

Information content of the alignments

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

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

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