

# BUSTED analysis

- **West Nile Virus NS3 protein**

- No statistical support for selection; ML point estimate allocates a small proportion of sites ( $\sim 1\%$ ) to the selected group ( $dN/dS \sim 2$ )
- The rest of the gene is very strongly conserved ( $dN/dS = 0.004$ )

- **HIV-1 transmission pair**

- Very strong evidence of strong episodic diversification ( $dN/dS \sim 100$ ) on a small proportion of sites (2%)

- The rest of the gene evolves with weak purifying selection ( $dN/dS = 0.6-0.7$ )

- **SARS-CoV-2 spike**

- Evidence of episodic diversification ( $dN/dS \sim 15$ ) on a small proportion of sites ( $\sim 2\%$ )
- Most of the rest of the gene evolves with purifying selection ( $dN/dS = 0.2$ )

# Where does the power come from for BUSTED?

*An analysis of ~9,000 curated gene alignments from `selectome.unil.ch`*

