

Information content of the alignments

	<u>WNV NS3</u>	<u>HIV-1 <i>env</i></u>	<u>SARS-CoV-2 spike</u>
<u>Sequences</u>	19	16	118
<u>Codons</u>	619	288	1273
<u>Tree Length</u> <u><i>MG94 model,</i></u> <u><i>subs/site</i></u>	0.67	0.20	0.134

How do you expect the measure to correlate with the ability to detect selection?

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Alignment-wide estimates

- Using standard MLE approaches it is straightforward to obtain point estimates of $dN/dS := \beta/\alpha$
- 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)