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

Model fits

Model	*log* L	#. params	AIC_c	Branch set	ω_1	ω_2	ω_3	
Unconstrained model	**-2040.0**	**45**	**4170.9**	**Test**	**0.58 (85.37%)**	**0.73 (12.50%)**	**93.41 (2.13%)**	
Constrained model	**-2076.6**	**44**	**4242.1**	**Test**	**0.00 (29.28%)**	**1.00 (54.27%)**	**1.00 (16.45%)**	

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 HIV-sets.fas --starting-points 5
```

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

BUSTED site-level 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

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