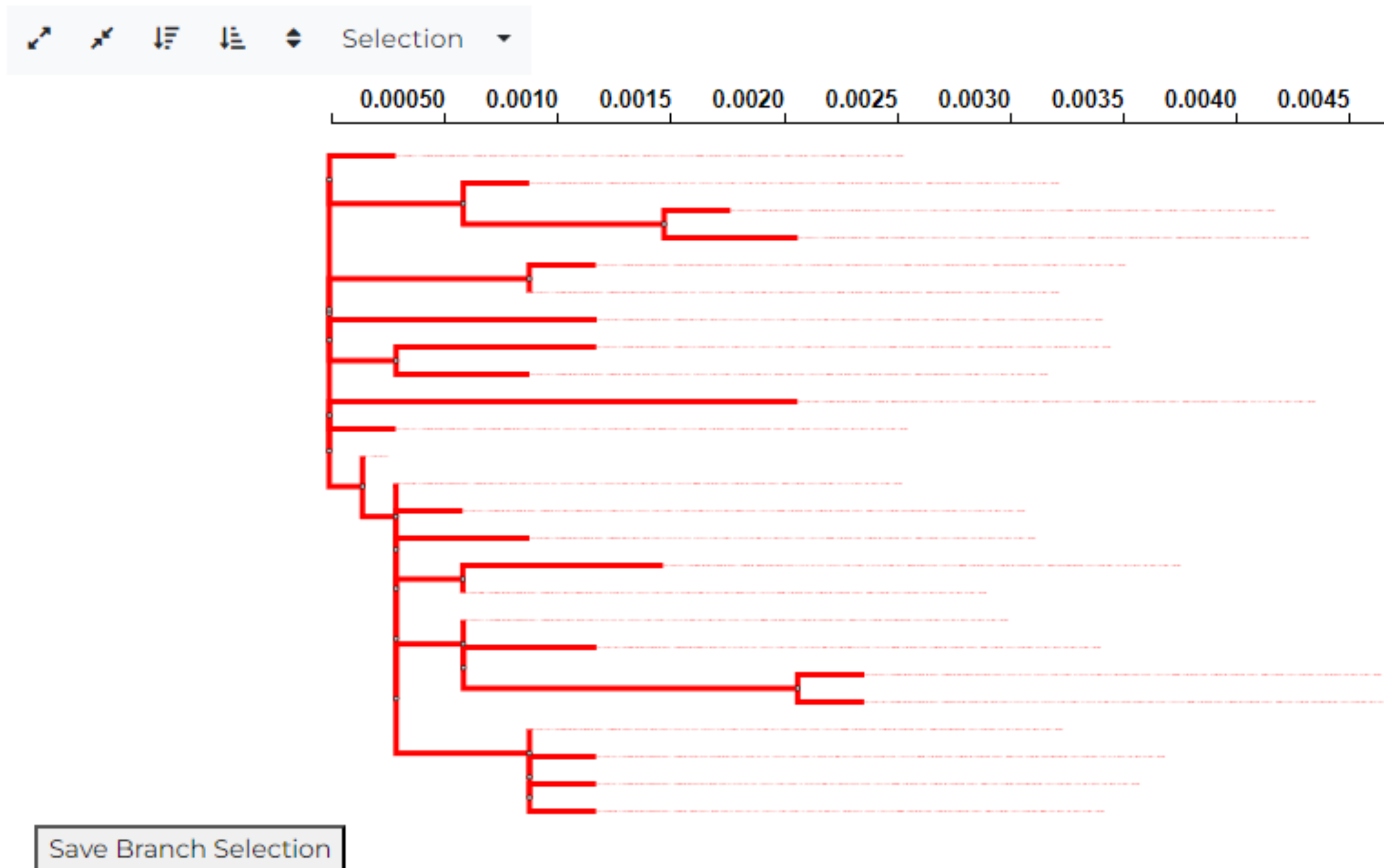


# BUSTED

Branch-site Unrestricted Statistical Test for Episodic Diversification

Select Test Branches



Datamonkey is funded jointly by MIDAS and NIH award R01 GM093939

Explore results - <https://www.datamonkey.org/busted/66815fd6ab6e044dbc7ffd8a>

# BUSTED

## Branch-site Unrestricted Statistical Test for Episodic Diversification

Based on the likelihood ratio test, there **is no** evidence of *episodic diversifying selection* in this dataset (p=0.5000). Export

BUSTED analysis (v4.5) was performed on the alignment from /home/datamonkey/datamonkey-js-server/production/app/busted/output/66815fd6ab6e044dbc7ffd8a using HyPhy v2.5.61. This analysis **included** site-to-site synonymous rate variation.

**Suggested citation** Gene-wide identification of episodic selection, Mol Biol Evol. 32(5):1365-73, 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  Update

25  
sequences in the alignment

567  
codon sites in the alignment

1  
partitions

47  
median branches/partition used for testing

3 classes  
non-synonymous rate variation

3 classes  
synonymous rate variation

0.50  
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
Tested w					
Unconstrained model	-2680.15	5503.02	71	0.1017 (100.00%) 0.00208 (0.0000%) 1.690 (0.0000%) Mean = 0.1017, CoV = 0.000	
Synonymous rates					
Unconstrained model				1.000 (100.00%) 1.179 (0.0000%) 2.673 (0.0000%) Mean = 1.000, CoV = 0.000	