

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 Bayesian 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	19.127	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