Information content of the alignments

	WNV NS3	**HIV-1 _env_**	**SARS-CoV-2 spike**
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Codons	619	288	1273
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Alignment-wide estimates

- Using standard MLE approaches it is straightforward to obtain point estimates of `dN/dS := ` β/α

- 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)