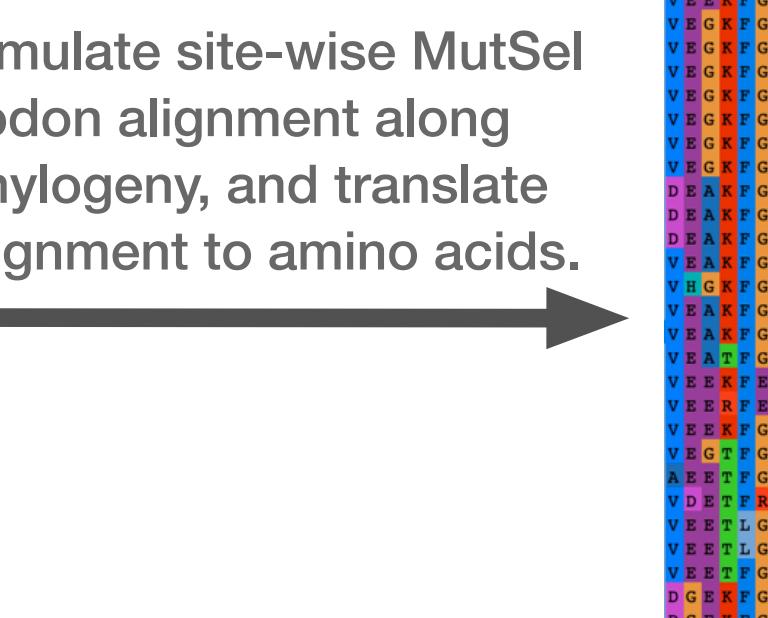
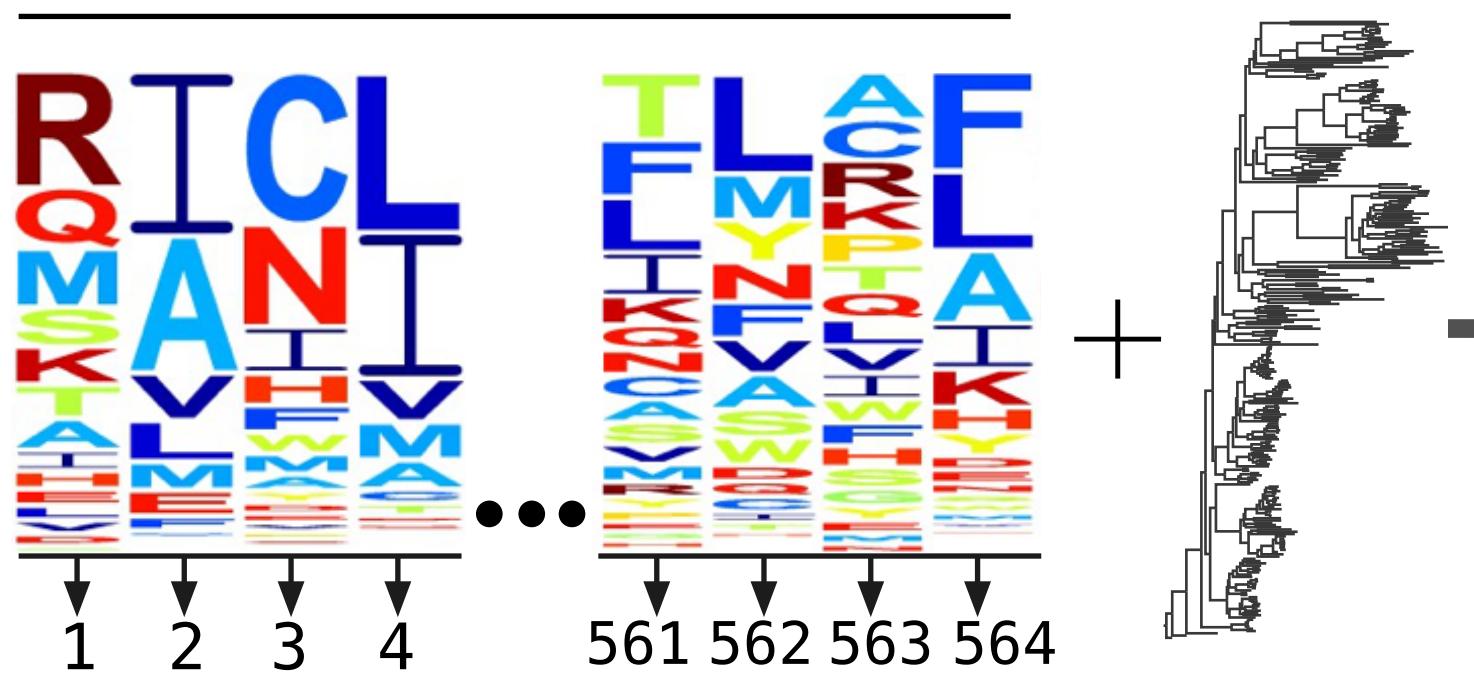
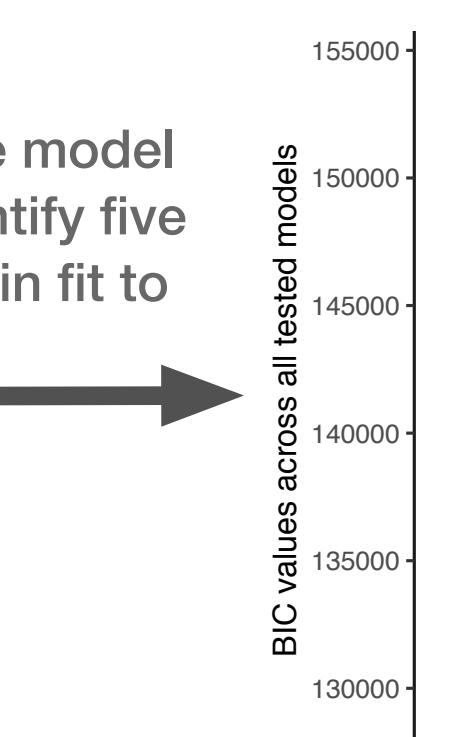


Site-wise amino-acid preferences
assessed by DMS, shown for HA
(Thyagarajan and Bloom 2014).



Simulate site-wise MutSel codon alignment along phylogeny, and translate alignment to amino acids.



m5 (mtART)

m4 (DCMut+I)

m3 (cpREV)

m2 (FLU+G4)

m1 (JTT+G4)

m5 tree

m2 tree

m3 tree

m4 tree

m5 tree

JC tree

GTR tree

Reconstruct phylogeny with five identified models, as well as JC and GTR. Compare each to true phylogeny.

m5 (mtART)

m4 (DCMut+I)

m3 (cpREV)

m2 (FLU+G4)

m1 (JTT+G4)

m5 tree

m2 tree

m3 tree

m4 tree

m5 tree

JC tree

GTR tree

m5 (mtART)

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m3 (cpREV)

m2 (FLU+G4)

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m5 tree

m2 tree

m3 tree

m4 tree

m5 tree

JC tree

GTR tree