Codon	Partition	alpha	beta	LRT	Selection detected?	dN/dS with confidence intervals
2	1	1.843	0.000	7.521	Neg. p = 0.0061	0.000(0.00- 0.09)
3	1	0.786	0.000	3.161	Neg. p = 0.0754	0.000(0.00- 0.16)
4	1	2.174	0.000	10.742	Neg. p = 0.0010	0.000(0.00- 0.07)
7	1	1.105	0.000	7.537	Neg. p = 0.0060	0.000(0.00- 0.11)
8	1	0.422	0.000	3.173	Neg. p = 0.0749	0.000(0.00- 0.28)
9	1	1.353	0.000	8.638	Neg. p = 0.0033	0.000(0.00- 0.08)
10	1	1.353	0.000	8.369	Neg. p = 0.0038	0.000(0.00- 0.09)
…						
247	1	1.353	0.000	8.088	Neg. p = 0.0045	0.000(0.00- 0.10)
248	1	0.451	0.000	3.496	Neg. p = 0.0615	0.000(0.00- 0.28)
249	1	0.000	2.700	7.881	Pos. p = 0.0050	10000.000(7599.84-10000.00)
250	1	0.220	0.000	2.797	Neg. p = 0.0945	0.000(0.00- 0.61)
388	1	0.220	0.000	2.797	Neg. p = 0.0945	0.000(0.00- 0.61)

hyphy fel --alignment data/WestNileVirus_NS3.fna –ci Yes

Mapping substitutions with SLAC

- SLAC capable of detecting selection, is fast, but generally lacks power
- It provides a number of intuitive metrics for interpreting selection results
- SLAC recovers ancestral states and allows one to “map” evolutionary history onto a tree.

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