

Detecting Individual Sites Subject to Episodic Diversifying Selection

Ben Murrell^{1,2}, Joel O. Wertheim³, Sasha Moola², Thomas Weighill², Konrad Scheffler^{2,4},
Sergei L. Kosakovsky Pond^{4*}



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- MEME = 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 ($p \leq 0.1$).

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.

16

sequences in the alignment

288

codon sites in the alignment

1

partitions

26

median branches/partition used for testing

N/A

bootstrap replicates

8

sites subject to episodic diversifying selection

0.50

median branches with support for selection/selected site

3

sites with variable ω across branches

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

Part.	Codon	α	β^-	p^-	β^+	p^+	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

```
hyphy meme --alignment data/HIV-sets.fas
```