FEL on internal branches of Spike finds most selected sites, including many known to be of functional significance

Codon	Partition	alpha	beta	LRT	Selection detected?
5	1	0.000	19.127	2.890	Pos. p = 0.0891
12	1	0.000	20.331	2.989	Pos. p = 0.0838
18	1	0.000	19.110	2.885	Pos. p = 0.0894
138	1	0.000	26.771	2.736	Pos. p = 0.0981
367	1	0.000	44.309	9.045	Pos. p = 0.0026
439	1	0.000	34.548	4.987	Pos. p = 0.0255
452	1	0.000	30.618	5.518	Pos. p = 0.0188
477	1	0.000	23.671	4.325	Pos. p = 0.0376
501	1	0.000	38.285	3.317	Pos. p = 0.0686
570	1	0.000	21.073	3.047	Pos. p = 0.0809
614	1	0.000	22.073	3.099	Pos. p = 0.0784
681	1	0.000	18.366	2.818	Pos. p = 0.0932
1176	1	0.000	21.955	3.039	Pos. p = 0.0813

```
hyphy fel --alignment spike.fas --tree spike.tree --branches Internal
```

More accurate testing via parametric bootstrap

- P-values for MEME/FEL etc are derived from asymptotic approximations (large N)

- Not clear how well these hold for smaller and low-divergence datasets

- Can use a **much slower** simulation based method to derive more accurate p-values at each site

- Can result both in improved power and lower rates of false positives