

# Accounting for recombination

- First screen the alignment to find putative non-recombinant fragments (e.g. using GARD)
- Apply a model-based test (MEME, FUBAR) using multiple phylogenies (one per fragment), but inferring other parameters (e.g. nucleotide substitution biases and base frequencies) from the entire alignment
- This has been shown to work very well on simulated and empirical data
- This is the approach does not work for analyses assuming a single tree (BUSTED, aBSREL).

**Table 4.** Effect of correcting for recombination when using fixed effects likelihood to detect positively selected sites.

Virus and gene	Positively Selected Codons	
	Uncorrected FEL	Corrected FEL
Cache Valley G	212,516,546,551	None
Canine Distemper H	158, <b>179, 264, 444</b>	<b>179, 264, 444</b> , 548
Crimean Congo hemm. fever NP	<b>195</b>	9, <b>195</b>
Hantaan G2	None	None
Human Parainfluenza (1) HN	37, <b>91, 358</b> , 556	<b>91, 358</b>
Influenza A (human H2N2) HA	<b>87</b> , 166, <b>252, 358</b>	<b>87</b> , 147, <b>252, 358</b>
Influenza B NA	<b>42,106,345,436</b>	<b>42,106,345,436</b>
Mumps F	<b>57, 480</b>	<b>57, 480</b>
Mumps HN	399	None
Newcastle disease F	1,4, <b>5,7,16</b> ,18, <b>108</b> ,516	<b>1,5,7,16,108</b> ,493,505
Newcastle disease HN	<b>2,54,58,228,262,284,306,471</b>	<b>2,58,228,262,284,306,471</b>
Newcastle disease N	<b>425, 430, 466</b>	<b>425, 430</b> , 462, <b>466</b>
Newcastle disease P	12, <b>56,65,174,179</b> ,188, <b>189, 204, 208, 213</b> ,217, <b>218,239,306,332</b>	<b>56, 65</b> , 146, 153, <b>174, 179, 189, 193, 204,208, 213, 218</b> , 261, <b>306,332</b>
Puumala NP	79	None

Test  $p < 0.1$  was used to classify sites as selected. Codon sites found under selection by both methods are shown in bold.