More on site-level selection

- Three more methods in HyPhy

- Fixed Effects Likelihood **(FEL)**

  - A simpler alternative to MEME (looks for pervasive selection)

  - May be more suited for smaller datasets or datasets of low divergence

- Single Likelihood Ancestor Counting (**SLAC**)

- A counting-based approach

- Good for data exploration and visualization

- Fast Unrestricted Bayseian AppRoximation (**FUBAR**)

  - A novel statistical approach for detecting pervasive adaptive evolution on large datasets (scales to 10000s of sequences)

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	19.047	2.891	Pos. p = 0.0891
12	1	0.000	20.331	2.990	Pos. p = 0.0838
18	1	0.000	19.108	2.886	Pos. p = 0.0893
138	1	0.000	26.726	2.738	Pos. p = 0.0980
367	1	0.000	44.298	9.049	Pos. p = 0.0026
439	1	0.000	34.504	4.989	Pos. p = 0.0255
452	1	0.000	30.455	5.519	Pos. p = 0.0188
477	1	0.000	23.695	4.327	Pos. p = 0.0375
501	1	0.000	38.294	3.319	Pos. p = 0.0685
570	1	0.000	21.078	3.049	Pos. p = 0.0808
614	1	0.000	22.071	3.101	Pos. p = 0.0783
681	1	0.000	18.297	2.820	Pos. p = 0.0931
1176	1	0.000	21.975	3.040	Pos. p = 0.0812

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