Pathogen Genomics Center of Excellence Situation Report

2024-04-26

Source: [Article Notebook](https://coe-test-org.github.io/sitrep-demo/index.qmd.html)

* 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

# 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

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| Figure 1: Proportion of variants by year. |

Source: [NorthWest Genomics Center of Excellence](https://coe-test-org.github.io/sitrep-demo/notebooks\nwcoe-preview.html#cell-fig-countprop)

Date Variant Proportion Count  
1 2023-01-01 Alpha 0.3000000 30  
2 2023-01-01 Delta 0.2979798 30  
3 2023-01-01 Omicron 0.2959596 30  
4 2023-01-02 Alpha 0.2939394 29  
5 2023-01-02 Delta 0.2919192 29  
6 2023-01-02 Omicron 0.2898990 29

# weights: 9 (4 variable)  
initial value 10986.122887   
final value 10985.946043   
converged

Source: [Article Notebook](https://coe-test-org.github.io/sitrep-demo/index.qmd.html)

* Washington State Department of Health - Alpha variant proportion is 33.50%
* 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 Deparment of Health - 33.50%

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| 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: [New England Genomics Center of Excellence](https://coe-test-org.github.io/sitrep-demo/notebooks\necoe-preview.html#cell-fig-state-analysis)

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| Figure 3: COVID-19 fatalities, outputs from New York Times modeling. |

Source: [Virginia Genomics Center of Excellence](https://coe-test-org.github.io/sitrep-demo/notebooks\vacoe-preview.html#cell-fig-fatality-plot)

## Citations

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

[[Figure 1](#fig-countprop) code source](https://coe-test-org.github.io/sitrep-demo/notebooks/nwcoe-preview.html#cell-fig-countprop)

[[Figure 2](#fig-state-analysis) code source](https://coe-test-org.github.io/sitrep-demo/notebooks/necoe-preview.html#cell-fig-state-analysis)

[[Figure 3](#fig-fatality-plot) code source](https://coe-test-org.github.io/sitrep-demo/notebooks/vacoe-preview.html#cell-fig-fatality-plot)

[main article code source](https://coe-test-org.github.io/sitrep-demo/index-preview.html)

Knuth, Donald E. 1984. “Literate Programming.” *Comput. J.* 27 (2): 97–111. <https://doi.org/10.1093/comjnl/27.2.97>.