## Detecting Individual Sites Subject to Episodic Diversifying Selection

Ben Murrell<sup>1,2</sup>, Joel O. Wertheim<sup>3</sup>, Sasha Moola<sup>2</sup>, Thomas Weighill<sup>2</sup>, Konrad Scheffler<sup>2,4</sup>, Sergei L. Kosakovsky Pond<sup>4</sup>\*

PLos Genetics | www.plosgenetics.org

1 July 2012 | Volume 8 | Issue 7 | e1002764

- Best-in-class power
- Able to detect episodes of selection, not just selection on average at a site
- Embarrassingly parallel (farm out each site), so runs reasonably fast

- Sample size is ~sequences, site level rate estimates imprecise
- Cannot estimate which individual branches are subject to selection with any precision
- Does not scale especially well with the number of sequences



Based on the likelihood ratio test, *episodic diversifying selection* has acted on **8** sites in this dataset ( $p \le 0.1$ ).

MEME analysis (v3.0) was performed on the alignment from /Users/sergei/Dropbox/Talks/VEME-current/data/HIV-sets.fas using HyPhy v2.5.40.

p-value threshold 0.1 Update

Suggested citation: Detecting Individual Sites Subject to Episodic Diversifying Selection.

PLoS Genet 8(7): e1002764.

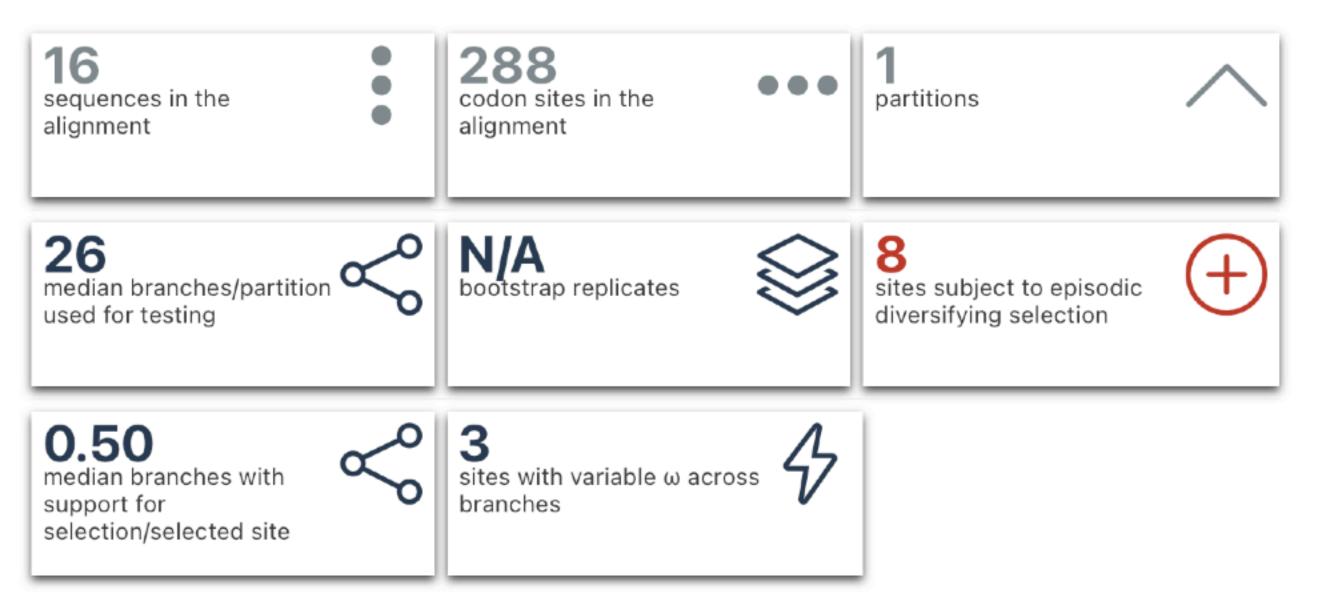


Table 1. Detailed site-by-site results from the MEME analysis

Part.	Codon	α	β-	p <sup>-</sup>	β+	p <sup>+</sup>	LRT	p-value	# branches under selection	MEME LogL	FEL LogL	Variation p
1	19	0	0	0.945	2,749.03	0.055	6.602	0.017	0	-14.847	-11.568	0.038
1	161	0	0	0.82	114.386	0.18	7.579	0.01	0	-16.568	-14.144	0.089
1	165	0	0	0.774	52.349	0.226	4.247	0.056	0	-15.506	-14.441	0.345
1	225	0	0	0.747	47.804	0.253	3.708	0.074	2	-13.869	-13.061	0.445
1	264	0	0	0.894	168.831	0.106	3.613	0.077	0	-11.753	-10.172	0.206
1	272	0	0	0.853	40.182	0.147	3.325	0.09	1	-10.449	-9.374	0.341
1	274	2.785	2.785	0.947	10,000	0.053	4.981	0.038	1	-20.161	-17.673	0.083
1	282	0	0	0	8.192	1	3.652	0.076	0	-19.326	-19.324	0.999