For a given set of SARS-CoV-2 genomic sites compare predicted probabilities of finding specific codons at given genomic sites (based on the evolutionary analysis of closely related animal sarbecoviruses) vs observed variation with a median of **3078961.5** consensus genomes per codon of SARS-CoV-2 from GISAID.

Download .JSON data

9440
genomic codon loci analyzed

8688
loci with observed variants

8723
loci with evolutionary predictions

4:8
Median (95%) observed codon variants per locus

4:8
Median (95%) predicted codon variants per locus

0
Median (predicted−observed) count difference per locus

8753
Loci with all variants at ≥ 0.1% predicted

1491
Loci with unpredicted variants at ≥ 0.01%

724
Sites with perfectly predicted minority variants at 0.01% threshold

0.356
Spearkman rank correlation between observed and predicted site entropies

0.274
Fraction of variable loci where the top minority codon was correctly predicted

1.74e+4
Prediction bit-score compared to a matched complexity random model (0.01% threshold)

December 2019   November 2020   May 2021

Continued evolution, complex selection dynamics, transition to endemic?

https://observablehq.com/@spond/sars-cov-2-pvo

The set of "unusual" changes
(compared to nCOV)

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