Alignment-wide estimates

- Using standard MLE approaches it is straightforward to obtain point estimates of `dN/dS := ` β/α

- Can also easily test whether or not `dN/dS > 1`, or `< 1` using the likelihood ratio test (LRT)

- Codon models also support the concepts of synonymous and non-synonymous distances between sequences using standard properties of Markov processes (exponentially distributed waiting times)

WNV NS3

Model	Log L	# p	dN/dS	LRT	p-value
Null	-7745.48	49	1		
Alternative	-6413.5	50	**0.009 [0.007-0.011]**	2512.6	~0

Very strongly conserved

HIV-1 env

Model	Log L	# p	dN/dS	LRT	p-value
Null	-2078.3	40	1		
Alternative	-2078.2	41	**1.122 [0.94-1.33]**	0.33	~0.6

Not significantly different from neutral

SARS-CoV-2 spike

Model	Log L	# p	dN/dS	LRT	p-value
Null	-9311.0	176	1		
Alternative	-9292.0	177	**0.54 [0.48-0.61]**	37.94	~0

Very strongly conserved