

Explore results - <https://www.datamonkey.org/busted/668160a0ab6e044dbc7ffdca>

Evidence ratio threshold Update

25

sequences in the alignment

567

codon sites in the alignment

1

partitions

22

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		
Tested ω						
Unconstrained model	-2679.26	5511.36	76	0.03200 (71.337%)	0.05756 (27.795%)	1.002 (0.86805%)
				Mean = 0.04752, CoV = 1.894		
Background ω						
Unconstrained model				0.08553 (24.916%)	0.1522 (75.084%)	0.4953 (0.0000%)
				Mean = 0.1356, CoV = 0.2126		
Synonymous rates						
Unconstrained model				1.000 (1.6086%)	1.000 (98.391%)	1.615 (0.00000000000010924%)
				Mean = 1.000, CoV = 3.332e-8		
Tested ω						
Constrained model	-2679.26	5509.34	75	0.03280 (71.983%)	0.05772 (27.171%)	1.000 (0.84600%)
				Mean = 0.04775, CoV = 1.857		
Background ω						
Constrained model				0.08643 (25.064%)	0.1520 (74.936%)	0.4670 (0.0000%)
				Mean = 0.1356, CoV = 0.2097		

Plot type

Support for positive selection ▾

Figure 1. Empirical Bayes Factors for $\omega > 1$ at a particular branch and site (only tested branches are included).

