

Analytical framework

- Key mutations have significant phenotypic and epidemiological significance.
- Analysis of substitution patterns in large sets of SARS-CoV-2 data can reveal genomic sites subject to **selective pressure** => **possibly important**
- Used a suite of stock and modified **dN/dS methods** for **coding sequence evolution** developed over ~2 decades and extensively used in other RNA viruses
- The methods are implemented in the HyPhy software package (www.hyphy.org)
- Our public servers (datamonkey.org) have processed >10,000 complex CoV evolutionary analyses from researchers worldwide.
- Spent considerable effort to scale up analyses and develop data reduction techniques to manage data sizes.
- Collaborative efforts, many other open source tools at covid-19.galaxyproject.org

