

Pathogen Genomics Center of Excellence Situation Report



2024-04-26

Source: Article Notebook

- Current data reflects a mixture of JN.1 descendents as the likely near term variants.
- Globally no other variants with unusual characteristics have been identified as having unusual growth.
- Some other point

initial value 10986.122887 final value 10985.946043 converged

Source: Article Notebook

Situation Update Details

- Based on what XYZ(?), JN.1 and descendents continue to dominate. Some recombinations from JN.1 and other BA.5 variants are being monitoredtracked, but have yet to show significant growth relative other variants.
- Together this diversity suggests steady evolution against general population immunity with no indications of a variant driven wave of COVID-19 infections.
- As of 2024-11-24, there were X samples from MM/DD/YYYY - MM/DD/YYYY, some comment on trend
- Some text here about image one. There is this variant that's here
- Some text about image two
- Image 3 has this
- Findings from a site's analysis of national data

Statewide COVID-19 Variants: Last 12 Weeks Percent of genetic mutations (or variants) of the COVID-19 virus by lineage for the past 6 weeks.

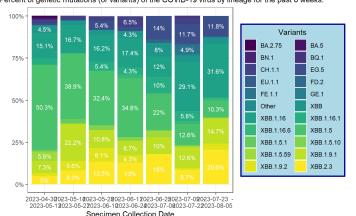


Figure 1: Proportion of variants by year.

- Georgia Department of Public Health probablity of detection: 33.38% and the consensus genomes are uploaded to public repositories like GISAID and GenBank.
- Massachusetts Department of Health prop 33.38%
- Virginia Department of Health 33.50%

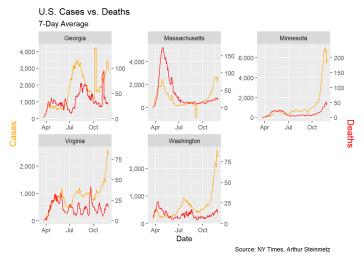


Figure 2: From the New York Times: A couple of observations are obvious. First when cases start to rise, deaths follow with a lag. Second, we have had three spikes in cases so far and in each successive instance the mortality has risen by a smaller amount. This suggests that, thankfully, we are getting better at treating this disease. It is NOT a function of increased testing because positivity rates have not been falling.

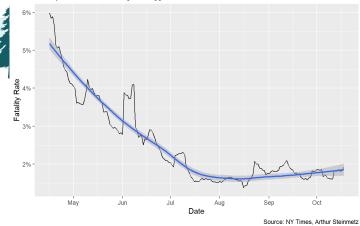
Source: NorthWest Genomics Center of Excellence

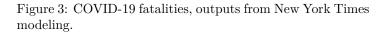
Date Variant Proportion Count 1 2023-01-01 0.3000000 Alpha 2 2023-01-01 Delta 0.2979798 30 2023-01-01 Omicron 0.2959596 30 29 2023-01-02 Alpha 0.2939394 2023-01-02 Delta 0.2919192 29 2023-01-02 Omicron 0.2898990 29

weights: 9 (4 variable)

Source: New England Genomics Center of Excellence

Fatality Rates are Creeping Up Fatality Rate as a Percentage of Lagged Cases





Source: Virginia Genomics Center of Excellence

Citations

This is a simple placeholder for the manuscript's main document (Knuth 1984).

 $Figure\ 1\ code\ source$

Figure 2 code source $\,$

Figure 3 code source

main article code source

Knuth, Donald E. 1984. "Literate Programming." Comput. J. 27 (2): 97–111. https://doi.org/10.1093/comjnl/27.2. 97.

