
Please cite [PMID 25701167](#) if you use this result in a publication, presentation, or other scientific work.

## Model fits i

Model	<i>log</i> L	#. params	AIC <sub>c</sub>	Branch set	ω <sub>1</sub>	ω <sub>2</sub>	ω <sub>3</sub>	
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
```

# BUSTED analysis

- **West Nile Virus NS3 protein**

- No statistical support for selection; ML point estimate allocates a small proportion of sites ( $\sim 1\%$ ) to the selected group ( $dN/dS \sim 2$ )
- The rest of the gene is very strongly conserved ( $dN/dS = 0.004$ )

- **HIV-1 transmission pair**

- Very strong evidence of strong episodic diversification ( $dN/dS \sim 100$ ) on a small proportion of sites (2%)

- The rest of the gene evolves with weak purifying selection ( $dN/dS = 0.6-0.7$ )

- **SARS-CoV-2 spike**

- Evidence of episodic diversification ( $dN/dS \sim 9$ ) on a small proportion of sites (5.2%)
- Most of the rest of the gene evolves with very strong purifying selection ( $dN/dS = 0.6-0.7$ )