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

Mean gene-wide dN/dS estimates

- Are not the way to go, **<u>except</u>** when you have very small (2-3 sequence) datasets

- **For example:**

  - The humoral arm of the immune system mounts a potent defense against viral infections

  - Existing successful vaccines are based on raising a neutralizing antibody (nAb) response to the pathogen

  - No simple host genetic basis (epitopes) of the specificity of neutralizing antibody responses is known

  - Need to measure these responses