Viewing the SARS-CoV-2 pandemic through a genomic lens

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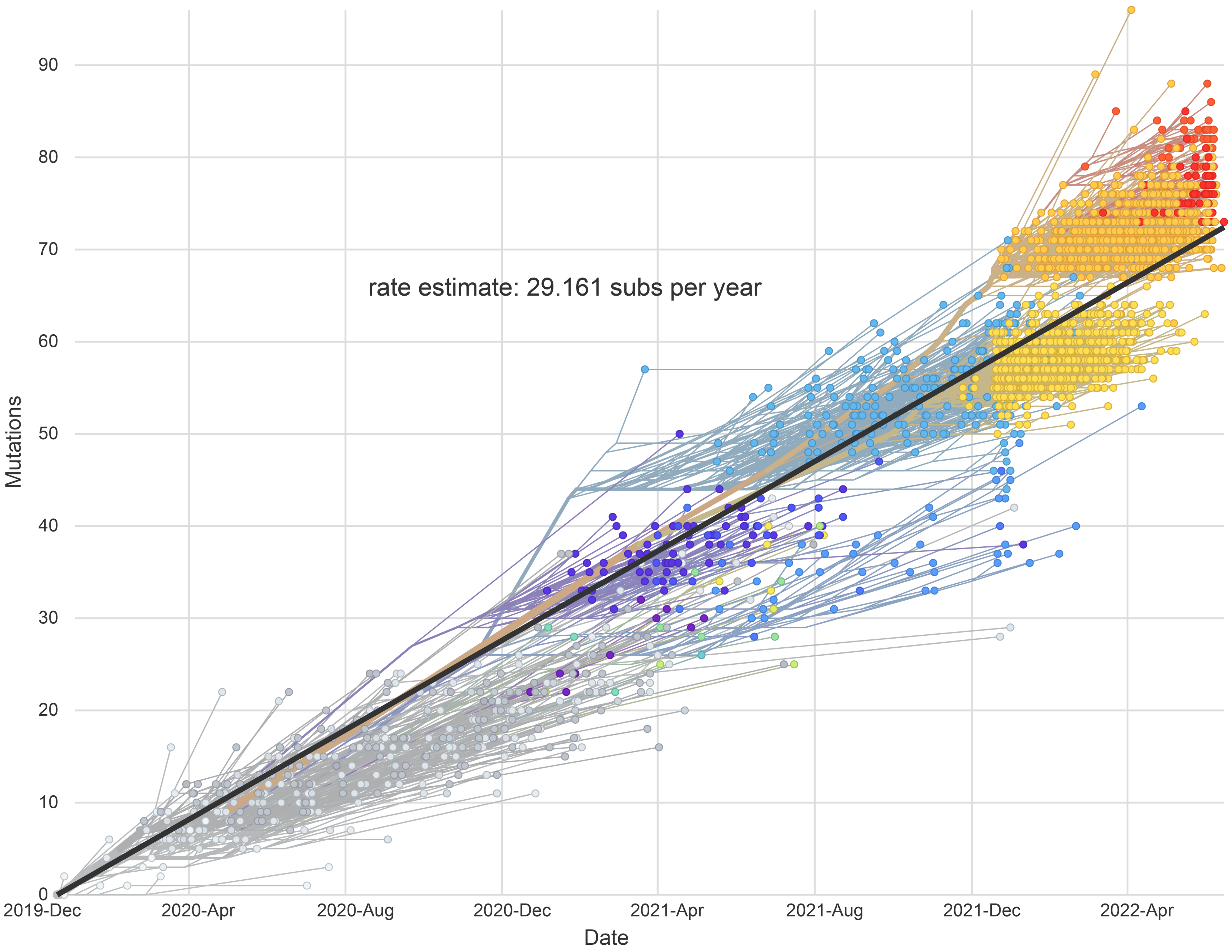
Classification of an evolving virus



https://nextstrain.org/

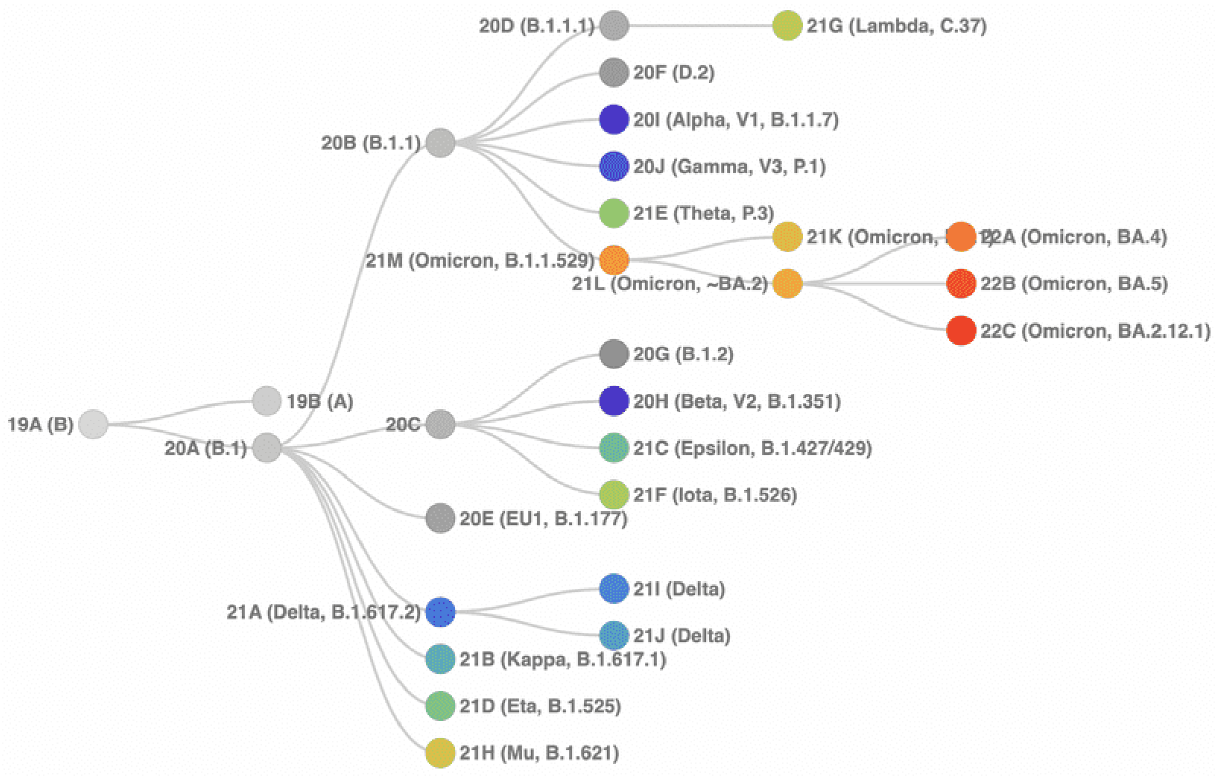
Key components of dynamic viral classification

- capture local and global patterns of genetic diversity in a timely and coherent manner
- track emerging lineages and their movement
- robust and flexible to changes in viral diversity
- ability to incorporate the emergence and disappearance of lineages over time

Rambaut et al. (2020) *Nature Microbiology*

Nextclade

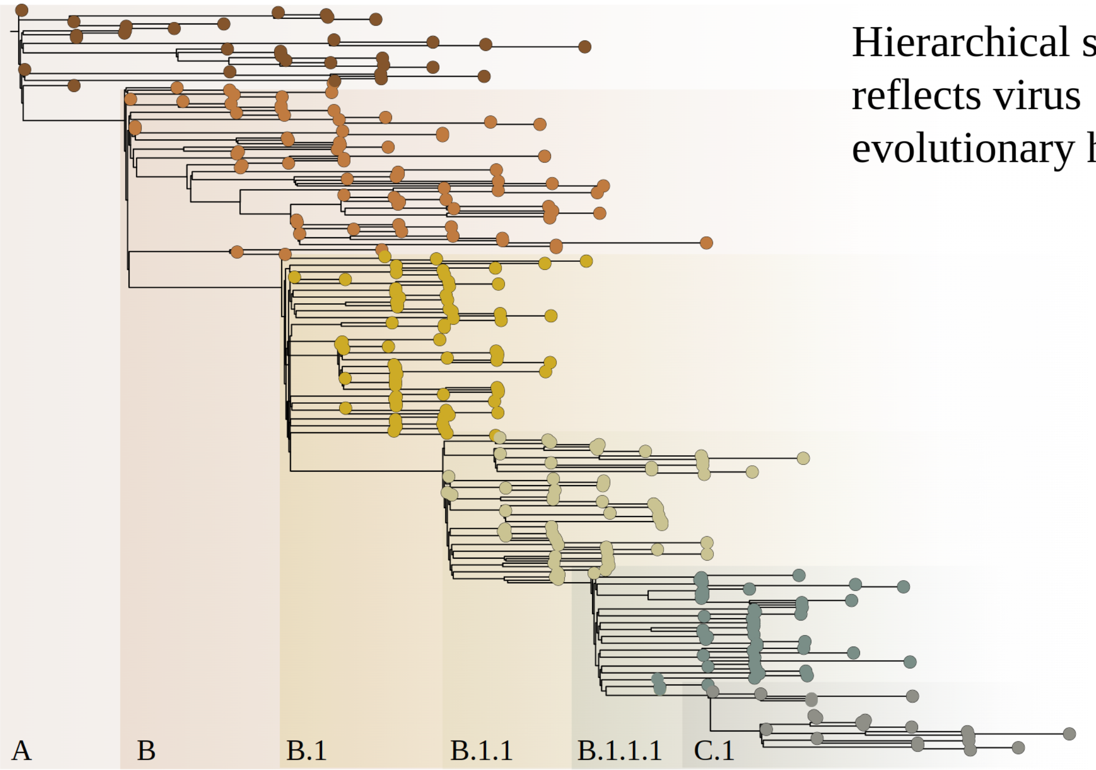
- A VOC or VOI is recognized by the WHO and given a Greek letter label
- A clade reaches >20% global frequency for 2 or more months
- A clade reaches >30% regional frequency for 2 or more months
- A clade shows consistent >0.05 per day growth in frequency where it is circulating and has reached >5% regional frequency



https://clades.nextstrain.org/

Pangolin

- Pango Committee maintains the "rules" of the nomenclature system
- Pango lineages are designed to represent the branches of the pandemic tree
- Pango lineages are intended to highlight epidemiologically-relevant events
- Pango lineages can be classified through two major methods
  - pangoLEARN: random forest based decision model
  - UShER: sample placement on pre-existing phylogenetic trees



Hierarchical system reflects virus evolutionary history

https://www.pango.network/

WHO Naming Convention

Currently circulating variants of concern (VOCs):

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Additional amino acid changes monitored°	Earliest documented samples	Date of designation
Omicron*	B.1.1.529	GR/484A	21K, 21L, 21M, , 22A, 22B, 22C	+S:R346K +S:L452X +S:F486V	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

* Includes BA.1, BA.2, BA.3, BA.4, BA.5 and descendent lineages. It also includes BA.1/BA.2 circulating recombinant forms such as XE. WHO emphasizes that these descendant lineages should be monitored as distinct lineages by public health authorities and comparative assessments of their virus characteristics should be undertaken.

The full list of Pango lineages can be found here: https://cov-lineages.org/lineage_list.html; for FAQ, visit: https://www.pango.network/faqs/

° Only found in a subset of sequences

https://www.who.int/activities/tracking-SARS-CoV-2-variants

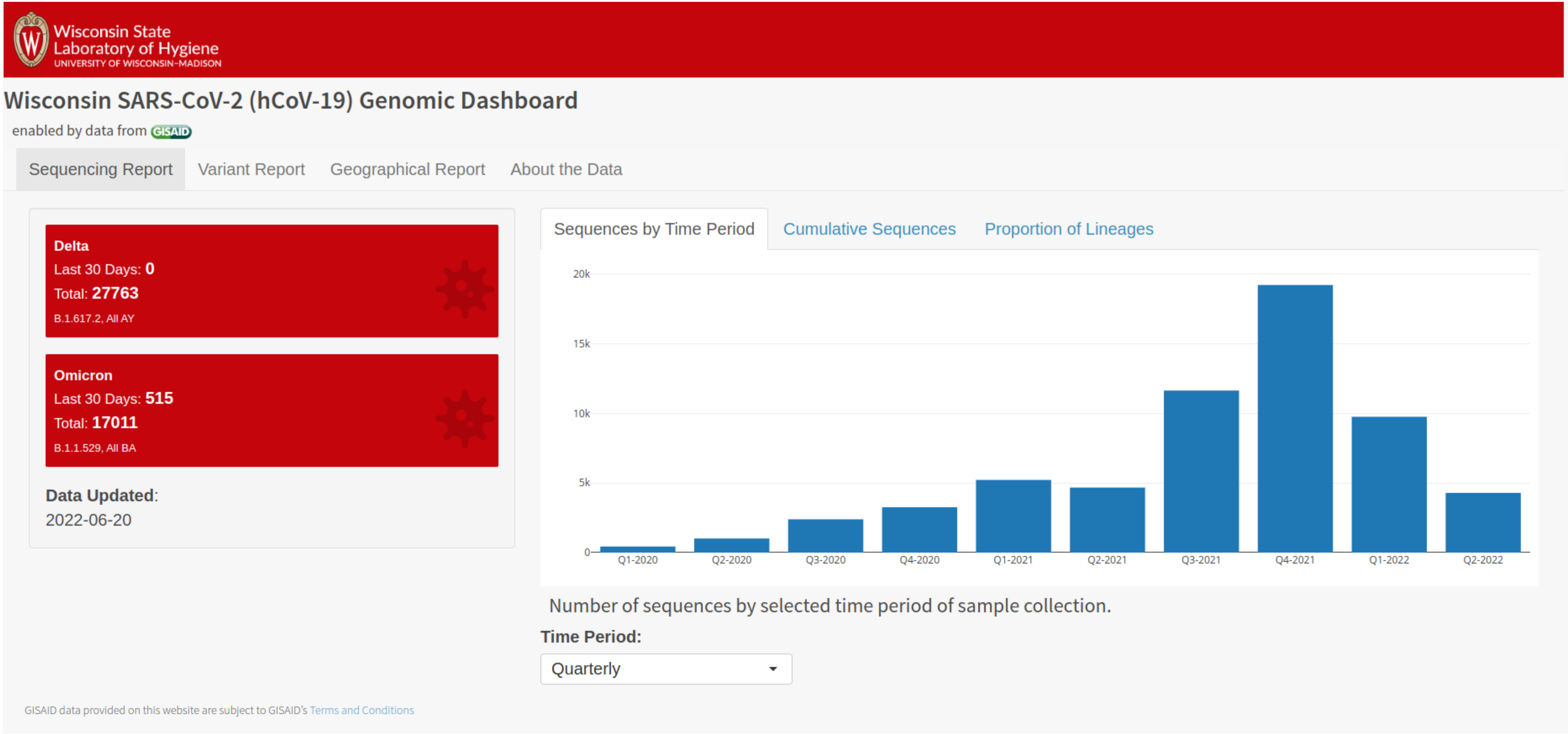
Previously circulating VOCs:

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	United Kingdom, Sep-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Beta	B.1.351	GH/501Y.V2	20H (V2)	South Africa, May-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Gamma	P.1	GR/501Y.V3	20J (V3)	Brazil, Nov-2020	VOC: 11-Jan-2021 Previous VOC: 09-Mar-2022
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021 Previous VOC: 7-Jun-2022

*Includes all descendent lineages.

Current SARS-CoV-2 Situation Report

Wisconsin SARS-CoV-2 Genomic Dashboard



Wisconsin SARS-CoV-2 (hCoV-19) Genomic Dashboard

enabled by data from GISAID

Delta
Last 30 Days: **0**
Total: **27763**
B.1.617.2, All AY

Omicron
Last 30 Days: **515**
Total: **17011**
B.1.1.529, All BA

Data Updated:
2022-06-20

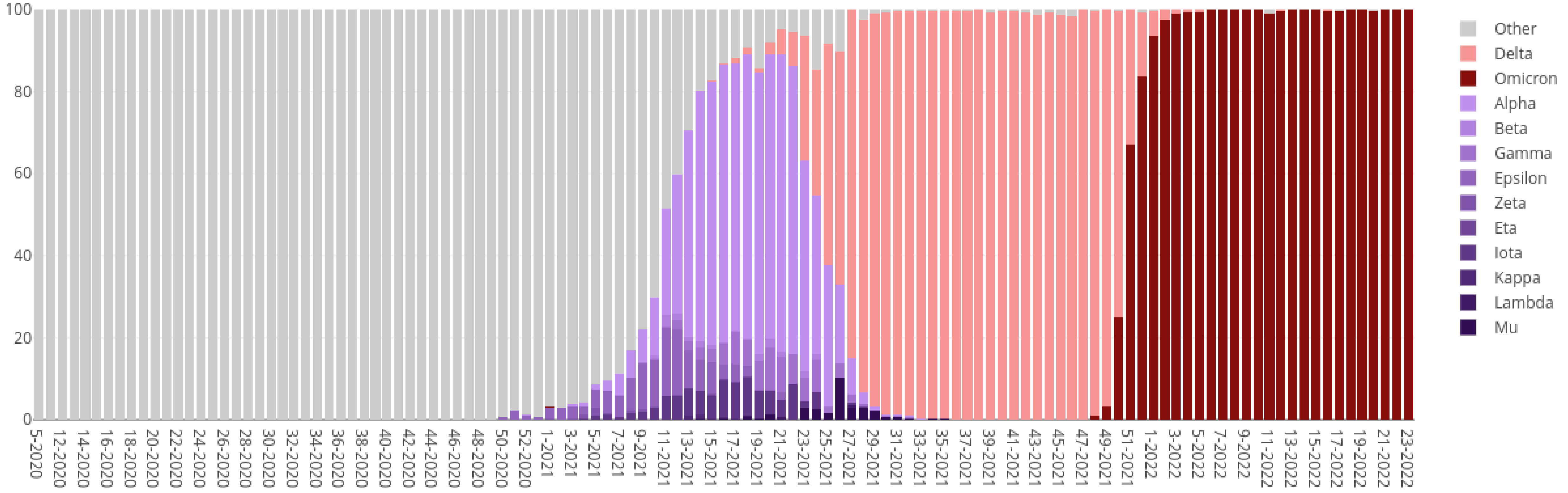
Number of sequences by selected time period of sample collection.

Time Period:
Quarterly

GISAID data provided on this website are subject to GISAID's Terms and Conditions

https://dataportal.slh.wisc.edu/sc2dashboard

Wisconsin Lineages



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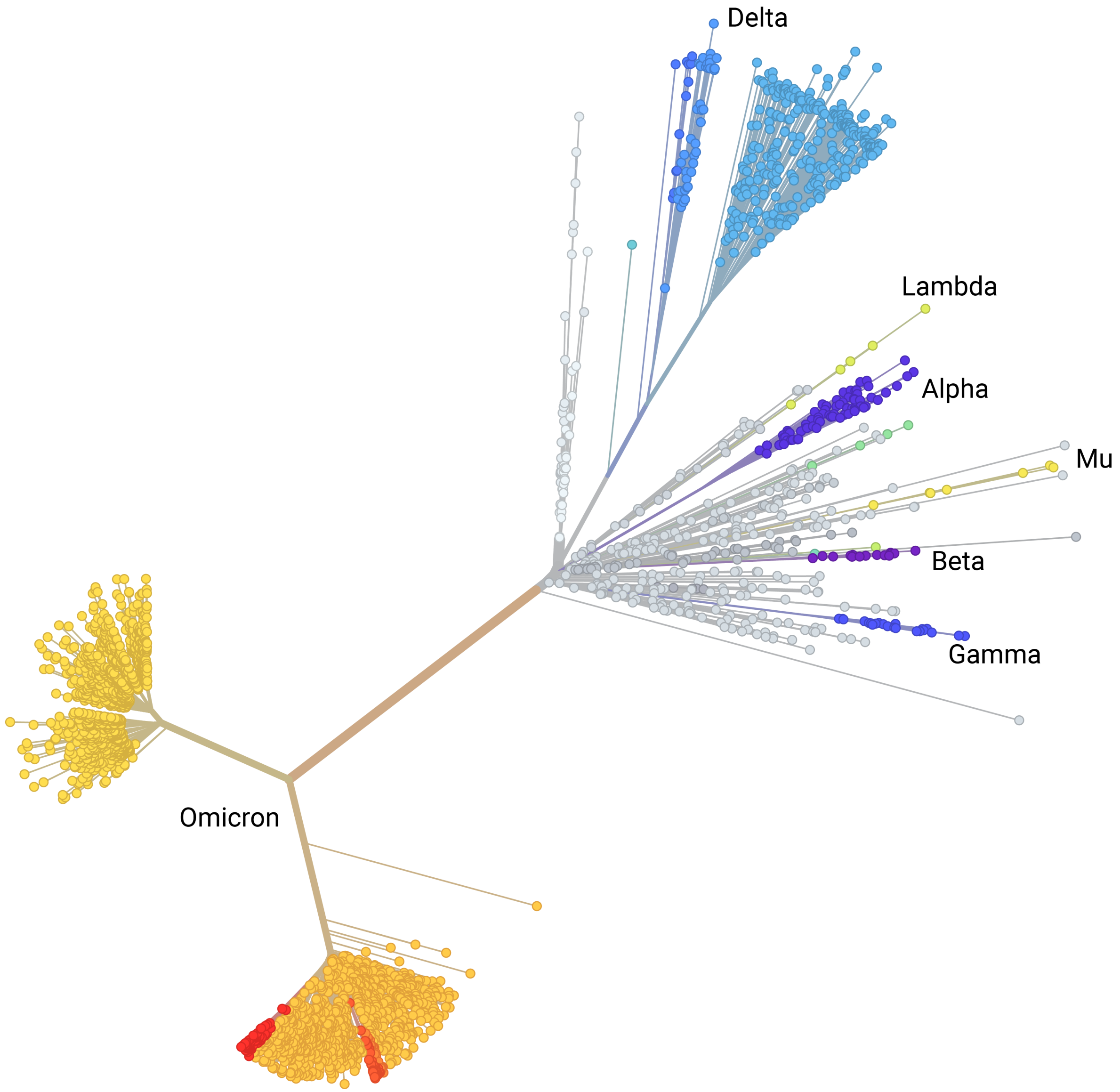
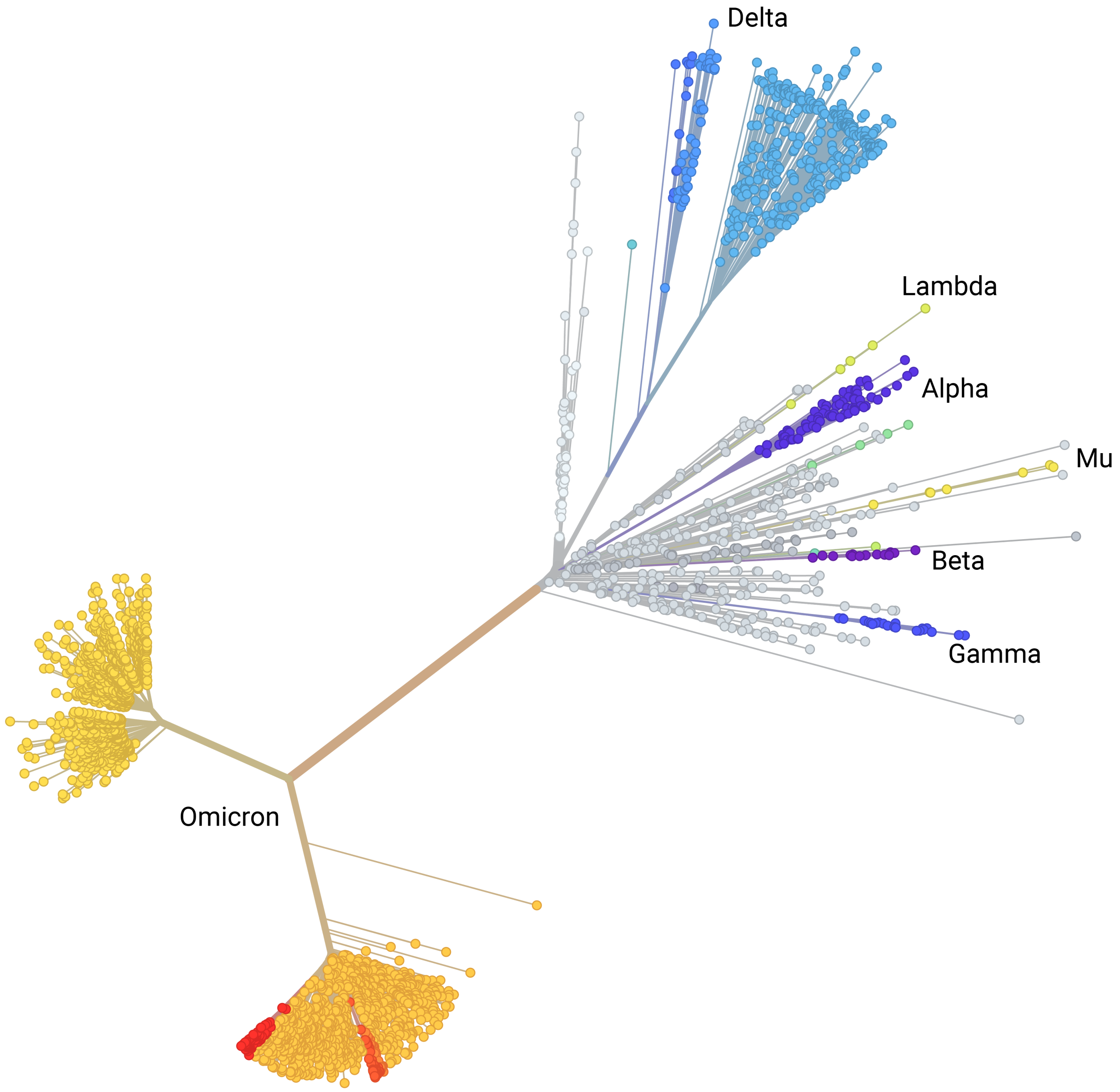
Emergence of Omicron



https://doi.org/10.1038/d41586-022-00215-2
https://nextstrain.org/

Emergence of Omicron



Three Theories

- Undetected Spread
- Animal Reservoir (Mouse/Rat)
- Chronic Infection

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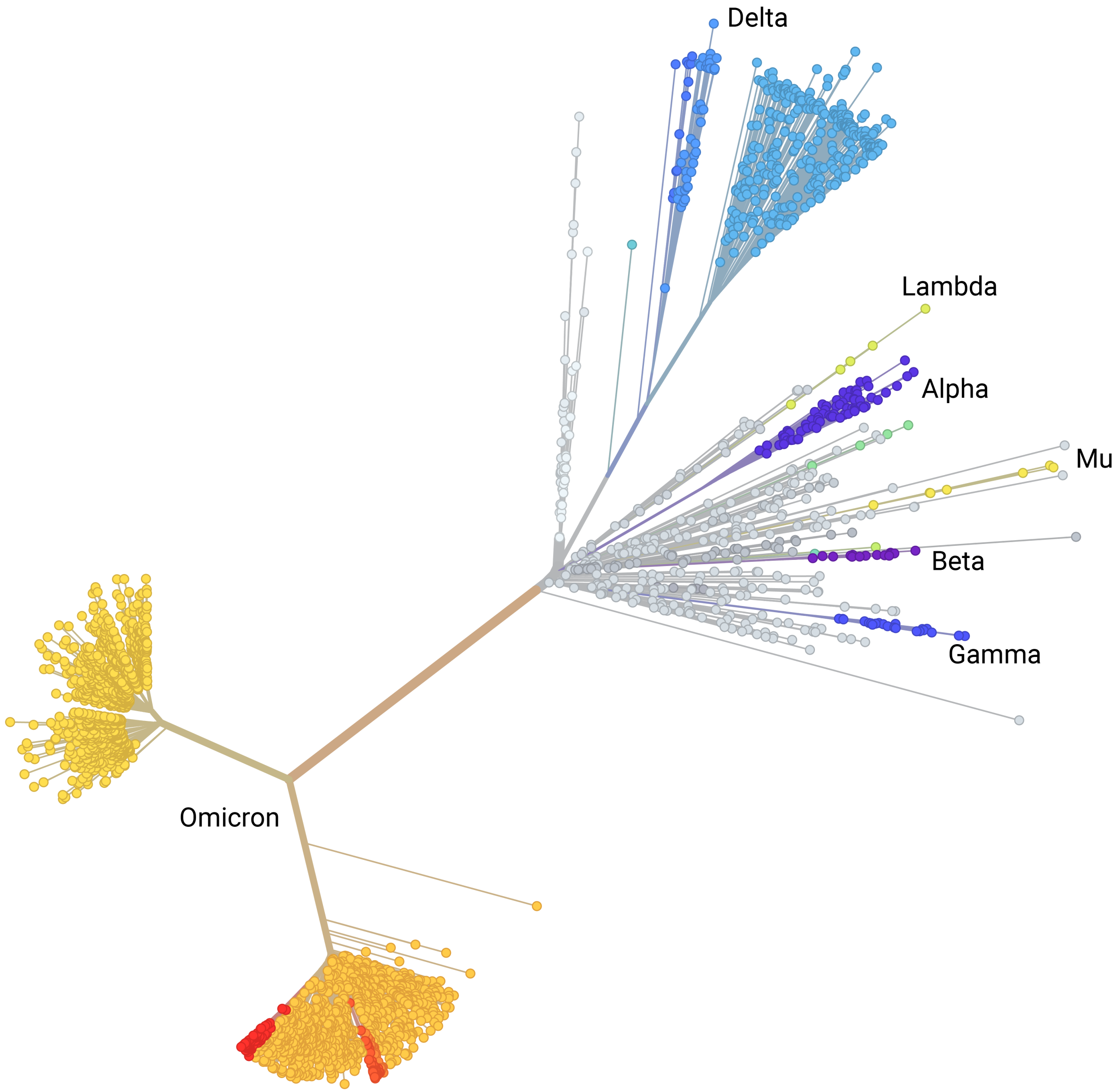
Omicron Today



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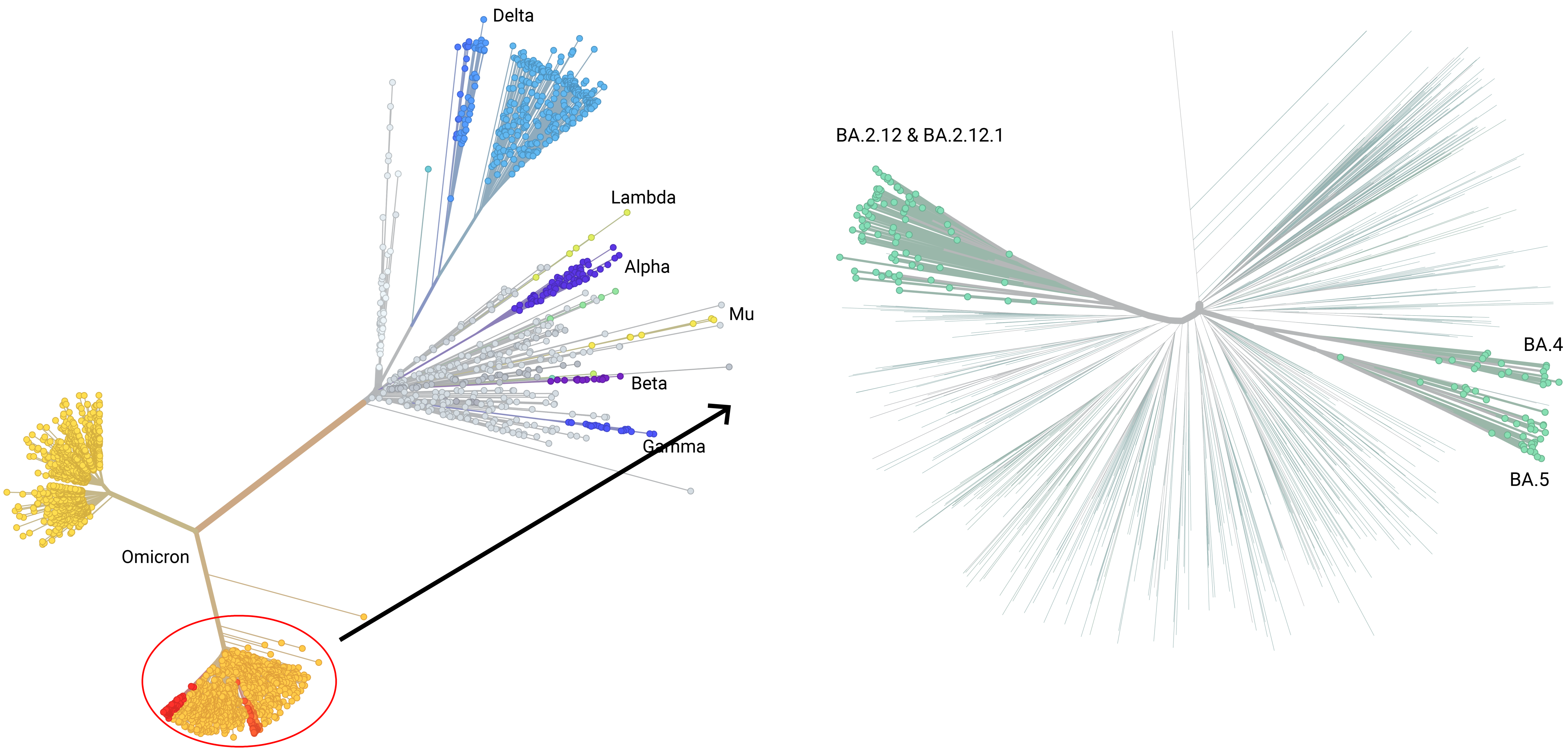
Omicron Today



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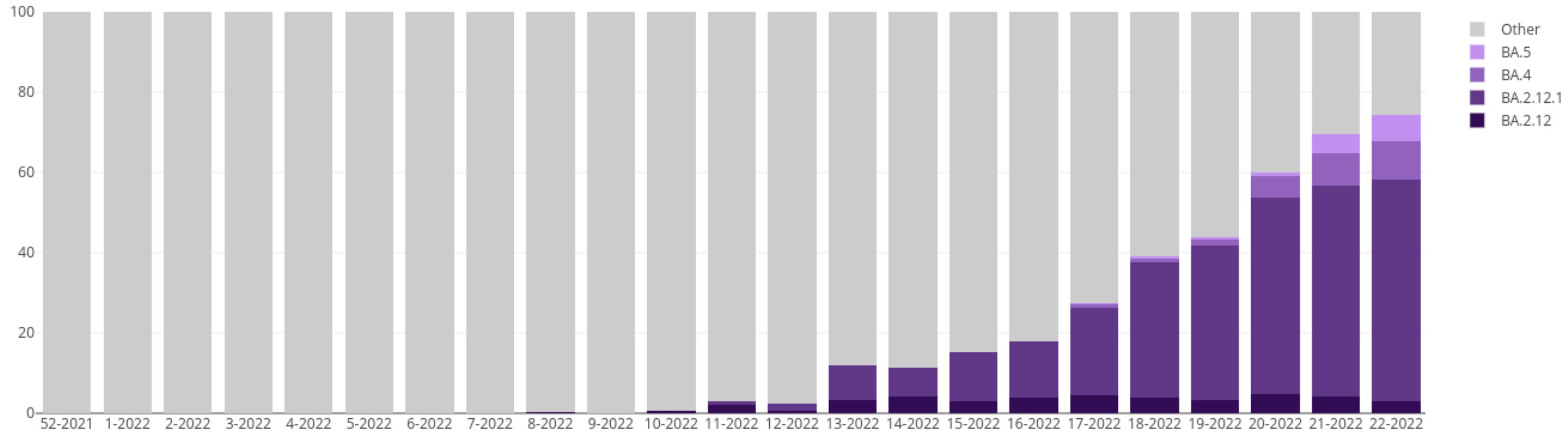
Omicron Today




nature https://doi.org/10.1038/s41586-022-04980-y

Accelerated Article Preview

BA.2.12.1, BA.4 and BA.5 escape antibodies elicited by Omicron infection

"Importantly, BA.2.12.1 and BA.4/BA.5 display stronger neutralization evasion than BA.2 against the plasma from 3-dose vaccination and, most strikingly, from post-vaccination BA.1 infections."

https://dataportal.slh.wisc.edu/sc2dashboard
Cao et al. 2022 *Nature*

Summary

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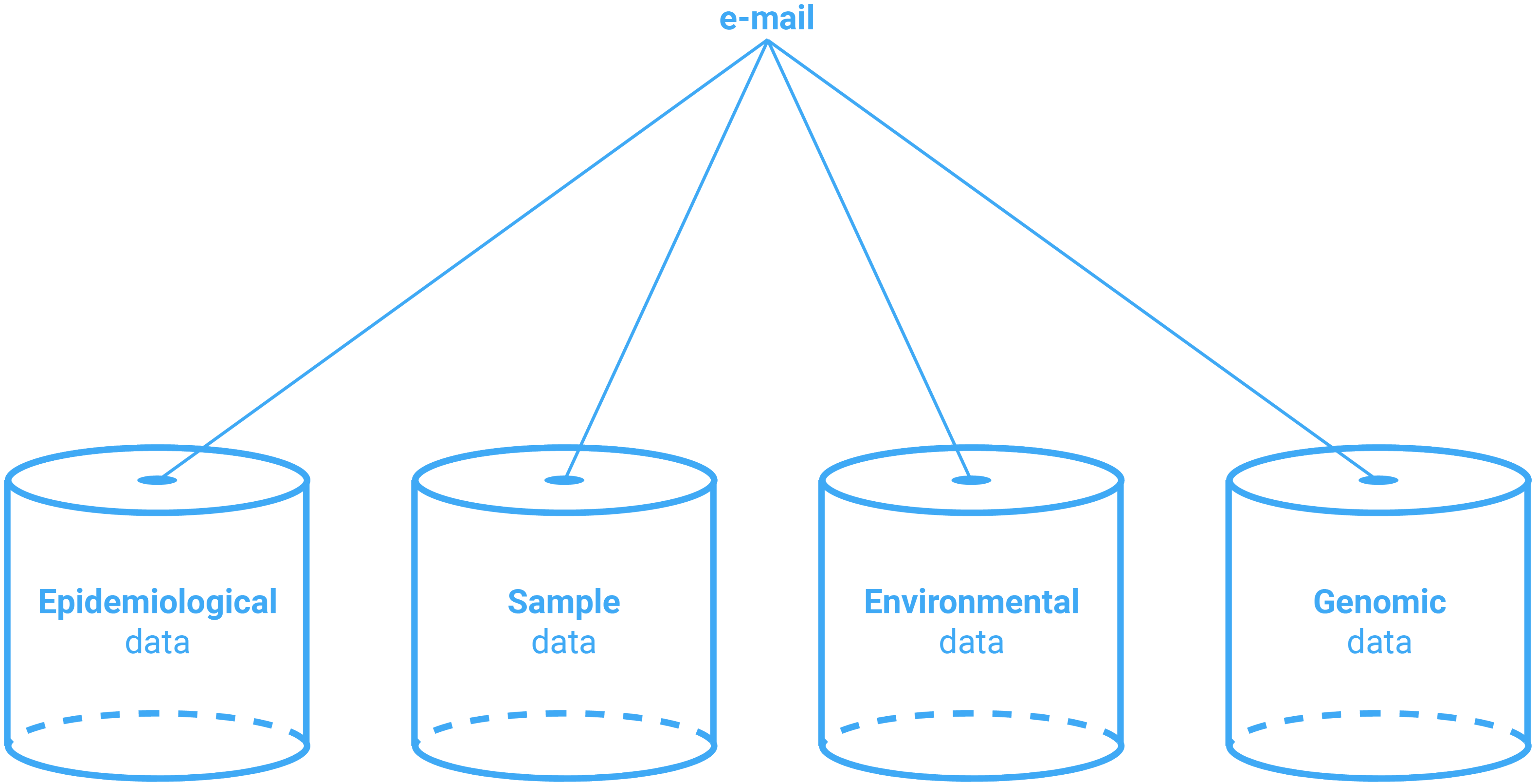
- It is very likely we will see new immune escape variants continue to emerge.
- Increases in at home testing has the potential to bias genomic surveillance.

Challenges in the application of genomic surveillance data

Public Health is currently a series of Data Silos



e-mail

Epidemiological data

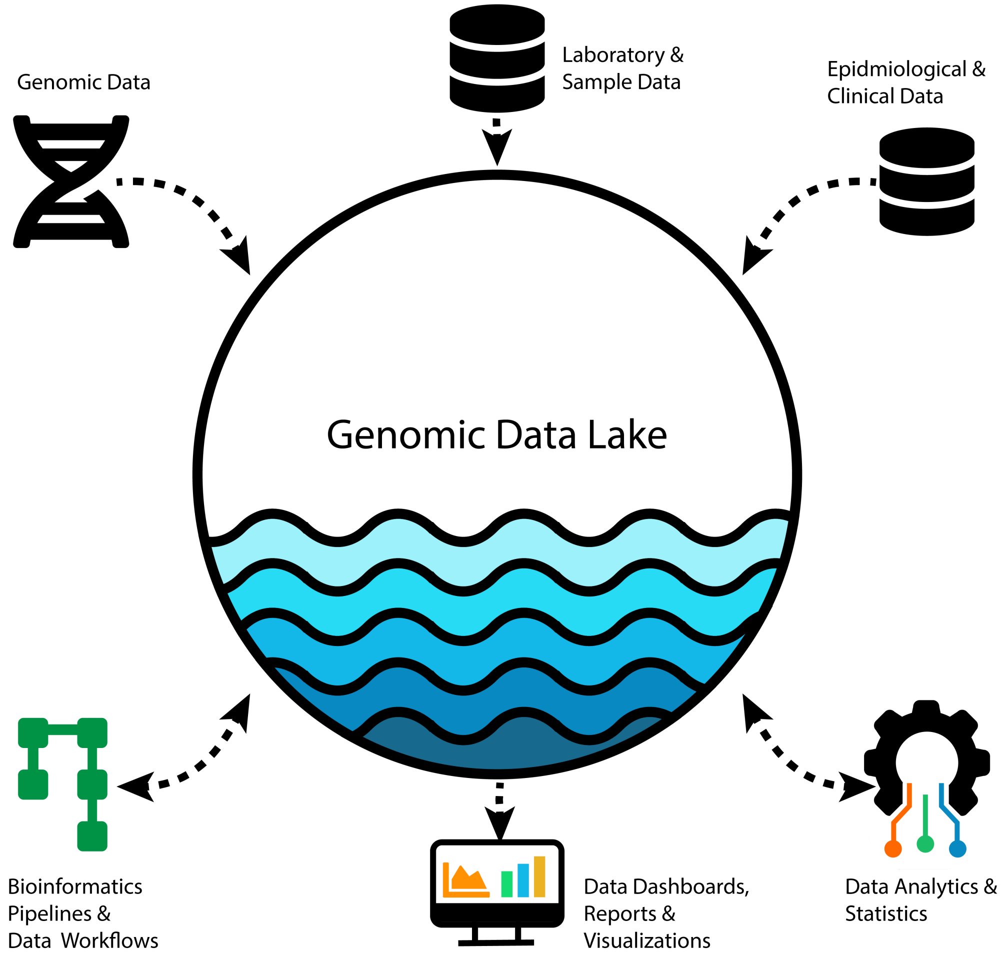
Sample data

Environmental data

Genomic data

Integrating environmental, epidemiological, and genomic data with a data lake

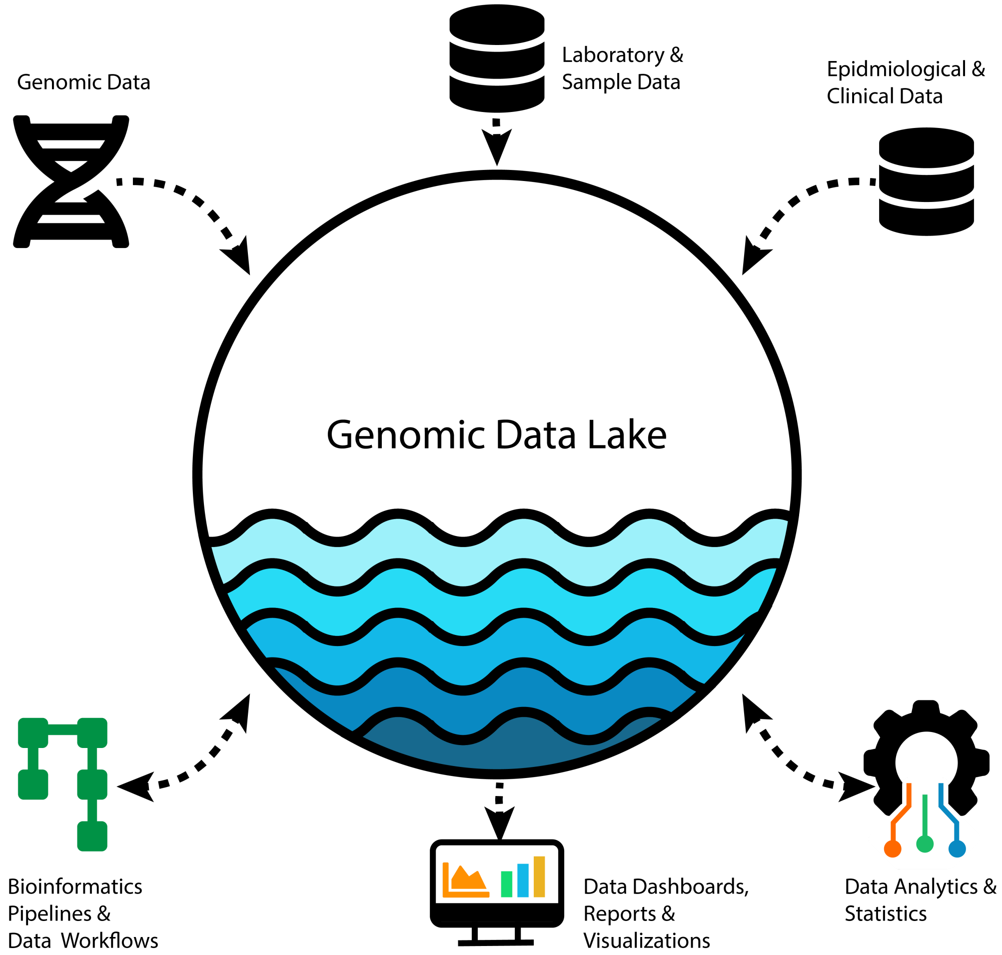
data lake: centralized repository designed to store, process, and secure large amounts of structured and unstructured data at any scale



Integrating environmental, epidemiological, and genomic data with a data lake

data lake: centralized repository designed to store, process, and secure large amounts of structured and unstructured data at any scale

- Data Lakes retain all data
- Support all data types
- Adapt easily to changes
- Require data scientists to navigate
- Require proper management to prevent a data swamp



Integrated data better supports public health

- Identify correlations between genetic variants and vaccination breakthroughs or increased symptom severity.
- Faster and more informed outbreak response.
- Application of machine learning models and AI to identify genomic patterns.
- Big data enables the application of precision public health efforts.

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Questions?