

BUSTED analysis

- **West Nile Virus NS3 protein**

- No statistical support for selection; ML point estimate allocates a small proportion of sites (~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 ($dN/dS \sim 9$) on a small proportion of sites (5.2%)
- Most of the rest of the gene evolves with very strong purifying selection ($dN/dS = 0.6-0.7$)

Where does the power come from for BUSTED?

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

