

# BUSTED inference

- **Because BUSTED is a random-effects method, it pools information across multiple sites and branches to gain power**
- The cost to this pooling is lack of site-level **resolution**, i.e., it is not immediately obvious which sites and/or branches drive the signal
- Standard ways to extract individual site contributions to the overall signal is to perform a post-hoc analysis, such as empirical Bayes, or “category loading”
- For BUSTED, “category loading” is faster and experimentally better
- Can also compute exploratory evidence for selection support along individual branches at specific sites

Based on the likelihood ratio test, there **is** evidence of *episodic diversifying selection* in this dataset (p=0.000).

BUSTED analysis (v4.0) was performed on the alignment from /Users/sergei/Dropbox/Talks/VEME-current/data/HIV-sets.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

16  
sequences in the alignment

288  
codon sites in the alignment

1  
partitions

26  
median branches/partition used for testing

3 classes  
non-synonymous rate variation

None  
synonymous rate variation

0.0  
p-value for episodic diversifying selection

13  
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	−2039.96	4170.83	45	<b>Tested ω</b> 0.5596 (86.941%) 0.9885 (10.960%) 96.09 (2.0981%) Mean = <b>2.611</b> , CoV = <b>5.242</b>	
Constrained model	−2078.31	4245.48	44	<b>Tested ω</b> 1.000 (14.819%) 1.000 (20.229%) 1.000 (64.952%) Mean = <b>1.000</b> , CoV = <b>NaN</b>	

# Gene-wide selection analysis using a branch-site method (BUSTED), **HIV-1 env**

hyphy busted --srv No --alignment data/HIV-sets.nex --starting-points 5

Produces *HIV-sets.nex.BUSTED.json* file  
View in <http://vision.hyphy.org/BUSTED>