

WNV NS3

| Model | Log L | # p | dN/dS | LRT | p-value |
|-------------|----------|-----|------------------------|--------|---------|
| <i>Null</i> | -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 |
|-------------|---------|-----|----------------------|------|---------|
| <i>Null</i> | -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 |
|-------------|---------|-----|---------------------|-------|---------|
| <i>Null</i> | -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, **except** 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