

Network Systems  
Science & Advanced  
Computing  
Biocomplexity Institute  
& Initiative  
University of Virginia

# Foresight and Analysis of Infectious Disease Threats to Virginia's Public Health

April 4<sup>th</sup>, 2024

(data current to March 27<sup>th</sup> – April 4<sup>th</sup>)

Biocomplexity Institute Technical report: TR BI-2024-20



---

**BIOCOMPLEXITY** INSTITUTE

[biocomplexity.virginia.edu](https://biocomplexity.virginia.edu)

# About Us

- Biocomplexity Institute at the University of Virginia
  - Using big data and simulations to understand massively interactive systems and solve societal problems
- Over 20 years of crafting and analyzing infectious disease models
  - Pandemic response for Influenza, Ebola, Zika, and others



## Points of Contact

Bryan Lewis  
[brylew@virginia.edu](mailto:brylew@virginia.edu)

Srini Venkatramanan  
[srini@virginia.edu](mailto:srini@virginia.edu)

Madhav Marathe  
[marathe@virginia.edu](mailto:marathe@virginia.edu)

Chris Barrett  
[ChrisBarrett@virginia.edu](mailto:ChrisBarrett@virginia.edu)

## Model Development, Outbreak Analytics, and Delivery Team

Abhijin Adiga, Aniruddha Adiga, Hannah Baek, Chris Barrett, Parantapa Bhattacharya, Chen Chen, Da Qi Chen, Jiangzhuo Chen, Baltazar Espinoza, Galen Harrison, Stefan Hoops, Ben Hurt, Gursharn Kaur, Brian Klahn, Chris Kuhlman, Bryan Lewis, Dustin Machi, Madhav Marathe, Sifat Moon, Henning Mortveit, Mark Orr, Przemyslaw Porebski, SS Ravi, Erin Raymond, Samarth Swarup, Pyrros Alexander Telionis, Srinivasan Venkatramanan, Anil Vullikanti, Andrew Warren, Amanda Wilson, Dawen Xie



# Overview

- **Goal:** Understand impact of current and emerging Infectious Disease threats to the Commonwealth of Virginia using modeling and analytics
- **Approach:**
  - Provide analyses and summaries of current infectious disease threats
  - Survey existing forecasts and trends in these threats
  - Analyze and summarize the current situation and trends of these threats in the broader context of the US and world
  - Provide broad overview of other emerging threats

# Key Takeaways

## **COVID-19 indicators have been in steady decline**

- Hospital admissions are higher than they were at this point last year, while ED visits with diagnosed COVID-19 are below and nearing an all-time low
- Wastewater viral activity levels have dropped significantly in recent weeks, with lows spread around Virginia
- Together this suggest continued declines easing into a low plateau

## **Influenza has dropped significantly in VA and across the US**

## **RSV hospitalizations remain at minimal activity**

# COVID-19 Surveillance

---



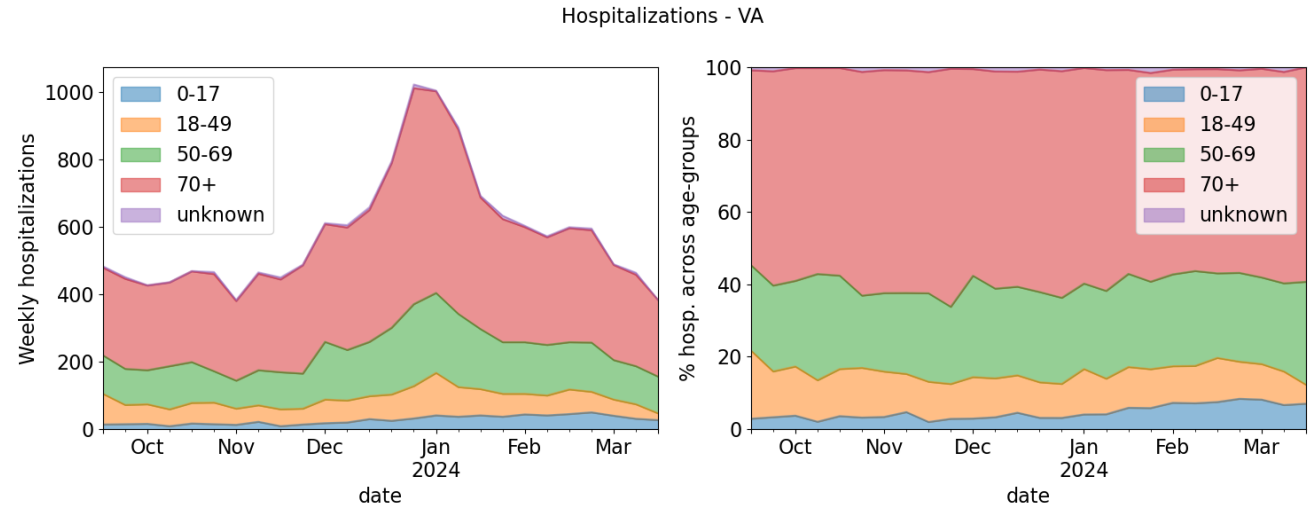
# Hospitalizations in VA by Age

## Age distribution in hospitals showing slight shift towards younger age groups

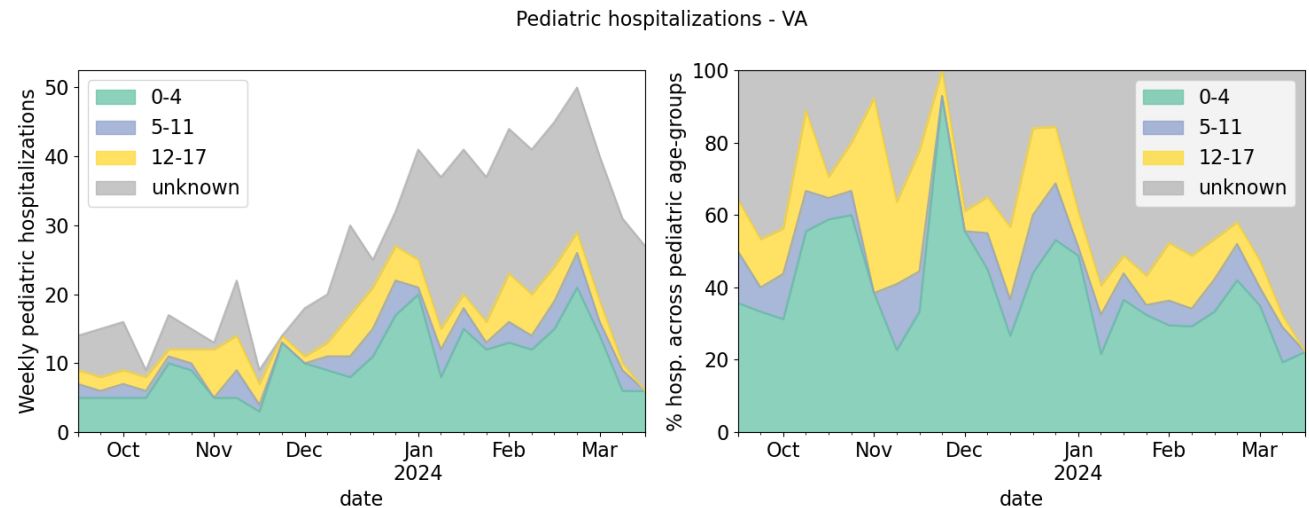
- Overall hospitalizations stable across all age groups
- Pediatric hospitalizations have fallen in recent weeks

Note: These data are lagged and based on HHS hospital reporting

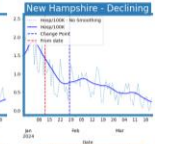
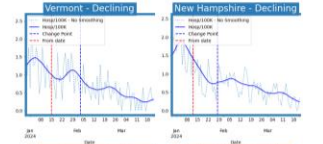
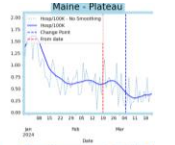
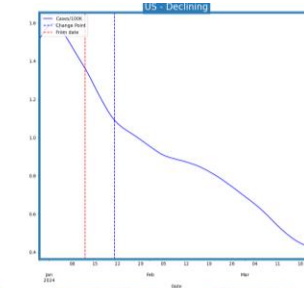
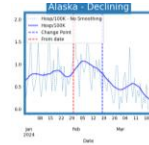
### Virginia Hospitalizations by Age (all ages)



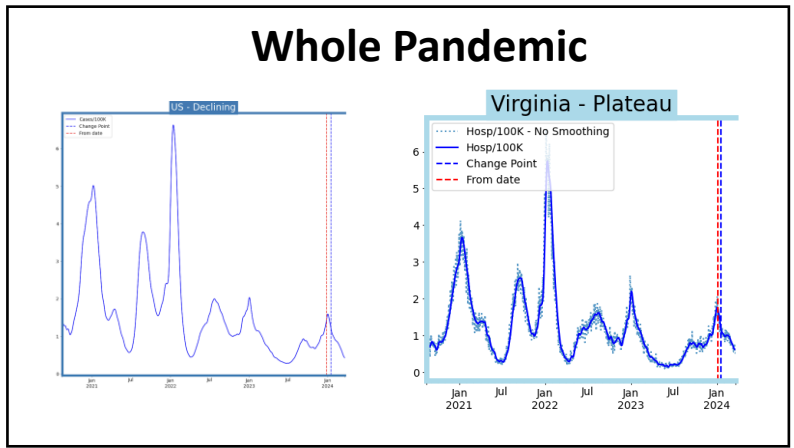
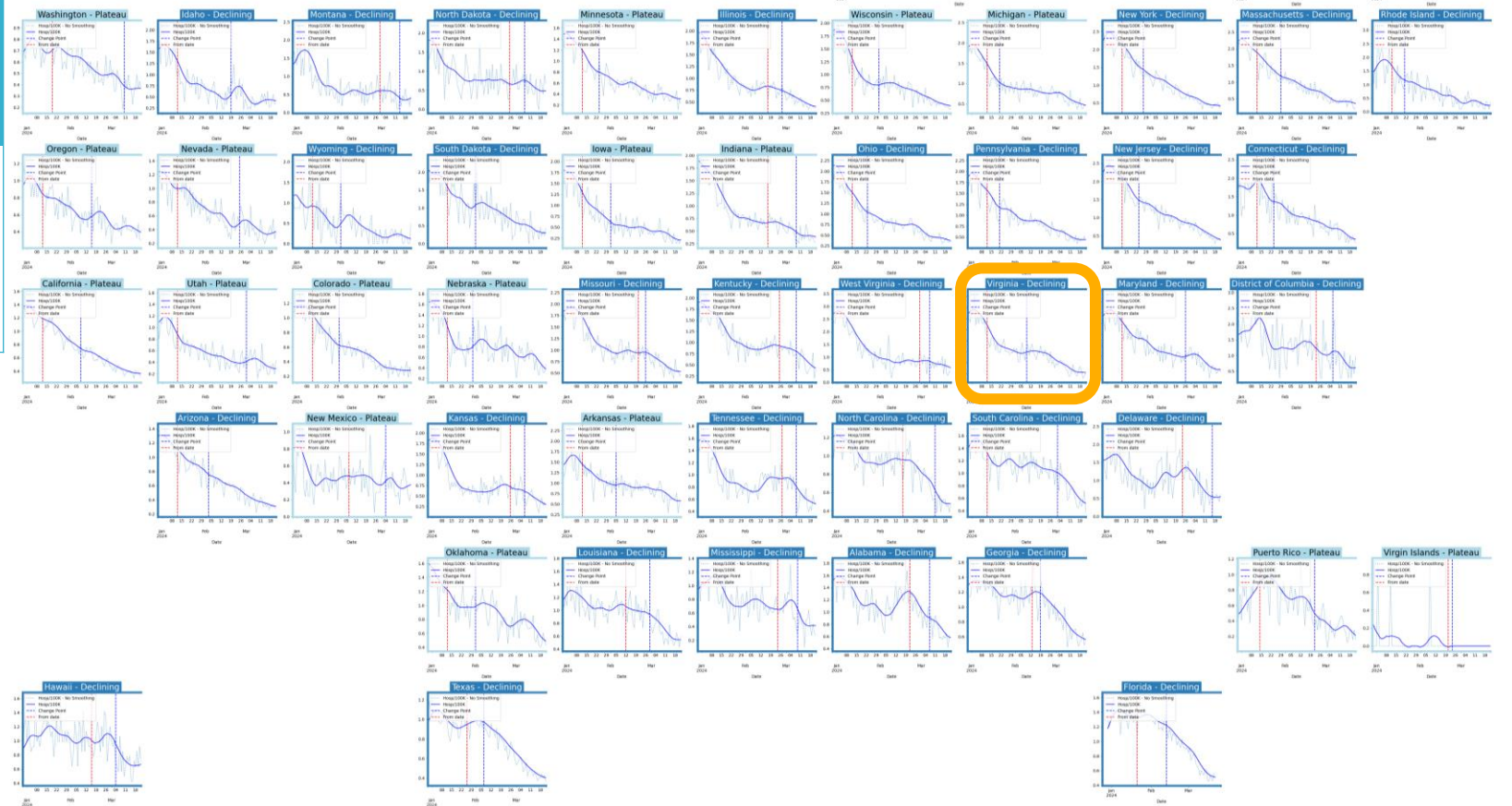
### Pediatric Hospitalizations by Age (0-17yo)



# United States Hospitalizations



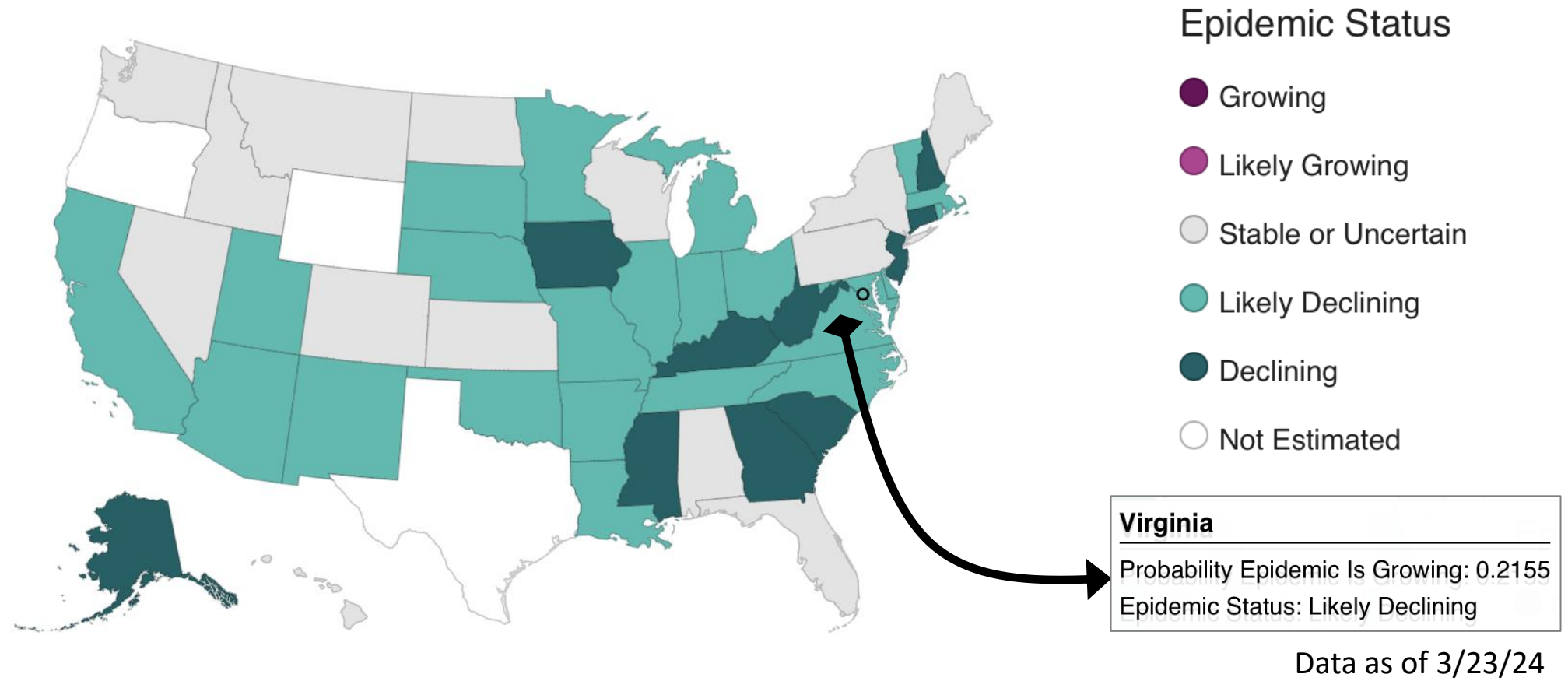
Status	Current Week	Last Week
Declining	35	27
Plateau	18	25
Slow Growth	0	1
In Surge	0	0



4/5/2024



# COVID-19 Hospitalizations – Epidemic Growth



Territories PR VI



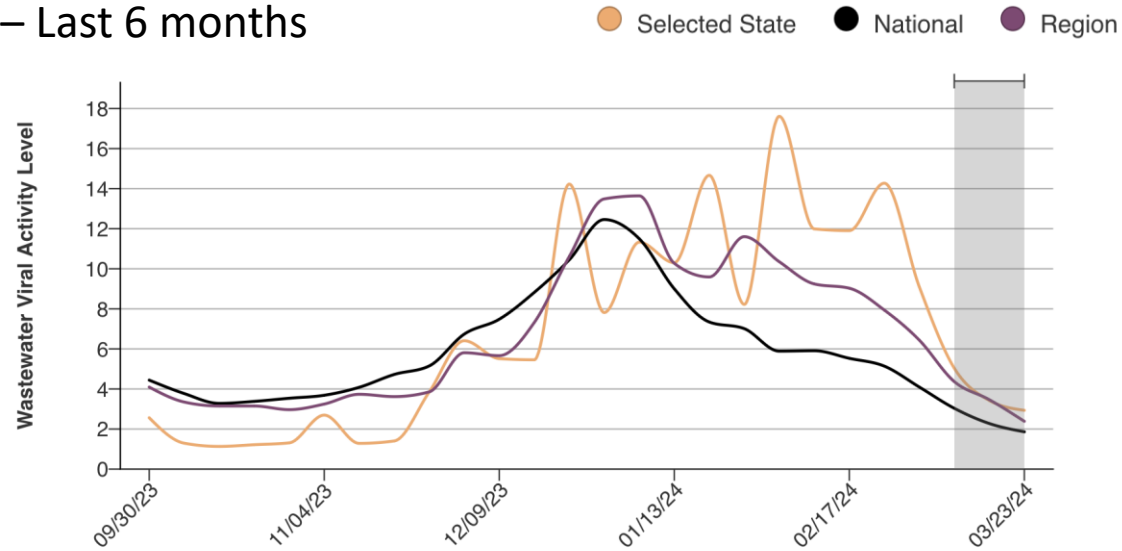
[CDC – CFA Epidemic Growth](#)

# Wastewater Monitoring – NWSS

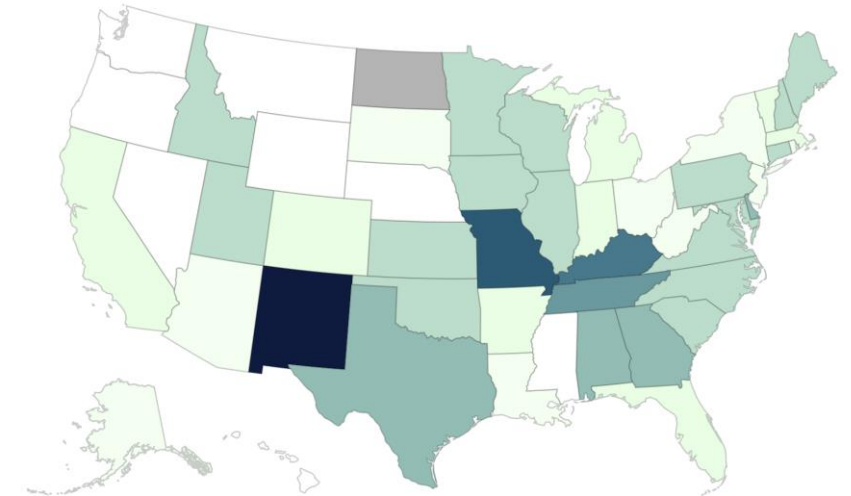
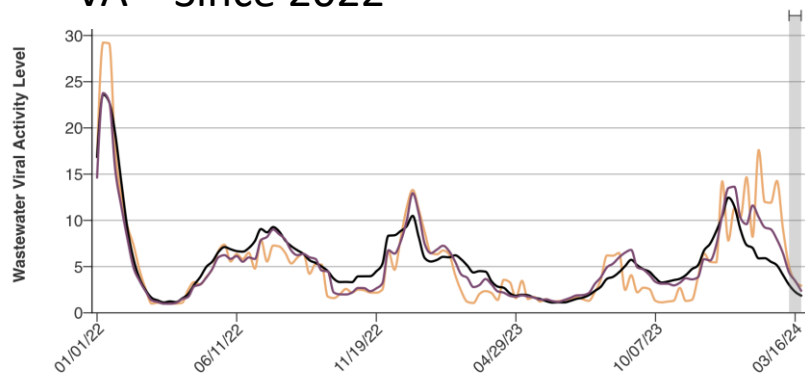
## Wastewater provides a coarse estimate of COVID-19 levels in communities

- VA down to “Low” after being “Moderate” last month
- Pervious, well observed, levels below region and national levels

VA – Last 6 months



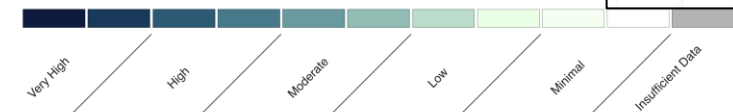
VA – Since 2022



Territories  GU  PR  VI

Current SARS-CoV-2 Wastewater Viral Activity Level

Select a level to add or remove it from the visualization.



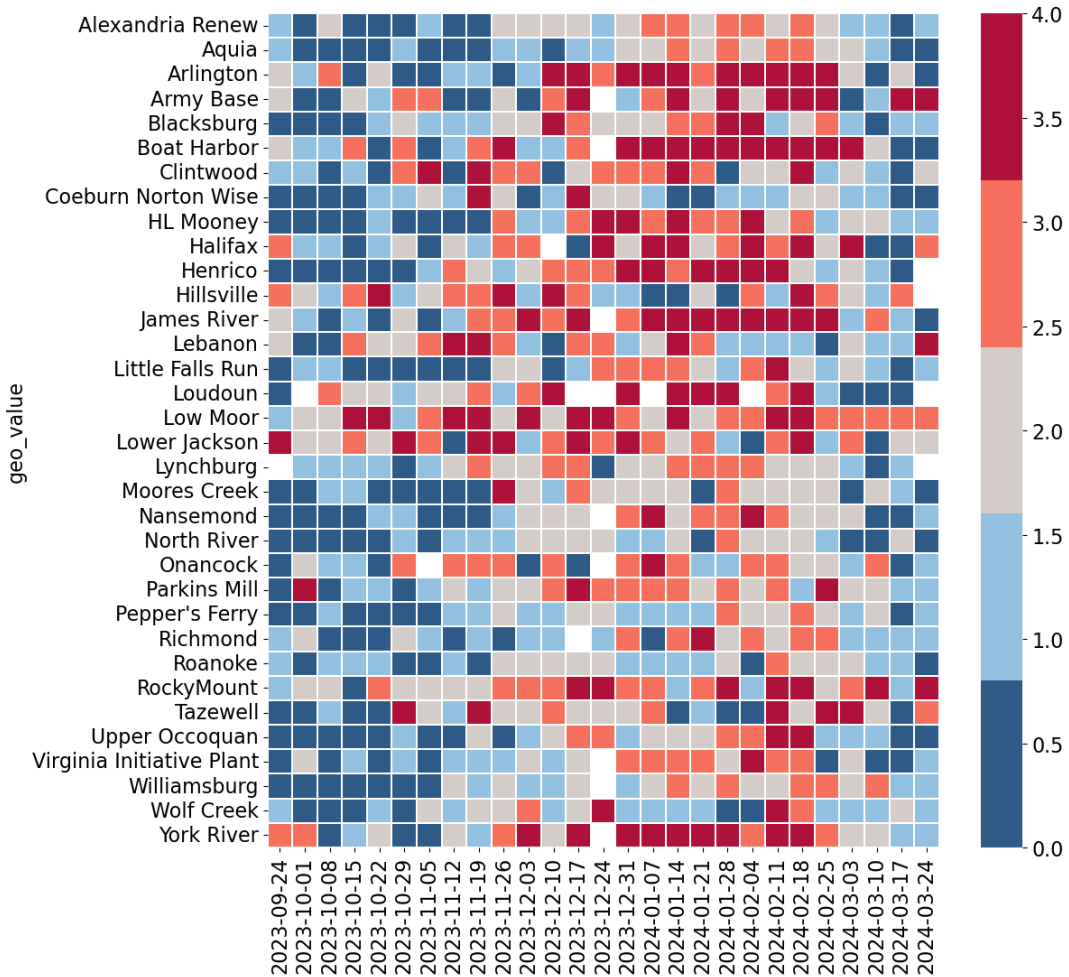
State/Territory: Virginia

Viral Activity Level: Low

Sites Currently Reporting: 18

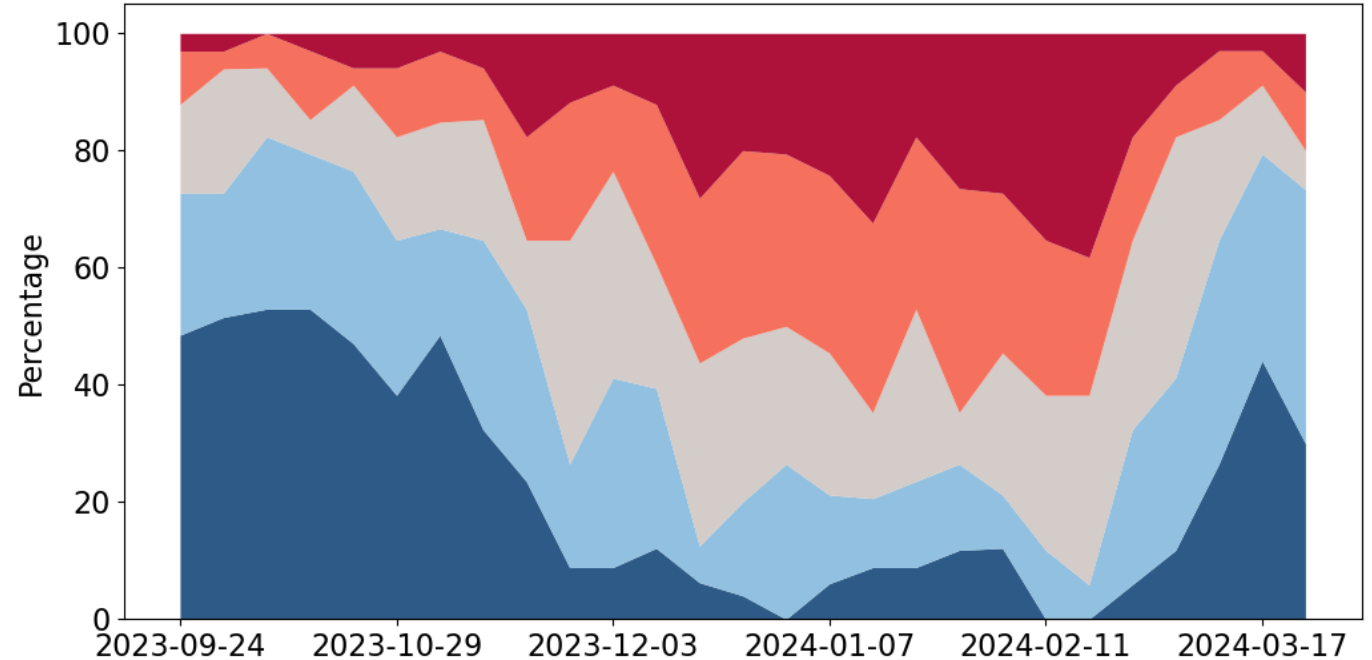
# Wastewater Monitoring – VA Sites

Wastewater provides COVID-19 levels in communities which correlate to disease burden



Last data point: **March 24<sup>th</sup>**

Viral Load Quintiles Over Time



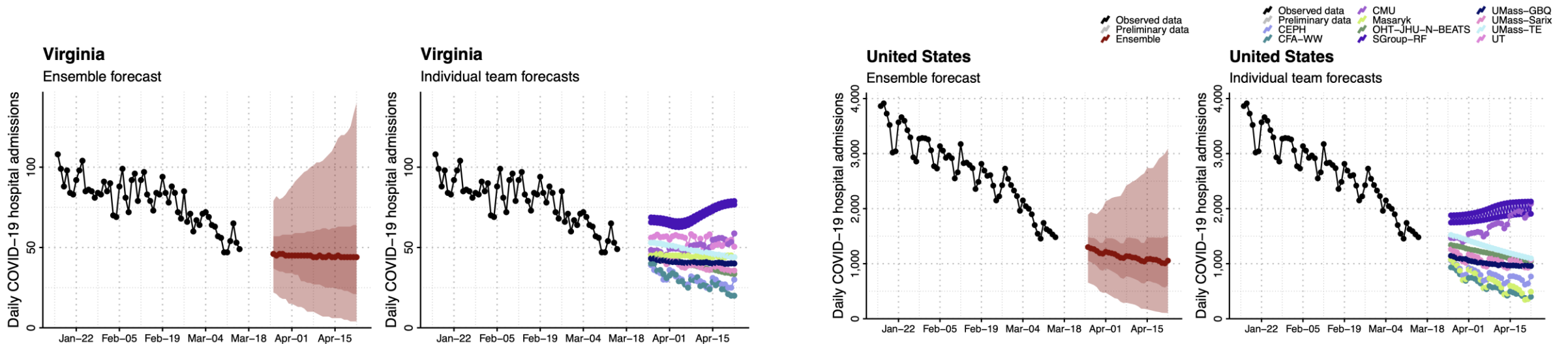
**Quintile proportions over time**  
Middle and higher are growing in past couple weeks

# Current COVID-19 Hospitalization Forecast

## Statistical models for submitting to CDC COVID Forecasting Hub

- Uses a variety of statistical and ML approaches to forecast weekly hospital admissions for the next 4 weeks for all states in the US

### Hospital Admissions for COVID-19 and Forecast for next 4 weeks (CDC COVID Ensemble) From March 25<sup>th</sup>



# COVID-19 Spatial Epidemiology

---

# ZIP Code Level Case Rates Since Last Meeting

## New cases per 100k in the last four weeks

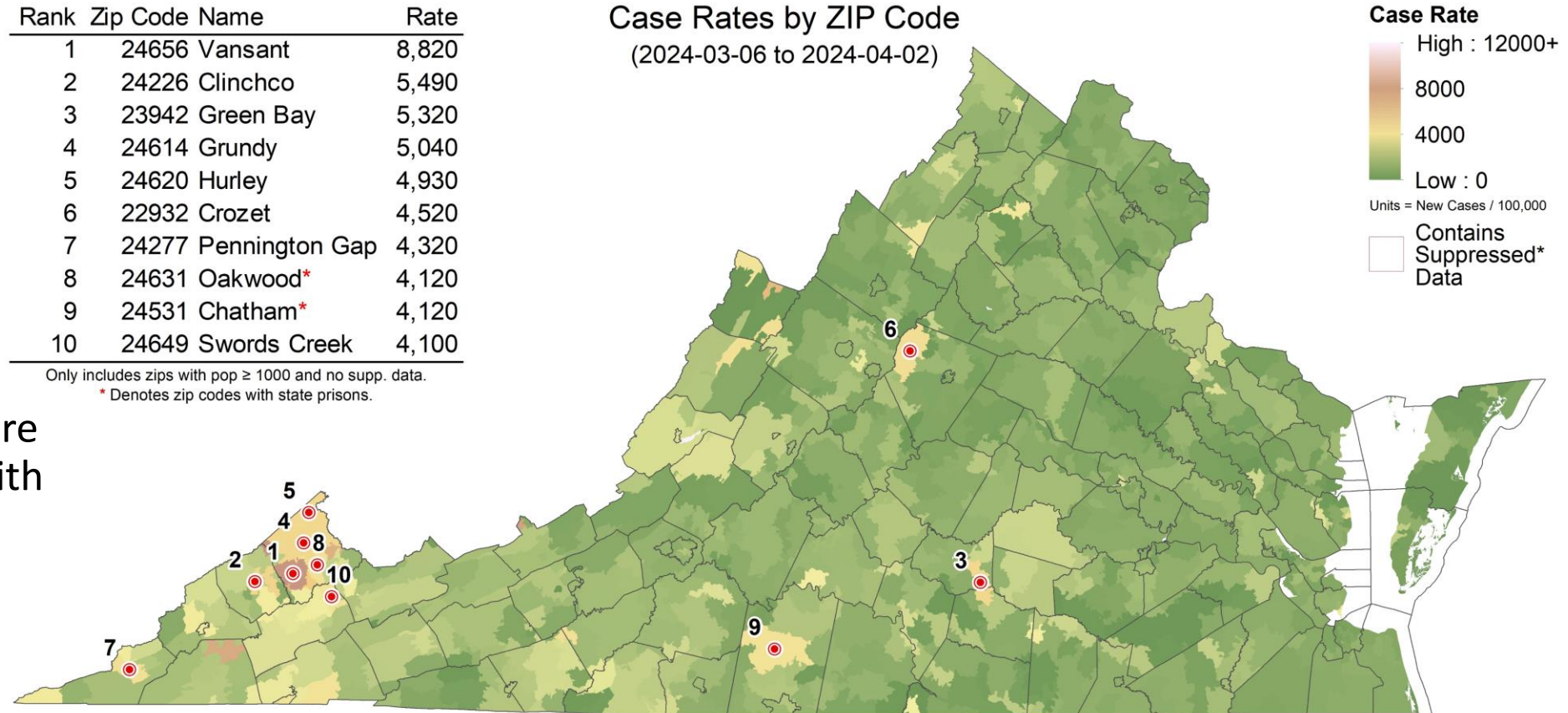
- Divide rates by **four** to calculate average weekly incidence.
- No change in color scale from last meeting.
- Case rates have fallen drastically across the Commonwealth.
- Oakwood and Chatham are the only two ZIP codes with prisons in this month's top 10.
- Most ZIP codes with elevated rates are in the Cumberland Plateau.

Rank	Zip Code	Name	Rate
1	24656	Vansant	8,820
2	24226	Clinchco	5,490
3	23942	Green Bay	5,320
4	24614	Grundy	5,040
5	24620	Hurley	4,930
6	22932	Crozet	4,520
7	24277	Pennington Gap	4,320
8	24631	Oakwood*	4,120
9	24531	Chatham*	4,120
10	24649	Swords Creek	4,100

Only includes zips with pop ≥ 1000 and no supp. data.

\* Denotes zip codes with state prisons.

Case Rates by ZIP Code  
(2024-03-06 to 2024-04-02)



Based on Spatial Empirical Bayes smoothed case rates, with an 8:1 ascertainment ratio, for four weeks ending 2024-04-02.

# Risk of Exposure / Spatial Clusters and Hot Spots

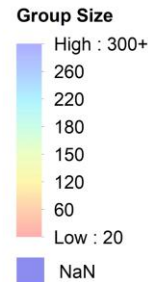
Case rates since last meeting by ZIP code used to calculate risk of encountering someone infected in a gathering of randomly selected people and find spatial hot spots

- **Group Size:** Assumes **8 undetected infections** per confirmed case (ascertainment rate from recent seroprevalence survey) and shows minimum size of a group with a 50% chance an individual is infected by ZIP code (e.g., in a group of 30 in Vansant, there is a 50% chance someone will be infected).
- **Spatial Clustering:** Getis-Ord  $G_i^*$  based hot spots compare clusters of ZIP codes with **four-week** case rates higher than nearby ZIP codes to identify larger areas with statistically significant deviations. SaTScan was used to corroborate this analysis and determine relative risk for identified clusters.

Rank	Zip Code	Name	Size
1	24656	Vansant	30
2	24226	Clinchco	49
3	23942	Green Bay	51
4	24614	Grundy	54
5	24620	Hurley	55
6	22932	Crozet	60
7	24277	Pennington Gap	63
8	24631	Oakwood*	66
9	24531	Chatham*	66
10	24649	Swords Creek	66

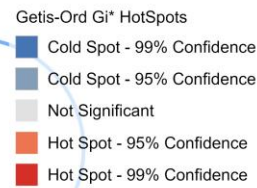
Only includes zips with pop ≥ 1000 and no supp. data.  
\* Denotes zip codes with state prisons.

Group Size Needed for 50% Likelihood of ≥1 Infected

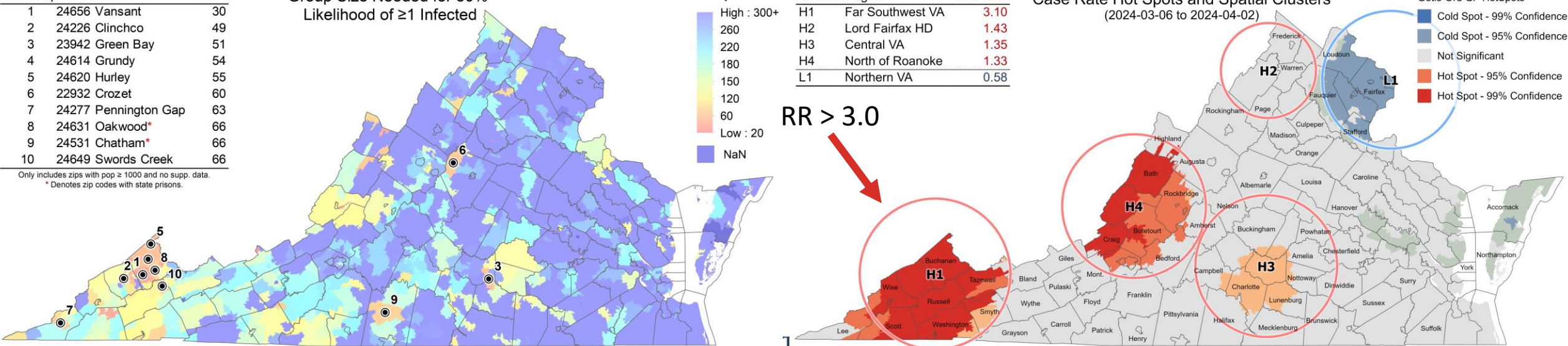


Cluster	Region	Rel. Risk
H1	Far Southwest VA	3.10
H2	Lord Fairfax HD	1.43
H3	Central VA	1.35
H4	North of Roanoke	1.33
L1	Northern VA	0.58

Case Rate Hot Spots and Spatial Clusters (2024-03-06 to 2024-04-02)



RR > 3.0



Based on Spatial Empirical Bayes smoothed point prevalence, with an 8:1 ascertainment ratio, for four weeks ending 2024-04-02.

SaTScan clusters have a minimum population of 50,000 and 10 locations, a RR ≥1.3 or RR ≤ 0.7, and a max radius of 75 km. Optimized Hot Spots based on Global Empirical Bayes smoothed point prevalence for the four weeks ending 2024-04-02.

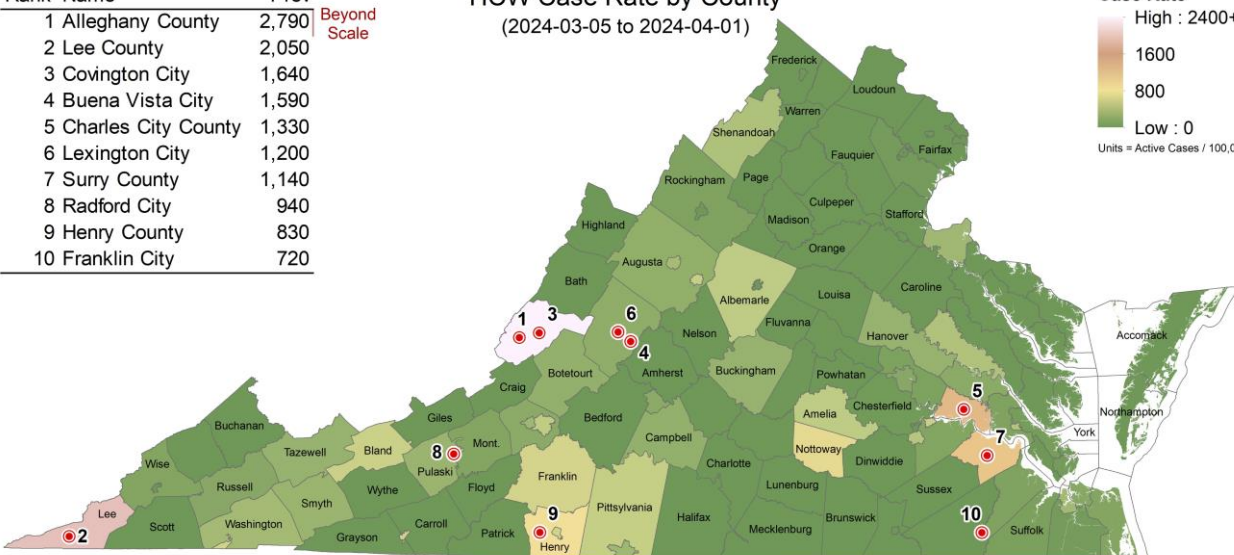
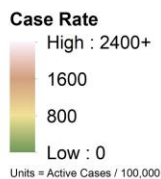
# COVID-19 among Healthcare Workers

**COVID-19 case rates for the public and for healthcare workers (HCW) were compared to find regions where HCW suffered unusually high burdens of disease**

- **HCW Rate:** Case rate among health care workers (HCW) over a four-week period ending April 1, 2024.
- **HCW Ratio:** Case rate among health care workers (HCW) over the same period using patient facing healthcare workers as the numerator, and the population's case rate as the denominator.
- The healthcare case to public case ratio is well below one in most counties. Alleghany, Charles City, Lee, and Surry counties are reporting elevated HCW case rates, and elevated HCW to public case ratios.

Rank	Name	Prev
1	Alleghany County	2,790
2	Lee County	2,050
3	Covington City	1,640
4	Buena Vista City	1,590
5	Charles City County	1,330
6	Lexington City	1,200
7	Surry County	1,140
8	Radford City	940
9	Henry County	830
10	Franklin City	720

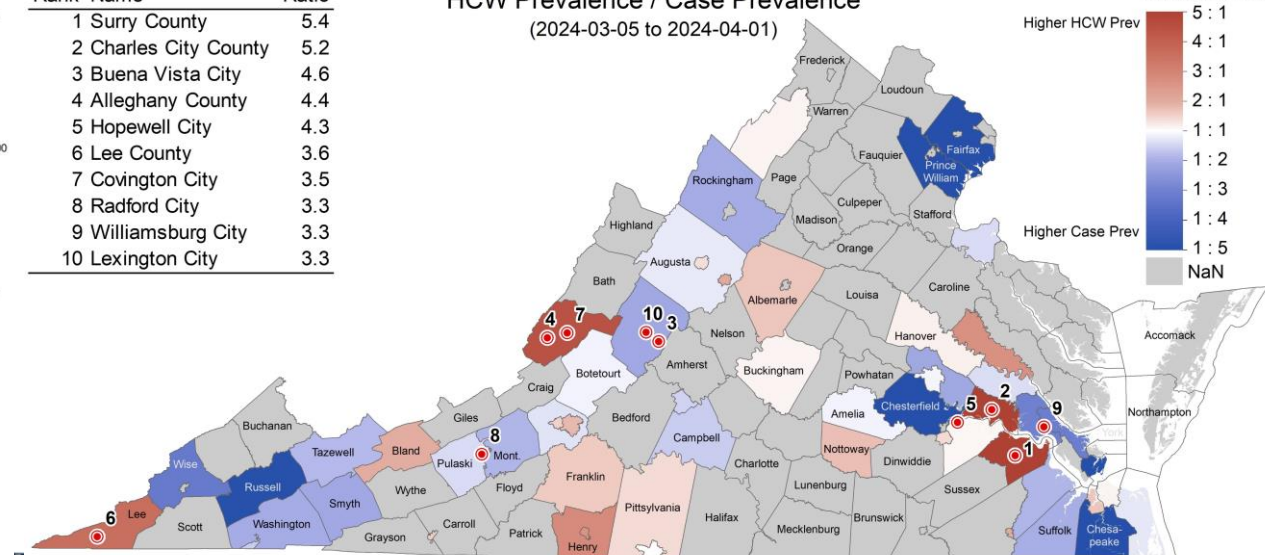
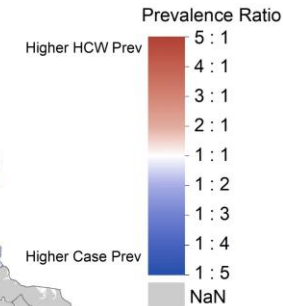
HCW Case Rate by County  
(2024-03-05 to 2024-04-01)



Note: Scale differs from general public prevalence maps.

Rank	Name	Ratio
1	Surry County	5.4
2	Charles City County	5.2
3	Buena Vista City	4.6
4	Alleghany County	4.4
5	Hopewell City	4.3
6	Lee County	3.6
7	Covington City	3.5
8	Radford City	3.3
9	Williamsburg City	3.3
10	Lexington City	3.3

HCW Prevalence / Case Prevalence  
(2024-03-05 to 2024-04-01)



Note: This assumes that the ascertainment rate of healthcare workers is double that of the public.

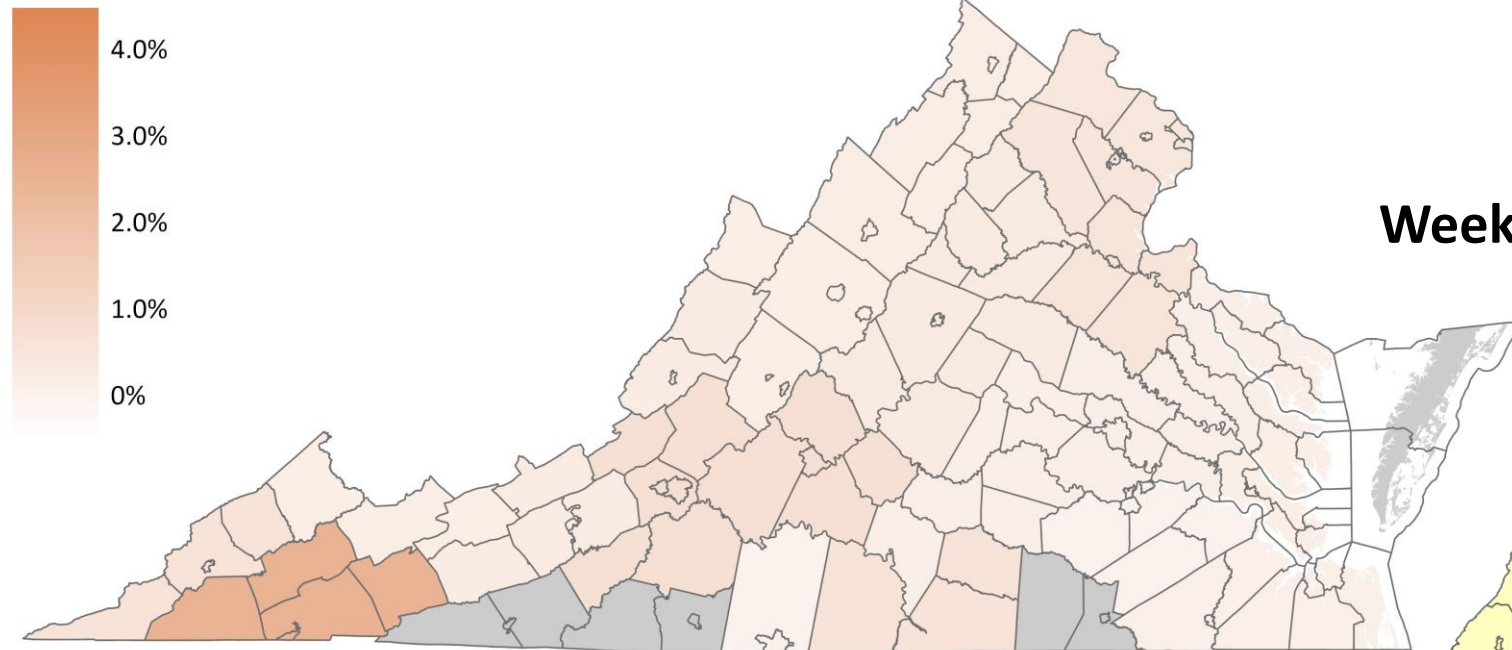


# Emergency Department Diagnosis Rate – COVID-19

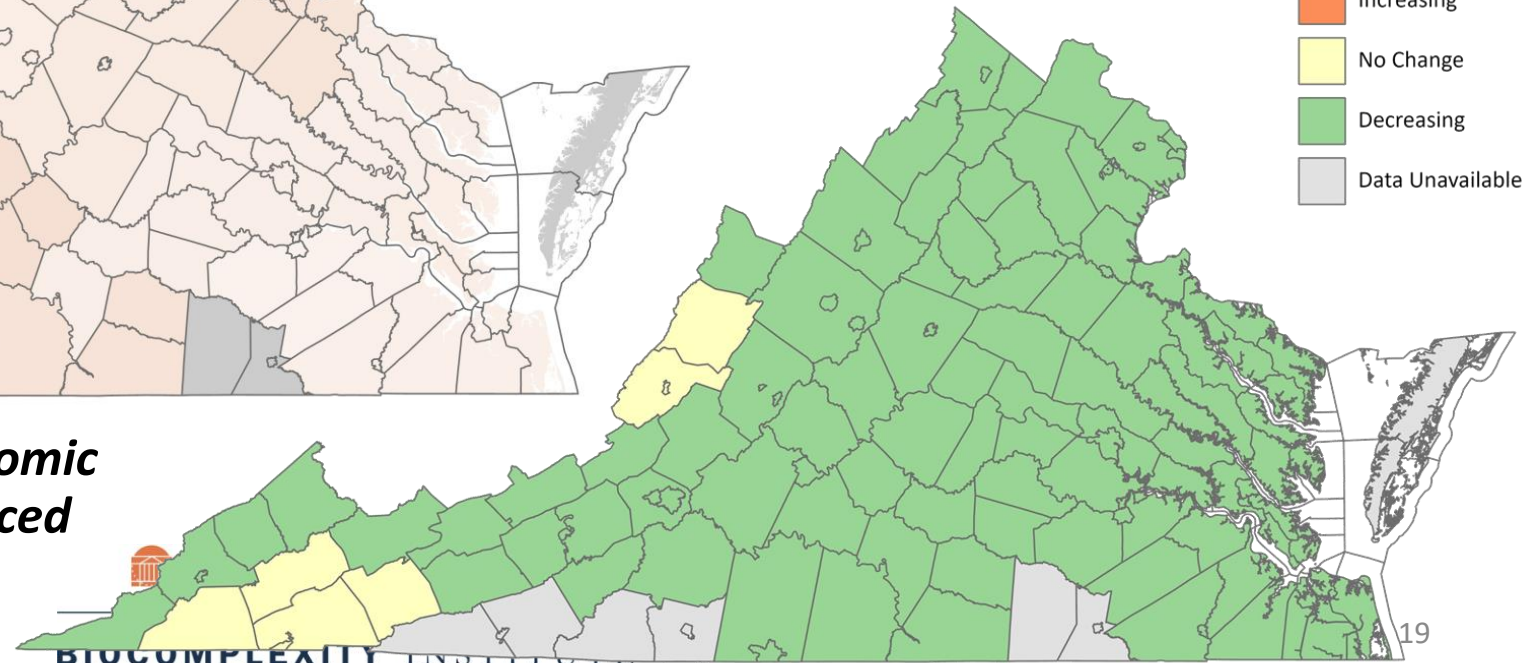
Far SW report the highest ED diagnosis rates, though no county reports higher than a 2.5%. Rates continue to fall statewide, except in the Far SW and the area around Covington.

## ED Diagnosis Rate

COVID-19 Diagnoses



## Weekly Trend of Diagnoses



*Derived from CDC National Syndromic Surveillance Program Data produced at the HSA level as of 2024-03-23.*

5-Apr-24

# COVID-19 Genomic Update

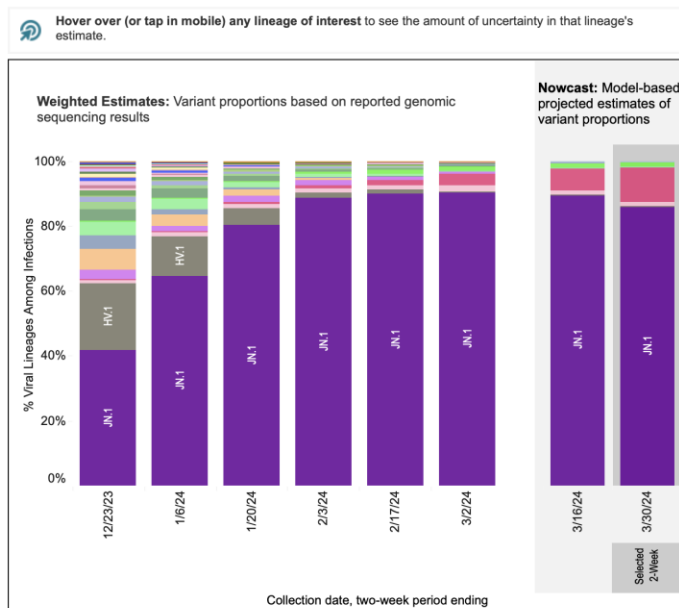
---

# SARS-CoV2 Variants of Concern

Emerging variants have potential to continue to alter the future trajectories of pandemic and have implications for future control

- Variants have been observed to: increase transmissibility, increase severity (more hospitalizations and/or deaths), and limit immunity provided by prior infection and vaccinations

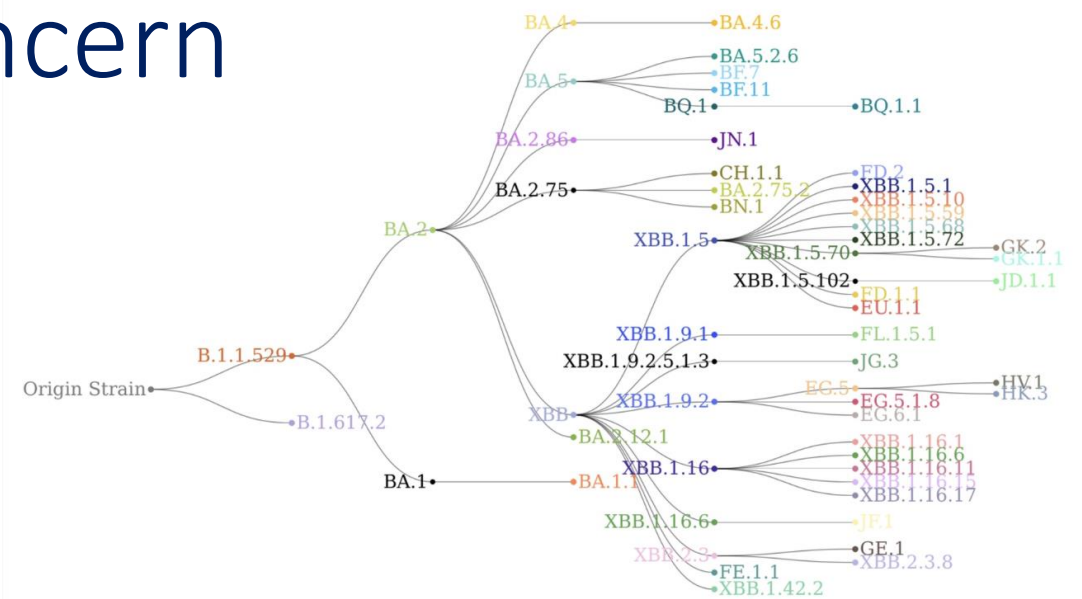
Weighted and Nowcast Estimates in United States for 2-Week Periods in 12/10/2023 – 3/30/2024



Nowcast Estimates in United States for 3/17/2024 – 3/30/2024

USA			
WHO label	Lineage #	%Total	95%PI
Omicron	JN.1	86.0%	80.3-90.3%
	JN.1.13	10.8%	6.6-16.8%
	JN.1.18	1.6%	1.0-2.4%
	BA.2	0.2%	0.0-0.8%
	BA.2.86	0.1%	0.1-0.2%
	HV.1	0.0%	0.0-0.1%
	GE.1	0.0%	0.0-0.1%
	JG.3	0.0%	0.0-0.0%
	JD.1.1	0.0%	0.0-0.0%
	B.1.1.529	0.0%	0.0-0.5%
	XBB	0.0%	0.0-0.0%
	HK.3	0.0%	0.0-0.0%
	EG.5	0.0%	0.0-0.0%
	XBB.1.16.15	0.0%	0.0-0.0%
	JF.1	0.0%	0.0-0.0%
	XBB.1.9.1	0.0%	0.0-0.0%
	XBB.2.3	0.0%	0.0-0.0%
	EG.5.1.8	0.0%	0.0-0.0%
	FL.1.5.1	0.0%	0.0-0.0%
	XBB.1.16.6	0.0%	0.0-0.0%
	XBB.1.16.11	0.0%	0.0-0.0%
	XBB.1.16	0.0%	0.0-0.0%
	GK.1.1	0.0%	0.0-0.0%
	HF.1	0.0%	0.0-0.0%
	GK.2	0.0%	0.0-0.0%
Other	Other*	1.2%	0.7-2.2%

\* Enumerated lineages are US VOC and lineages circulating above 1% nationally in at least one 2-week period. "Other" represents the aggregation of lineages which are circulating <1% nationally during all 2-week periods displayed.  
 \*\* These data include Nowcast estimates, which are modeled projections that may differ from weighted estimates generated at later dates.  
 # While all lineages are tracked by CDC, those named lineages not enumerated in this graphic are aggregated with their parent lineages, based on Pango lineage definitions, described in more detail here: <https://www.pango.network/the-pango-nomenclature-system/statement-of-nomenclature-rules/>.



## Omicron Updates\*

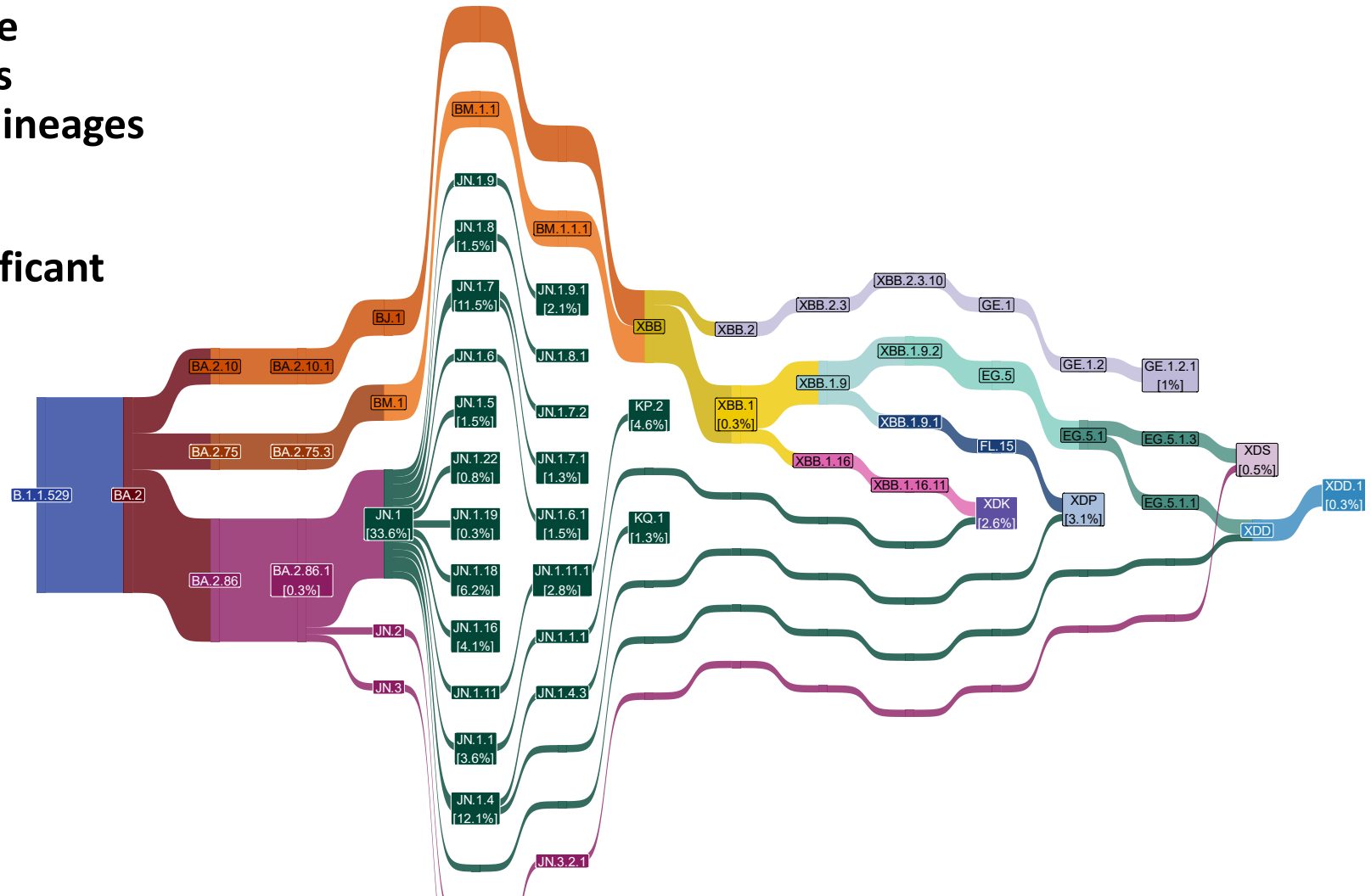
- JN.1 and descendants completely saturate
- JN.1.13 now at 11%

\*percentages are CDC NowCast Estimates

# SARS-CoV2 Variants of Concern

A variety of co-circulating variants have emerged with multiple recombinations between JN.1 lineages and other XBB lineages

JN.1.18 and JN.1.7 have the most significant weekly growth rate in the UK



Data shown as of March 27<sup>th</sup>, 2024.  
 Proportions are given for lineages that are observed in sequences with a specimen date between 11 March 2024 and 25 March 2024.

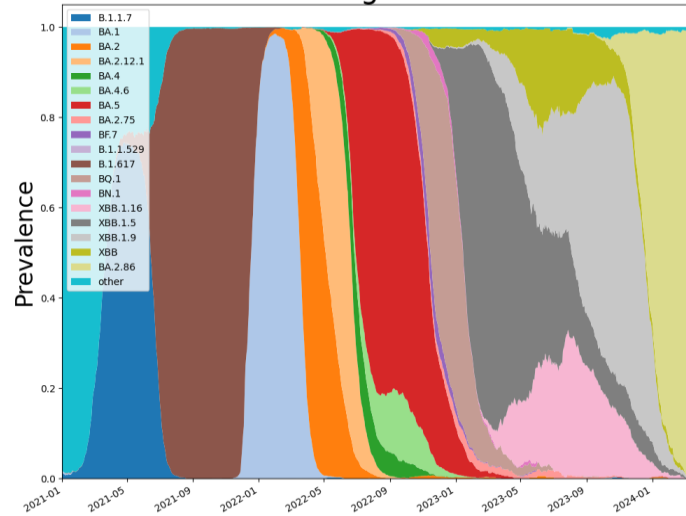
<https://www.gov.uk/government/publications/sars-cov-2-genome-sequence-prevalence-and-growth-rate/sars-cov-2-genome-sequence-prevalence-and-growth-rate-update-27-march-2024>

# SARS-CoV2 Omicron Sub-Variants

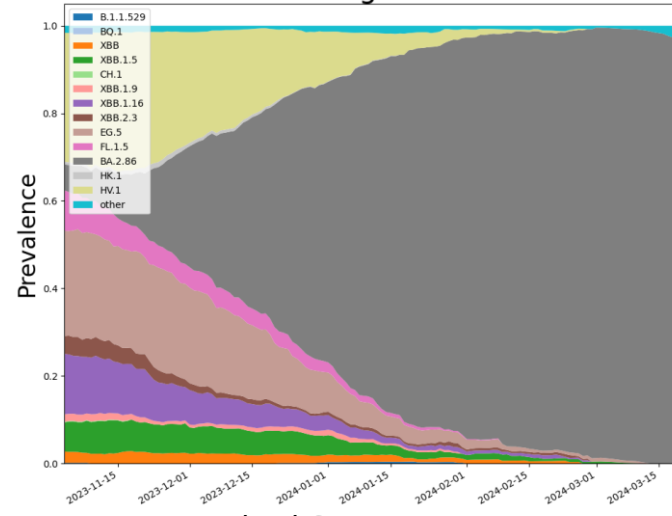
As detected in whole Genomes in public repositories

VoC Polynomial Fit Projections

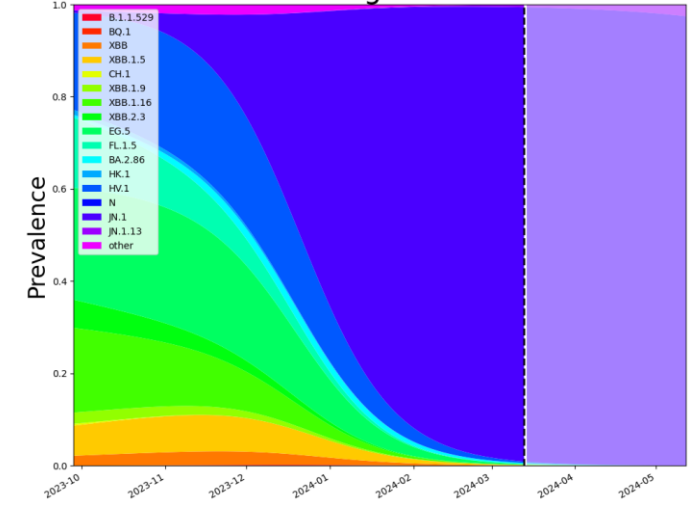
Virginia



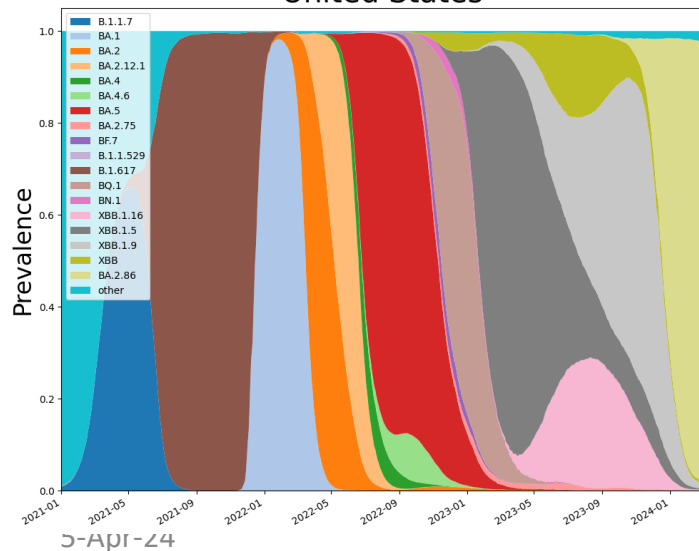
Virginia



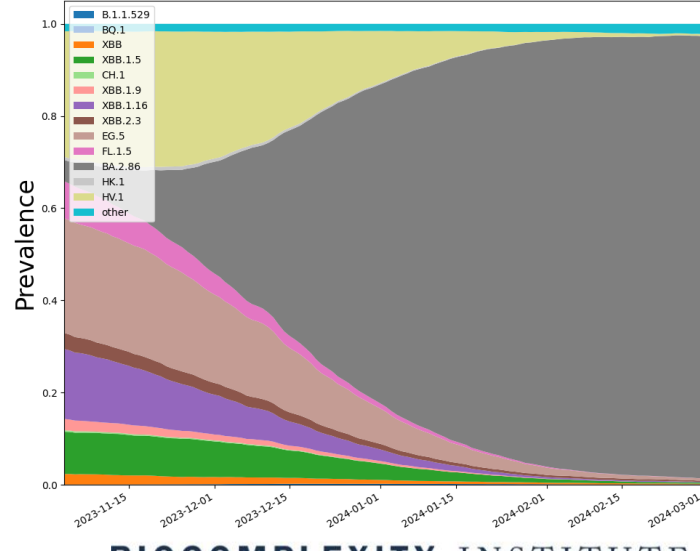
Virginia



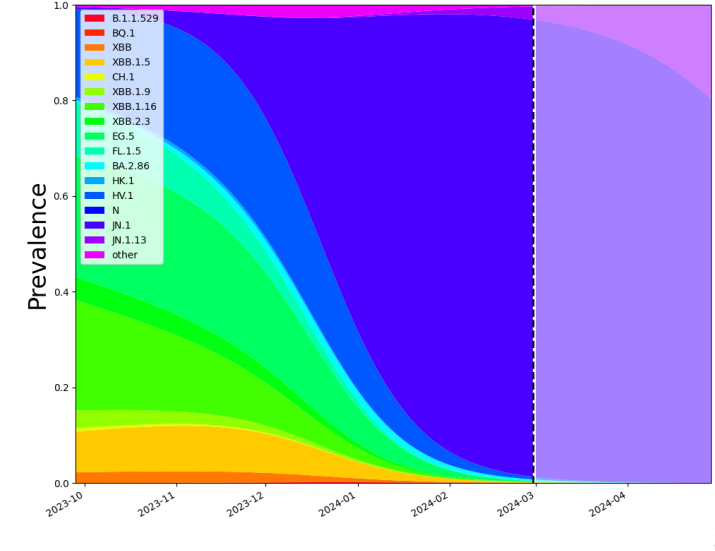
United States



United States



United States

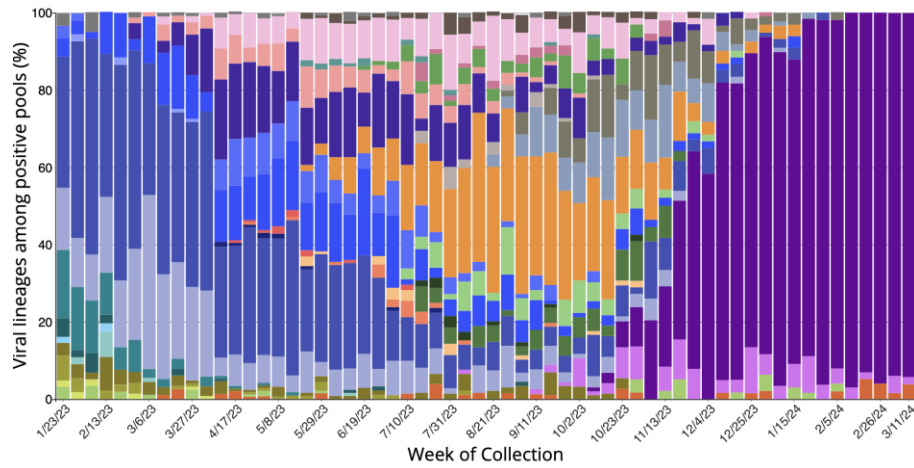


Note:  
Everything  
from dotted  
line forward is  
a projection.

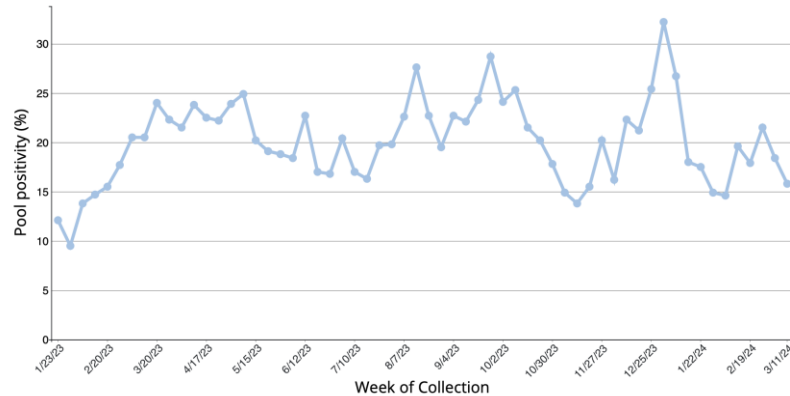
# Global SARS-CoV-2 Variant Status

## Traveller Surveillance

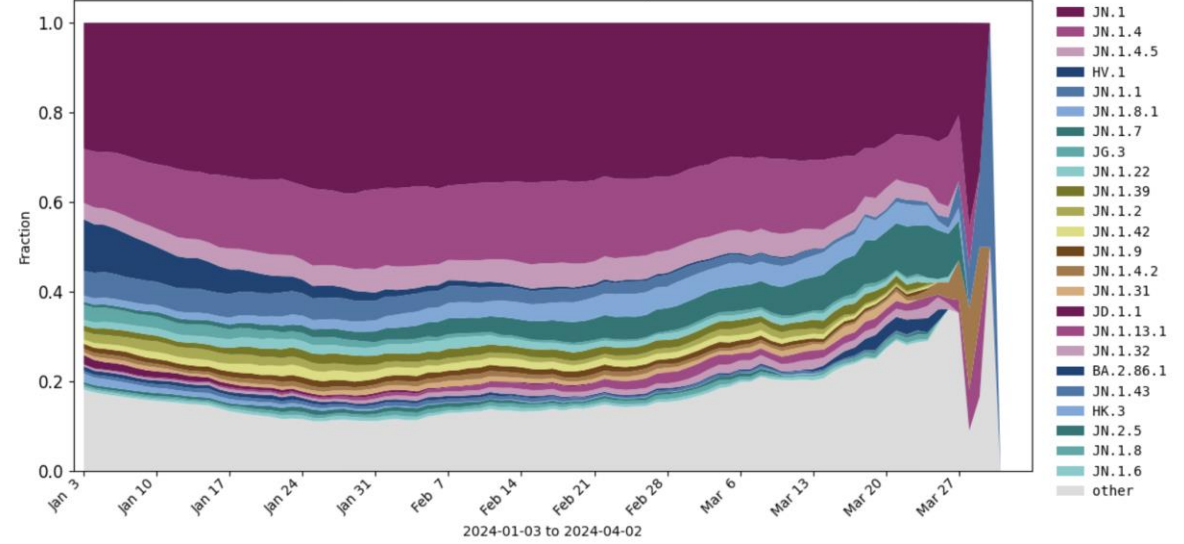
Variants Detected, by Collection Week



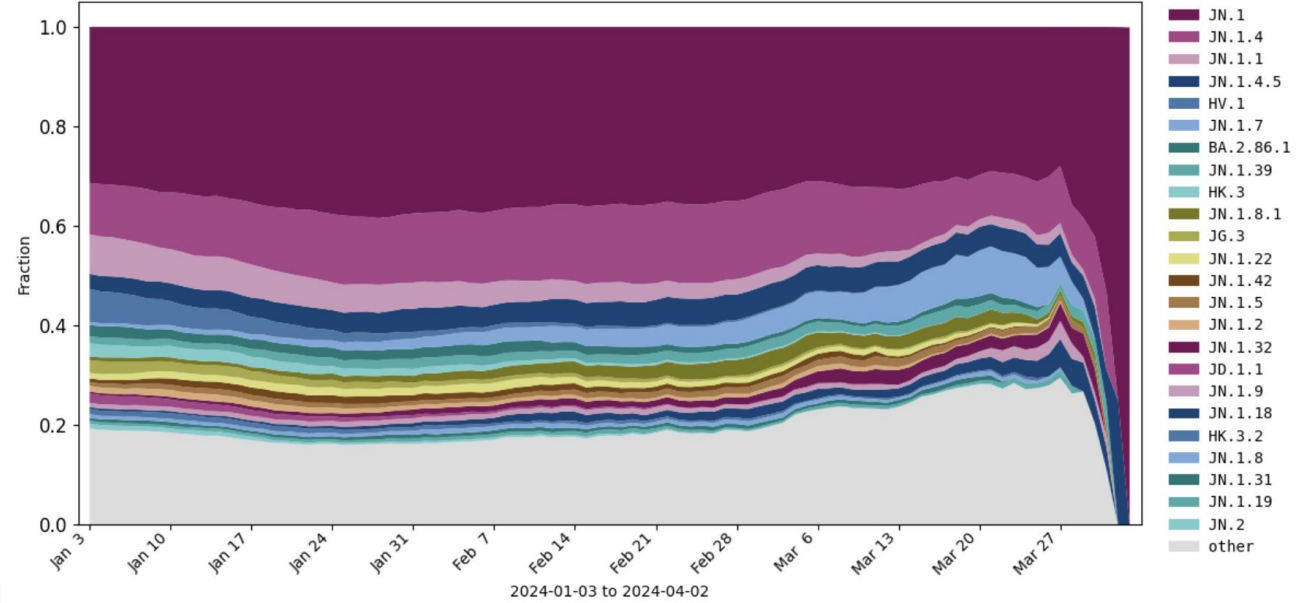
Positivity Rate for Pooled Samples, by Collection Week



North-America: 69096 sequences

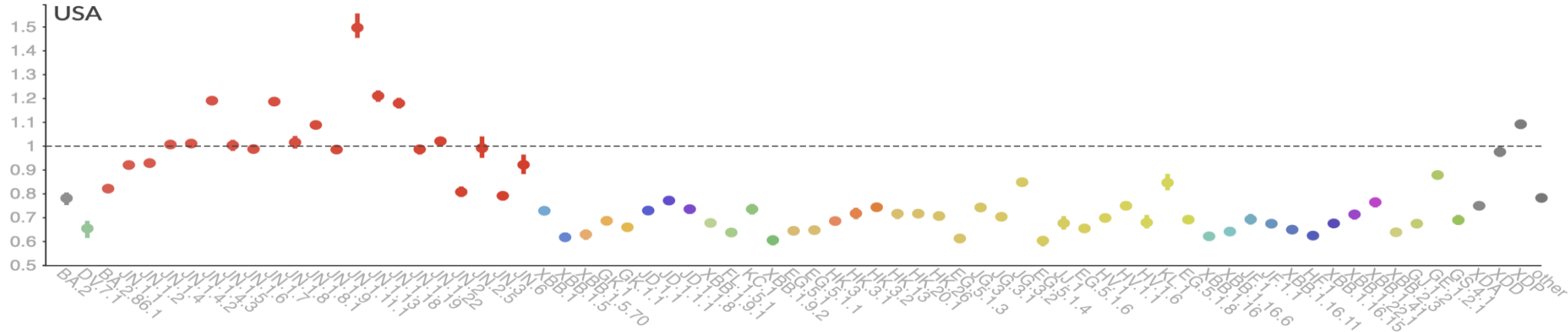


Global: 132958 sequences



# Global SARS-CoV2 Variant Status

<https://nextstrain.org/sars-cov-2/forecasts/>

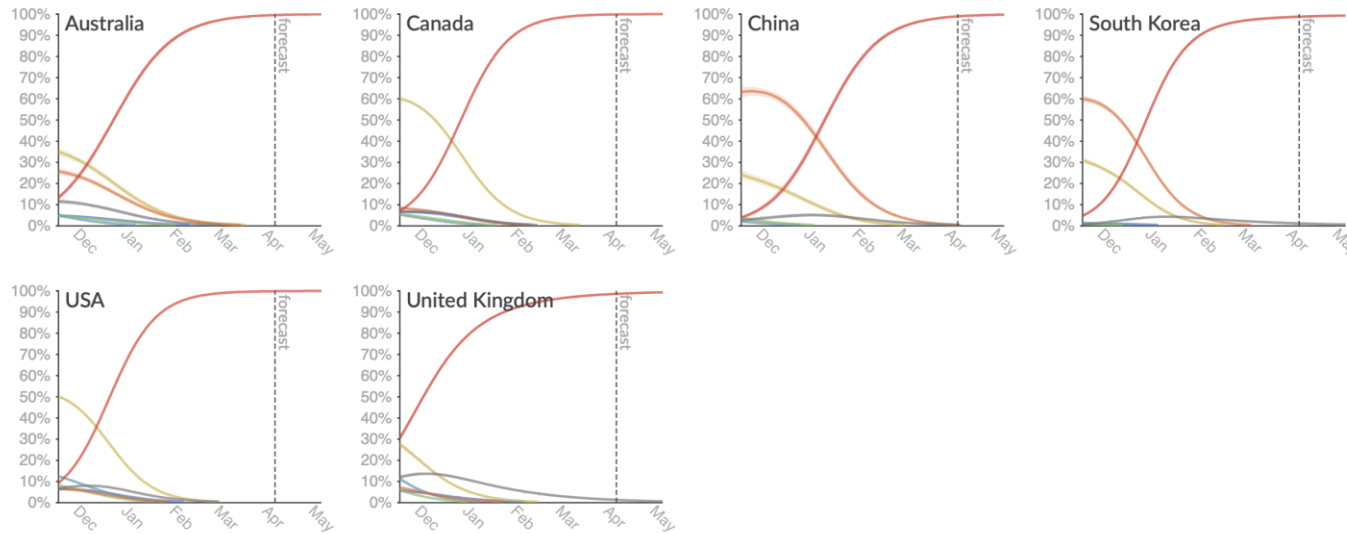


## Clade frequencies over time

Each line represents the estimated frequency of a particular clade through time. Equivalent Pango lineage is given in parenthesis, eg clade 23A (lineage XBB.1.5). Only locations with more than 100 sequences from samples collected in the previous 150 days are included. Results last updated 2024-04-04.

Logit transform  Daily raw data  Weekly raw data

● 23A (XBB.1.5) ● 23B (XBB.1.16) ● 23D (XBB.1.9) ● 23F (EG.5.1) ● 23H (HK.3) ● other ● 23I (BA.2.86)



## Lineage growth advantage

These plots show the estimated growth advantage for given Pango lineages relative to lineage JN.1. This describes how many more secondary infections a variant causes on average relative to lineage JN.1. Vertical bars show the 95% HPD. The "hierarchical" panel shows pooled estimate of growth rates across different locations. Results last updated 2024-03-05.

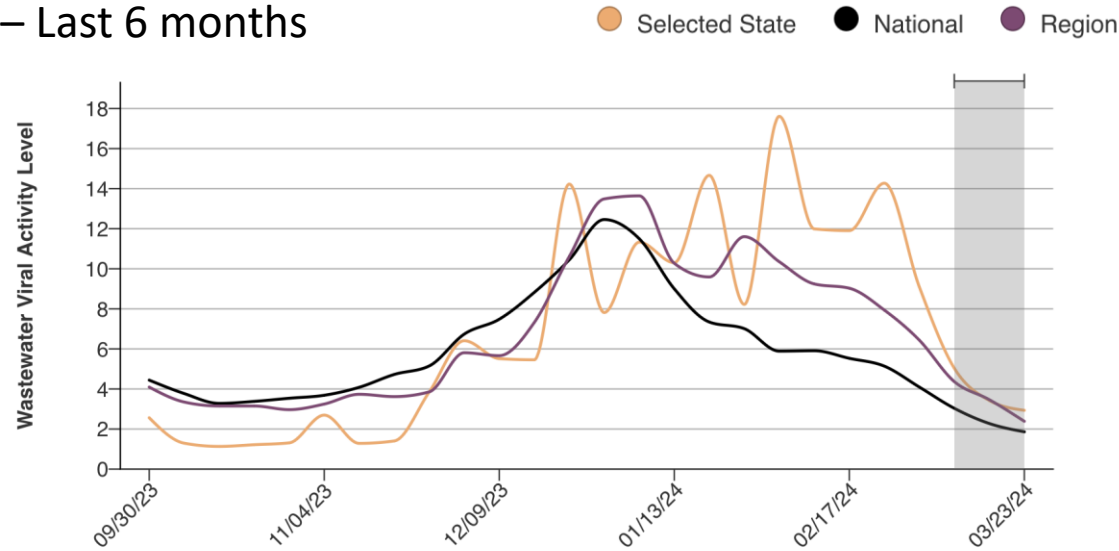
- BA.2 ● DV.7.1 ● BA.2.86.1 ● JN.1.1 ● JN.1.2 ● JN.1.4 ● JN.1.4.2 ● JN.1.4.3 ● JN.1.5 ● JN.1.6
- JN.1.7 ● JN.1.8 ● JN.1.8.1 ● JN.1.9 ● JN.1.11.1 ● JN.1.13 ● JN.1.18 ● JN.1.19 ● JN.1.22 ● JN.2
- JN.2.5 ● JN.3 ● JN.6 ● XBB.1 ● XBB.1.5 ● XBB.1.5.70 ● GK.1 ● GK.1.1 ● JD.1.1 ● JD.1.1.1
- JD.1.1.8 ● XBB.1.9.1 ● FL.1.5.1 ● KC.1 ● XBB.1.9.2 ● EG.5.1 ● EG.5.1.1 ● HK.3 ● HK.3.1 ● HK.3.2
- HK.13 ● HK.20.1 ● HK.26 ● EG.5.1.3 ● JG.3 ● JG.3.1 ● JG.3.2 ● EG.5.1.4 ● JJ.1 ● EG.5.1.6
- HV.1 ● HV.1.1 ● HV.1.6 ● KL.1 ● EG.5.1.8 ● XBB.1.16 ● XBB.1.16.6 ● JF.1 ● JF.1.1 ● XBB.1.16.11
- HF.1 ● XBB.1.16.15 ● XBB.1.22.1 ● XBB.1.41 ● XBB.2.3 ● GJ.1.2 ● GE.1.2.1 ● GS.4.1 ● XDA
- XDD ● XDP ● other ● JN.1

# Wastewater Monitoring – NWSS

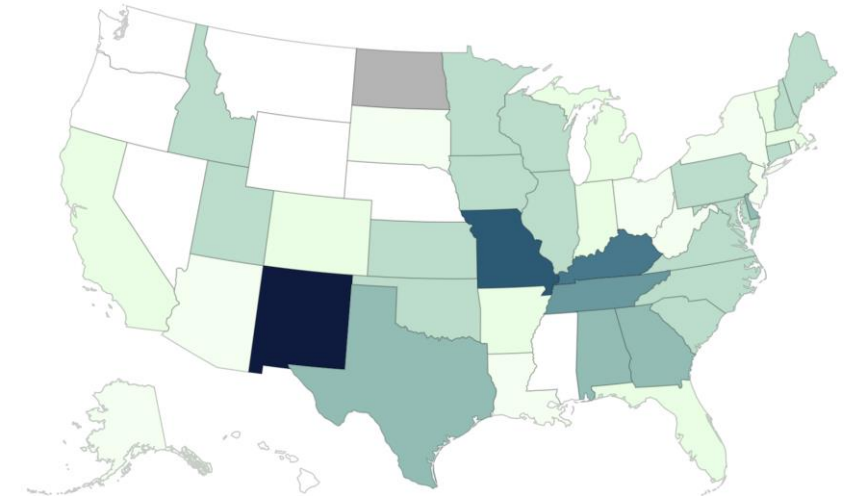
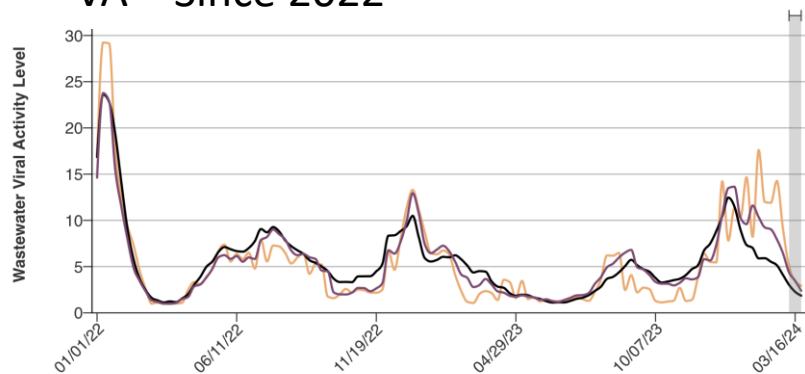
**Wastewater provides a coarse estimate of COVID-19 levels in communities**

- VA down to “Low” after being “Moderate” last month
- Pervious, well observed, levels below region and national levels

VA – Last 6 months



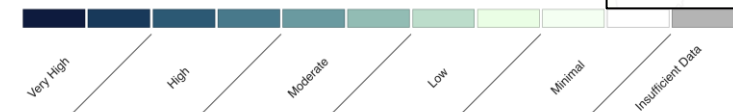
VA – Since 2022



Territories  GU  PR  VI

Current SARS-CoV-2 Wastewater Viral Activity Level

Select a level to add or remove it from the visualization.



**State/Territory: Virginia**

Viral Activity Level: Low

Sites Currently Reporting: 18





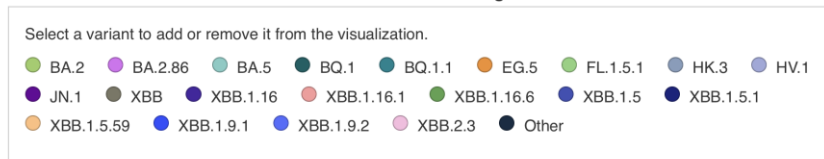
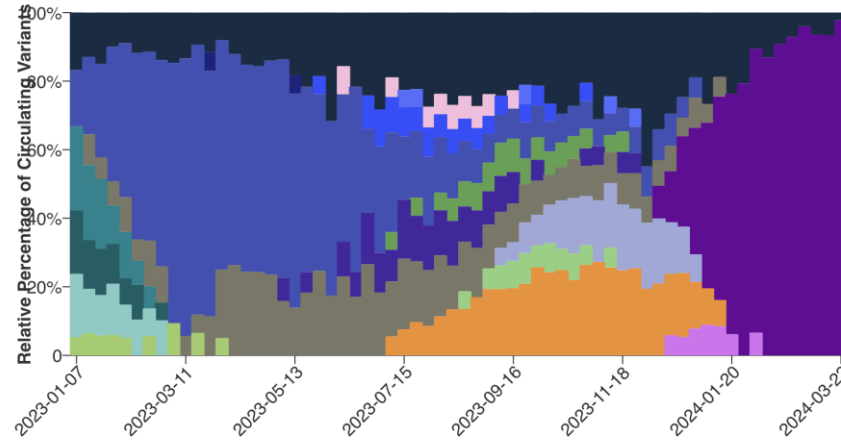
# National Wastewater Variant Status

## CDC Wastewater

The BA.2.86 variant category includes all JN.\* sublineages except JN.1 which is separated out into its own callout group.

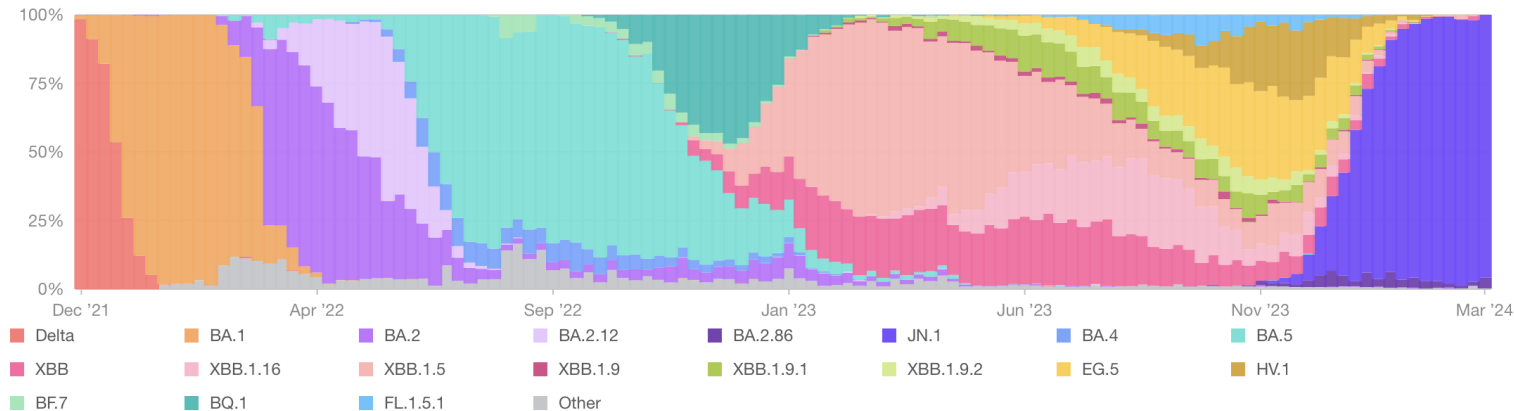
**Week Ending: 2024-03-23**

JN.1: 98%  
Other: 2%



## Biobot Wastewater

**Variants:** Percentage of variant lineage sequenced from SARS-CoV-2 genome found in wastewater



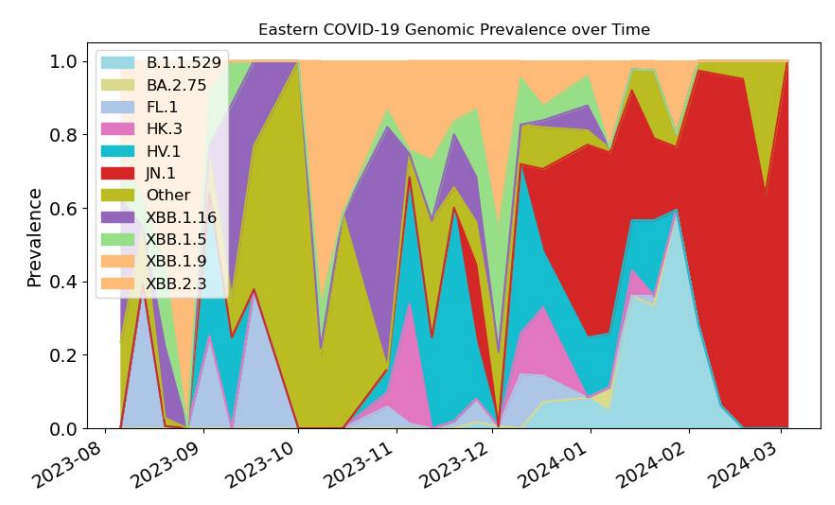
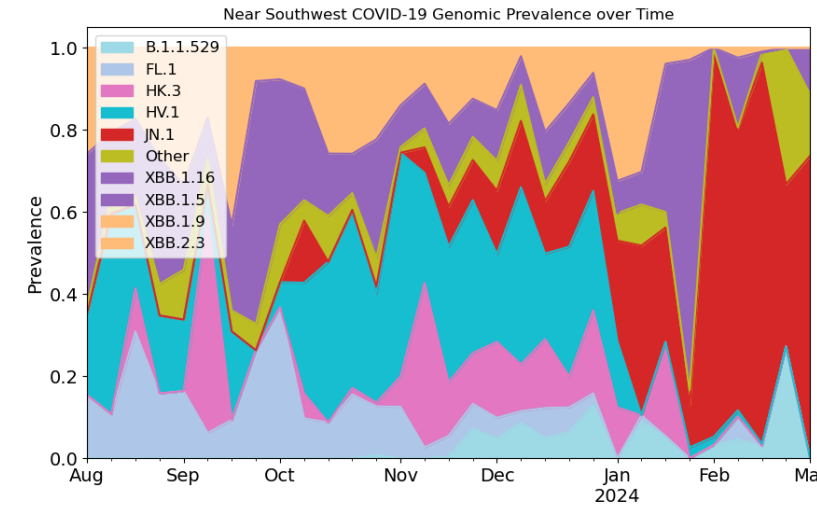
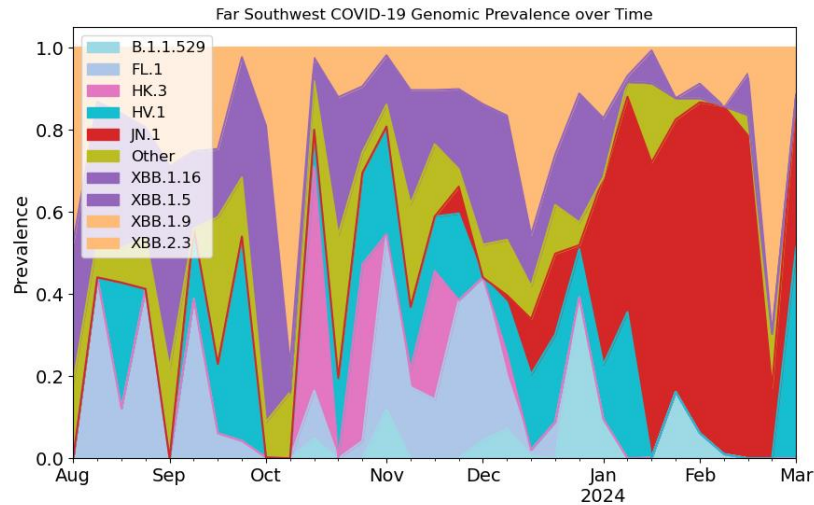
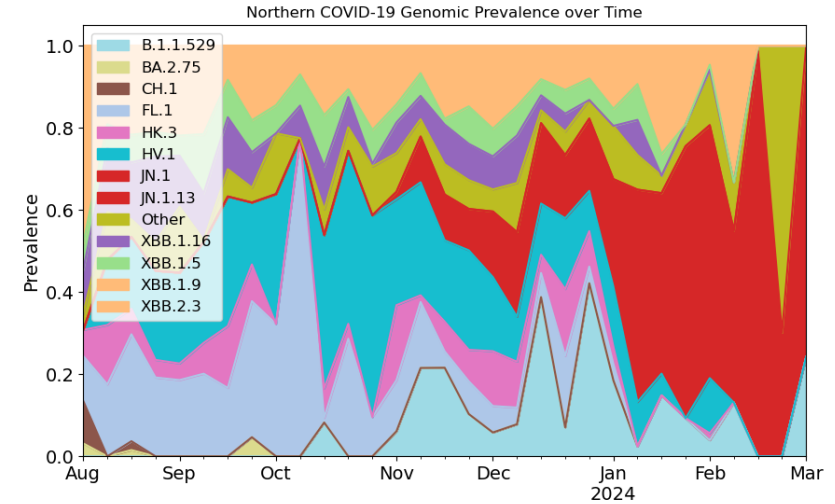
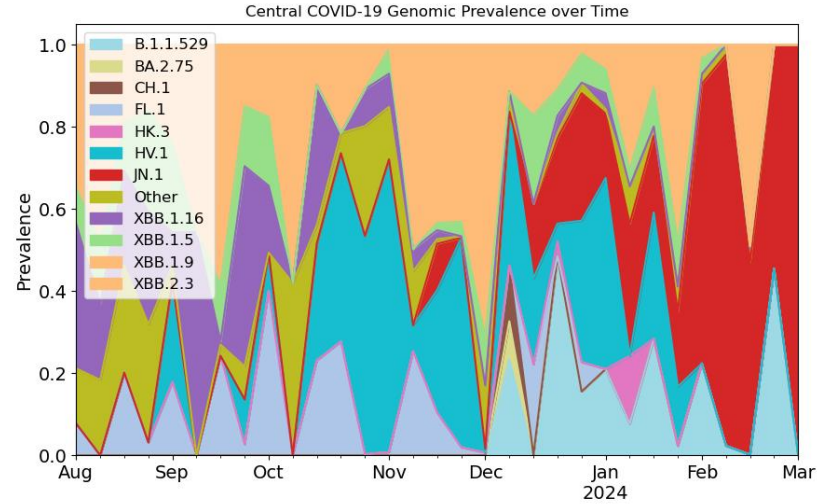
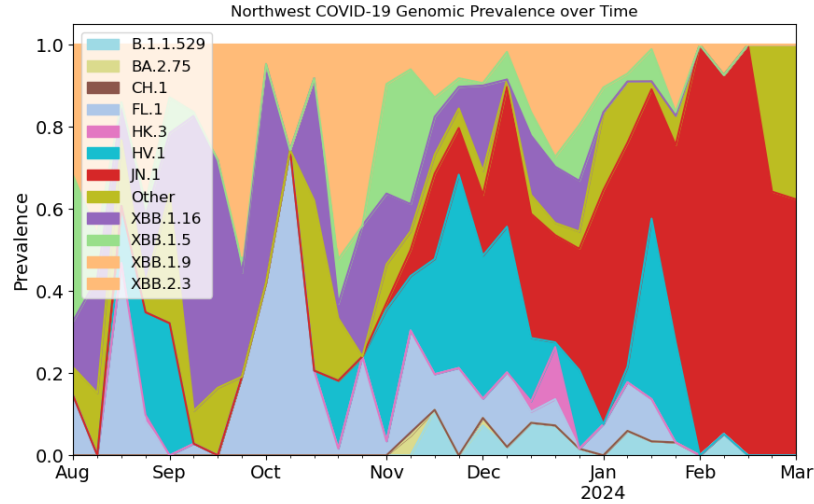
**March 13, 2024**

JN.1: **95.8%**

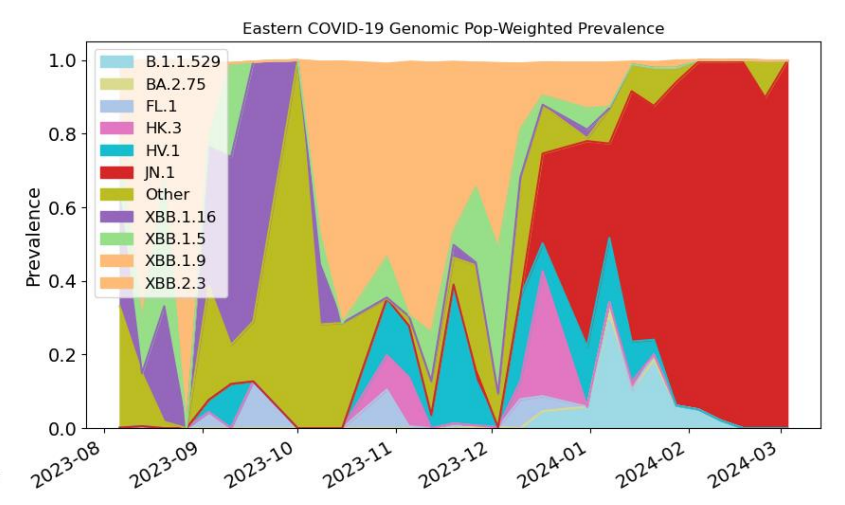
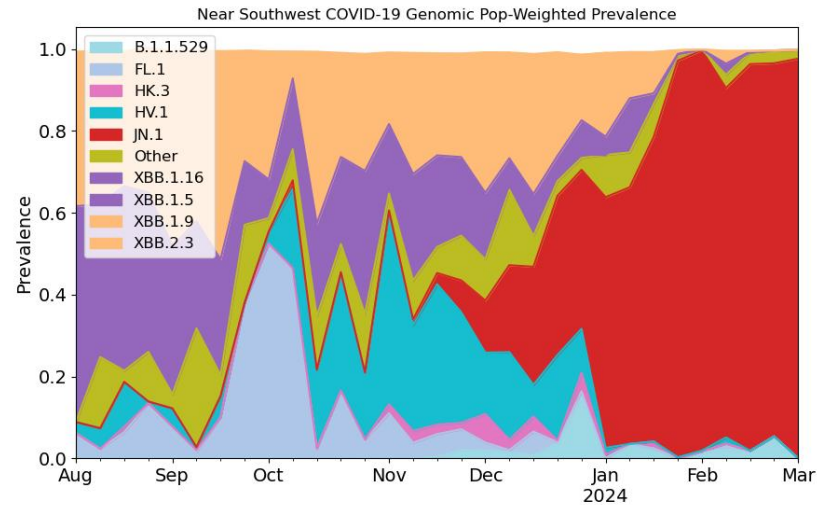
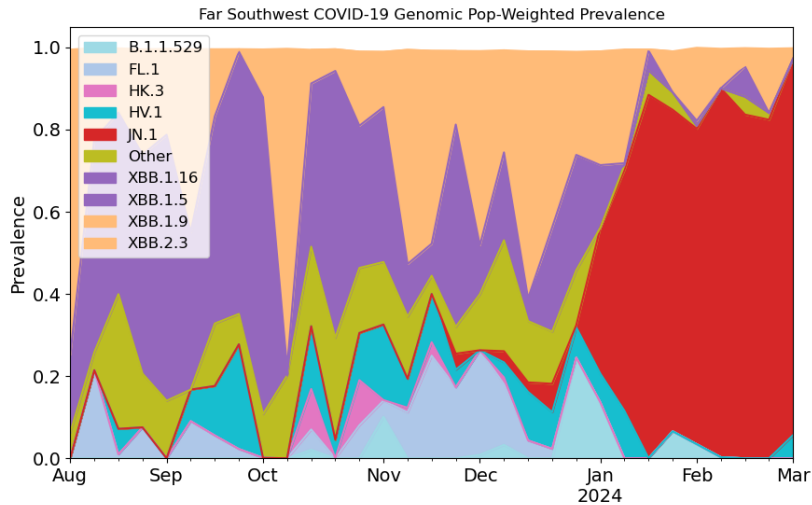
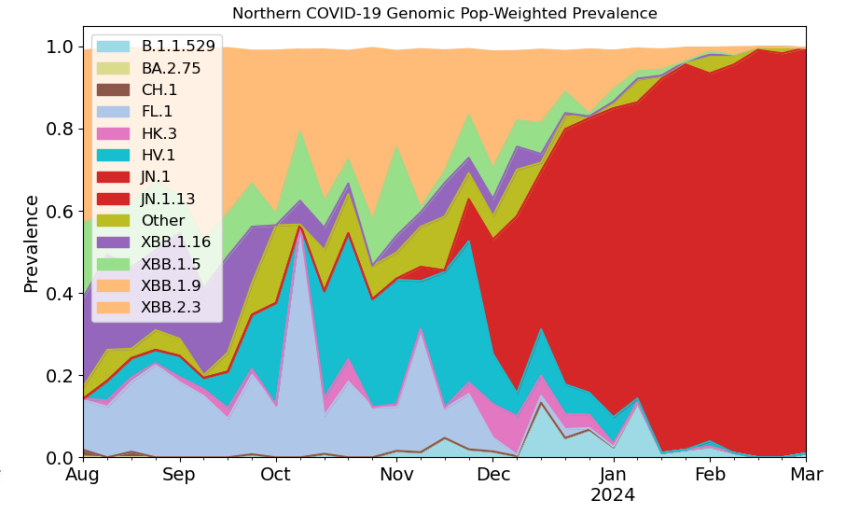
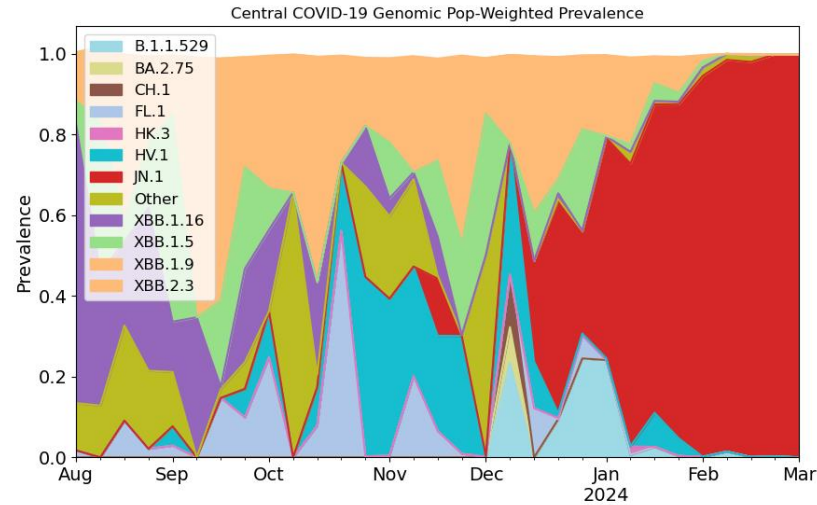
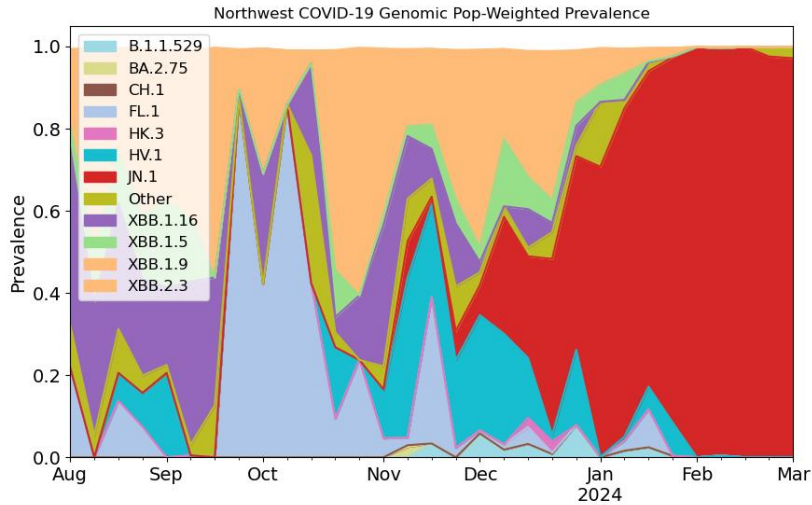
BA.2.86: **3.9%**

Other: **0.3%**

# Virginia Regional Wastewater Variant Status (median)



# Virginia Regional Population-Weighted Wastewater Variant Status



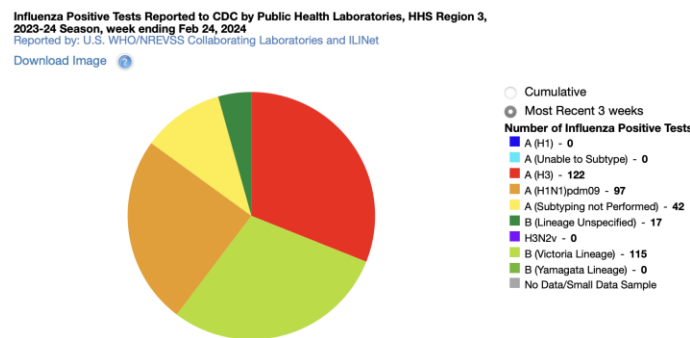
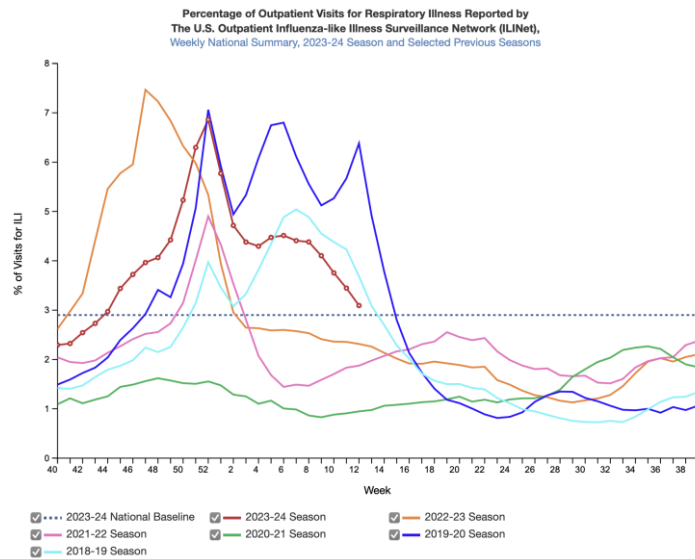
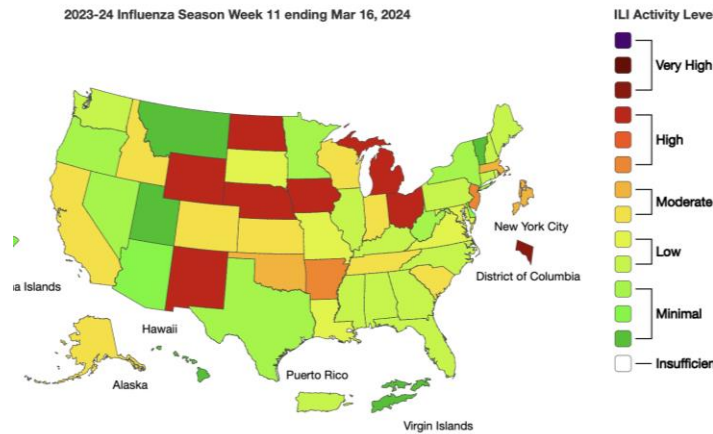
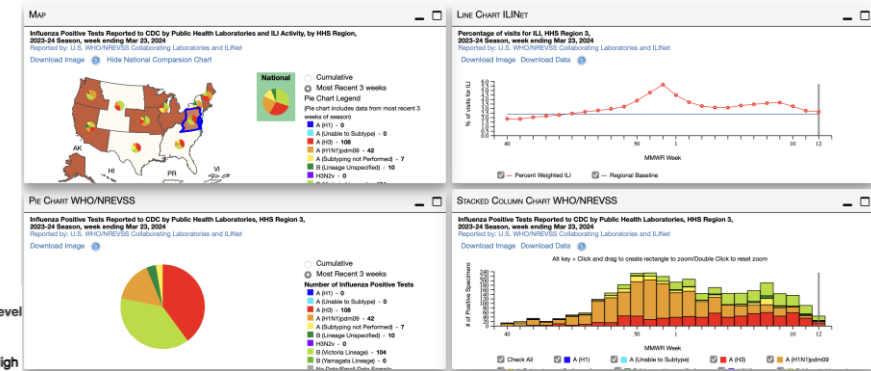
# Influenza Update

---

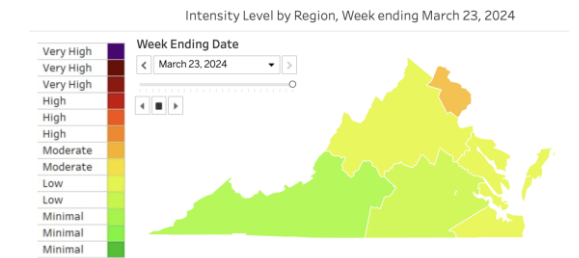
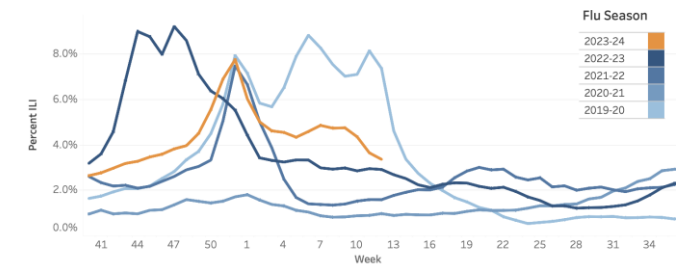
# Current Influenza Situation – ILI Activity

All regions remain above threshold and many are steady

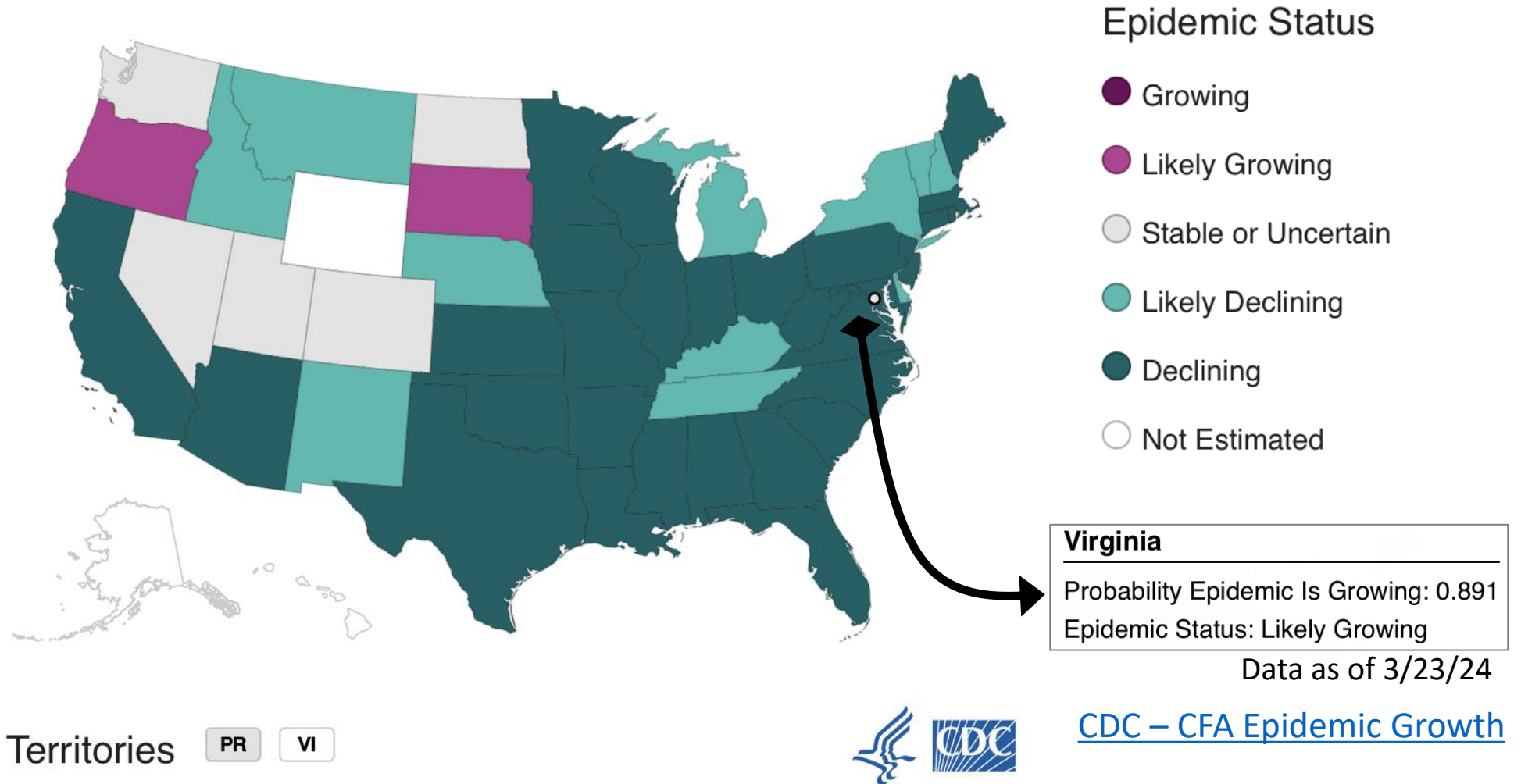
- Virginia is now in a "Low" level of Influenza activity
- National ILI activity has also dropped and is nearly below seasonal thresholds (as is VA)



## Virginia (ED & UC Visits – Mar 23, 2024)

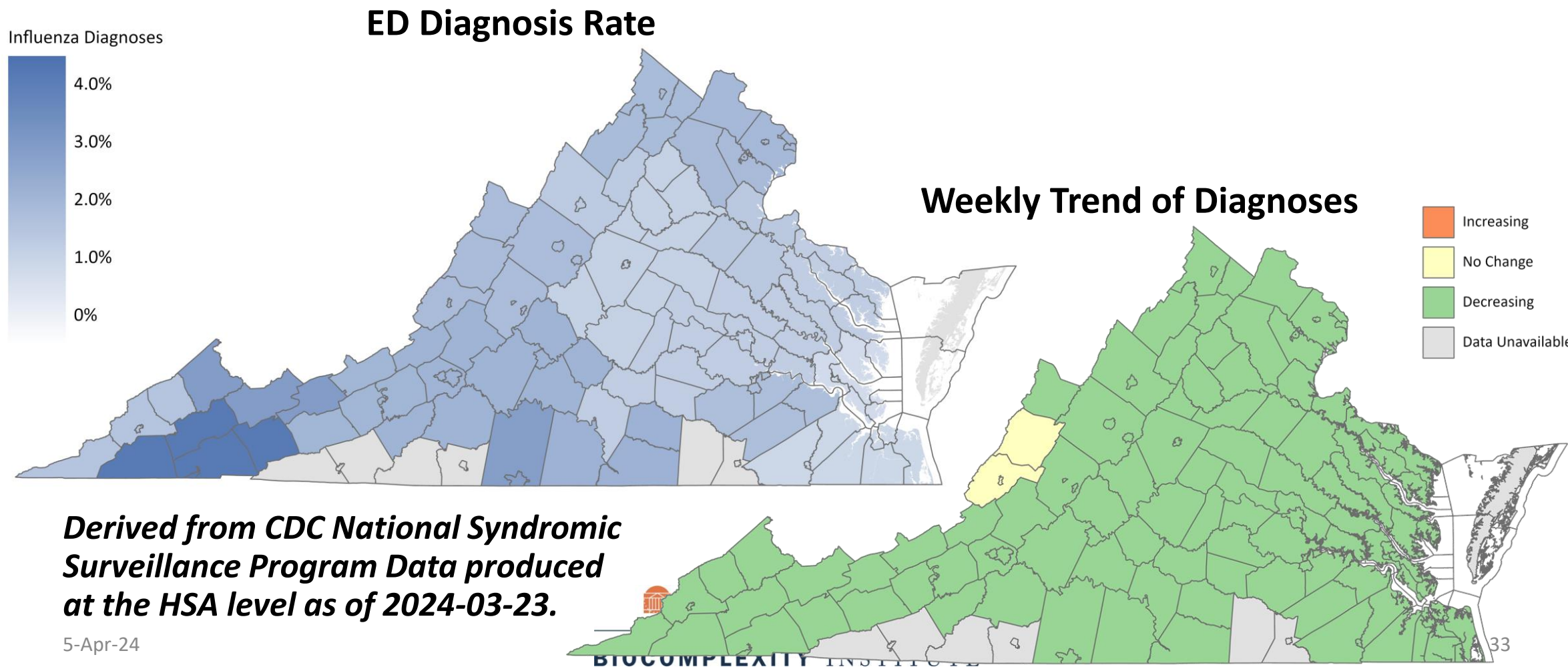


# Influenza Hospitalizations – Epidemic Growth



# Emergency Department Diagnosis Rate – Influenza

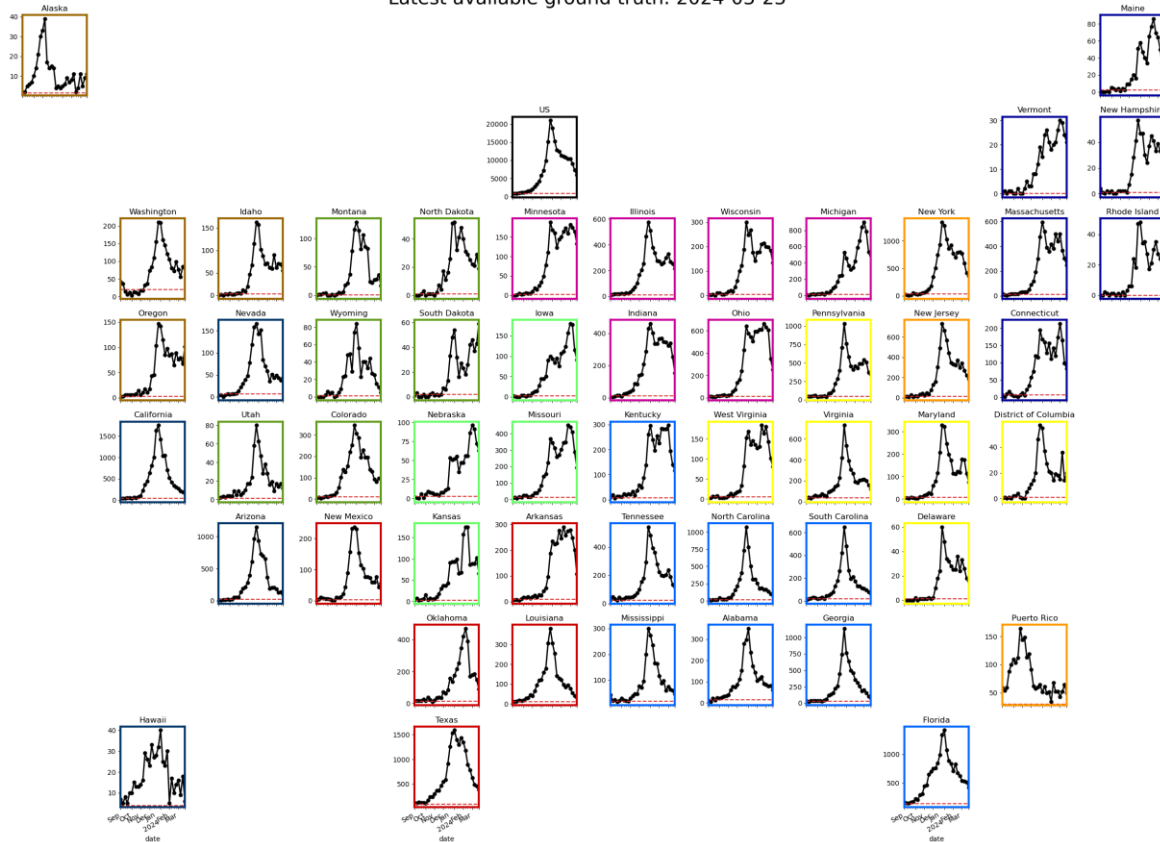
Flu diagnoses are still highest in the far Southwest and the Pittsylvania/Danville region. Rates continue to decline across the Commonwealth except in the Covington area.



# Influenza – Hospitalization Admissions

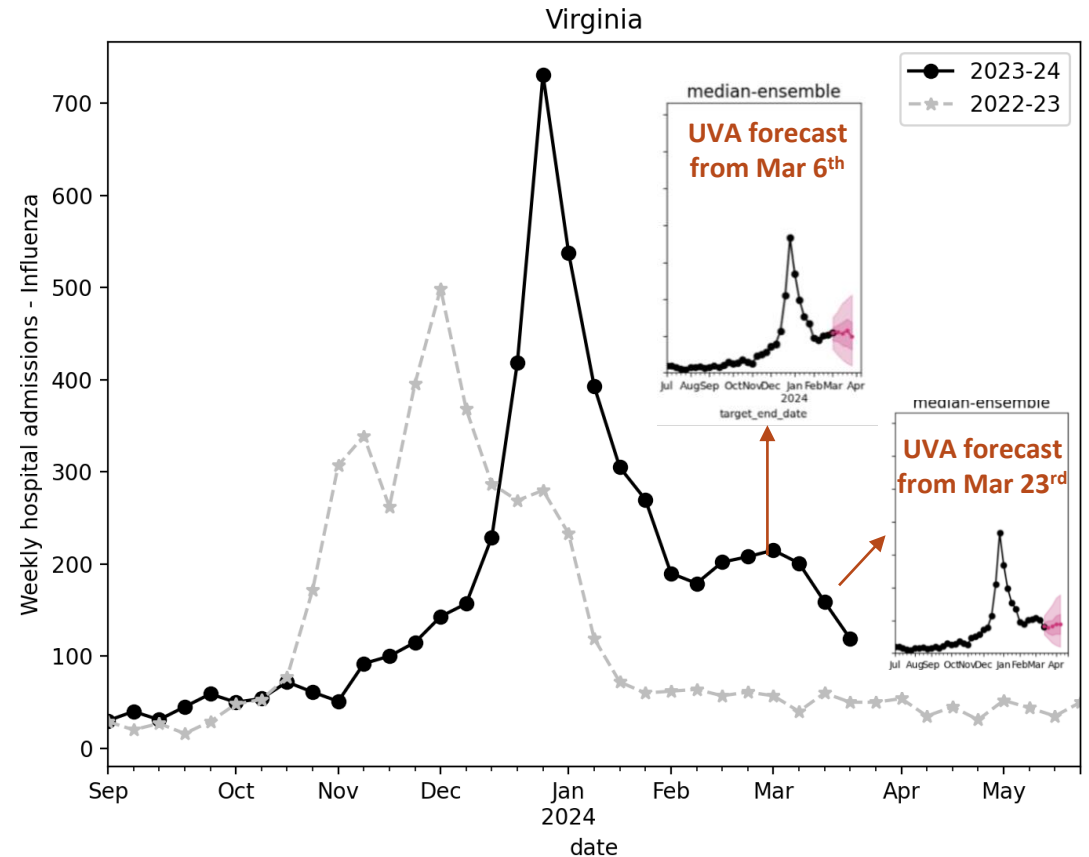
## National picture

Latest available ground truth: 2024-03-23



## Virginia Flu Hospital Admissions

Last update: March 30<sup>th</sup>, 2024





# Current Influenza Hospitalization Forecast

## Statistical models for submitting to [CDC Influenza Forecasting Hub](https://www.cdc.gov/flu/forecasting/)

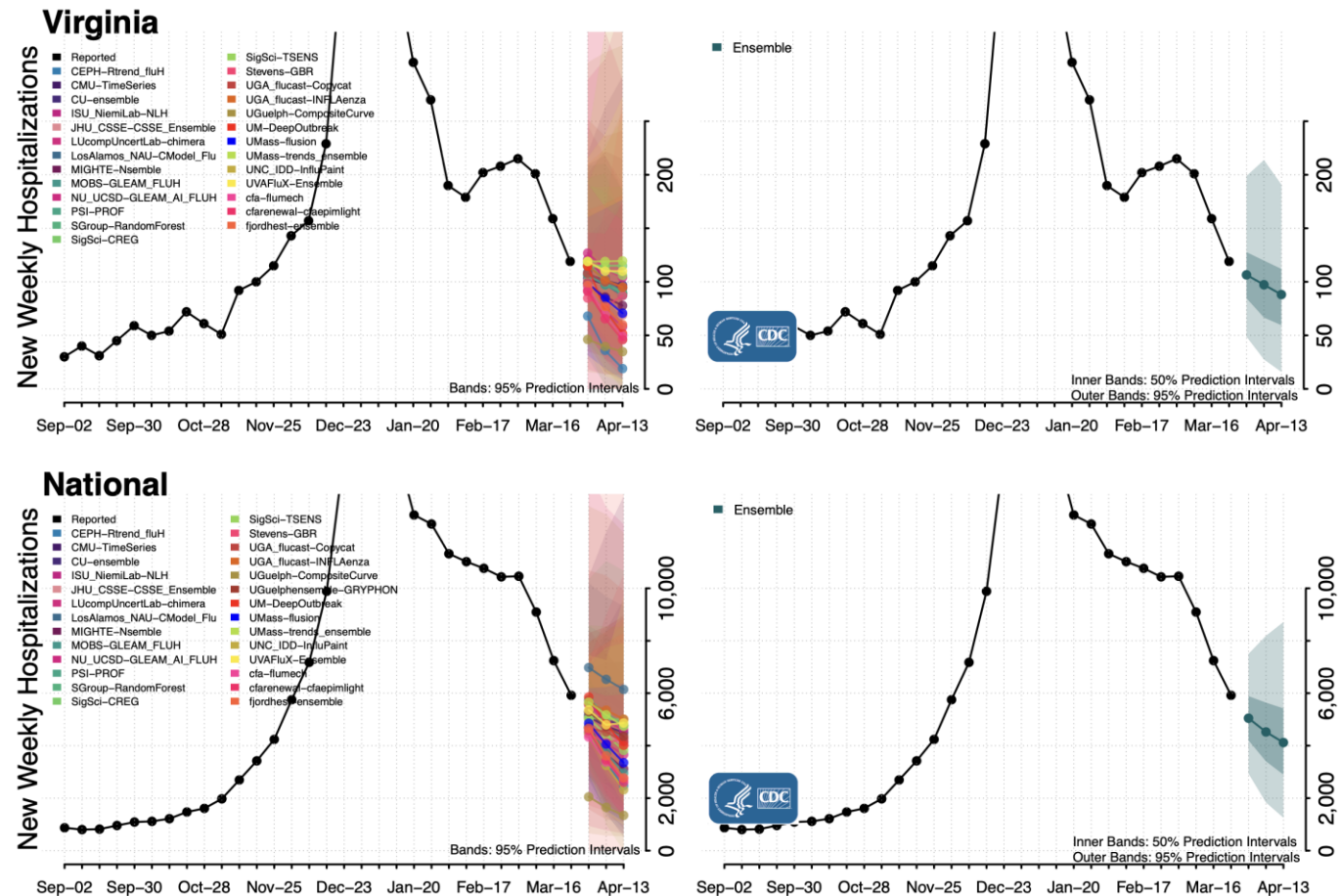
- Uses a variety of statistical and ML approaches to forecast weekly hospital admissions for the next 4 weeks for all states in the US

### Hospital Admissions for Influenza and Forecast for next 4 weeks (CDC Influenza Ensemble)

From March 27<sup>th</sup>

### CDC Flu Activity Surveillance

<https://www.cdc.gov/flu/weekly/fluactivitysurv.htm>

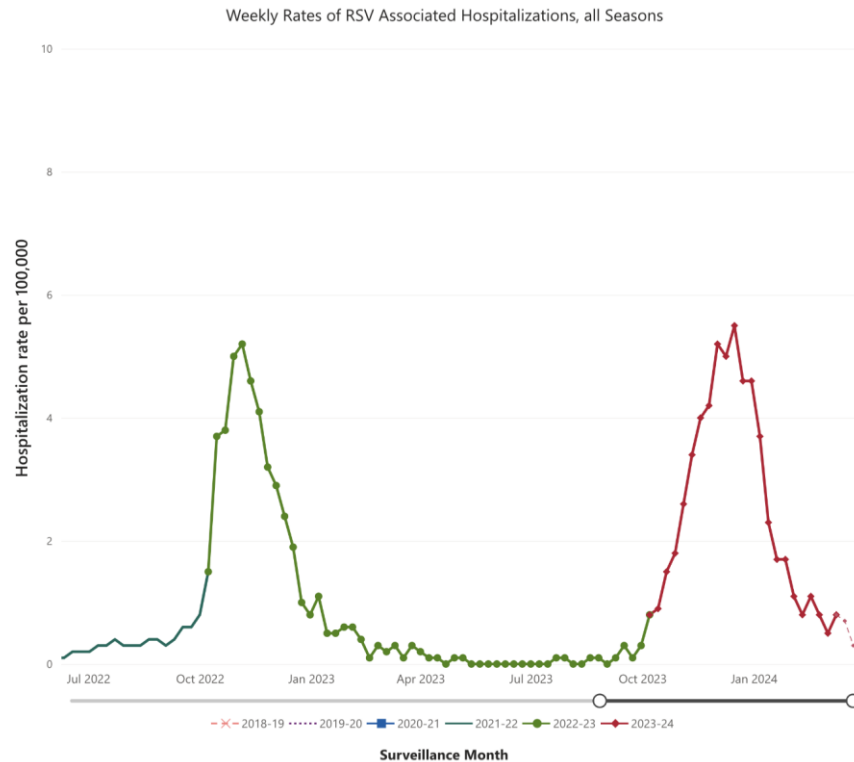


# RSV Update

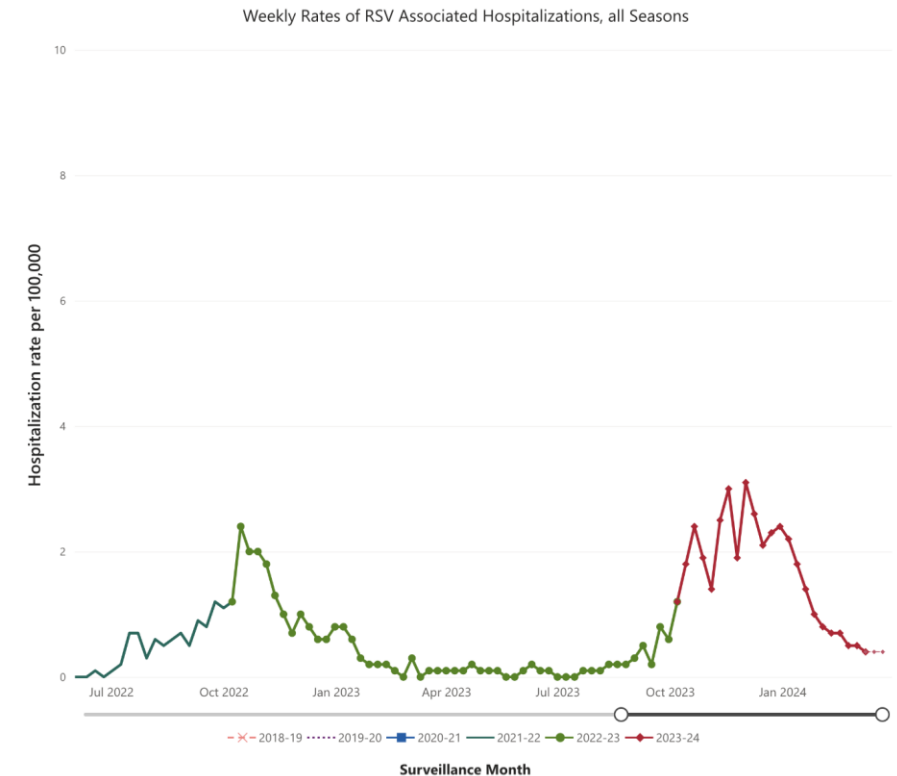
---

# Current RSV Situation – Hospitalization Rates (RSV-Net)

## Maryland (RSV-Net)



## Tennessee (RSV-Net)



Surveillance data as of:

3/09 (last solid data)

3/23 (last recent but likely to be updated)

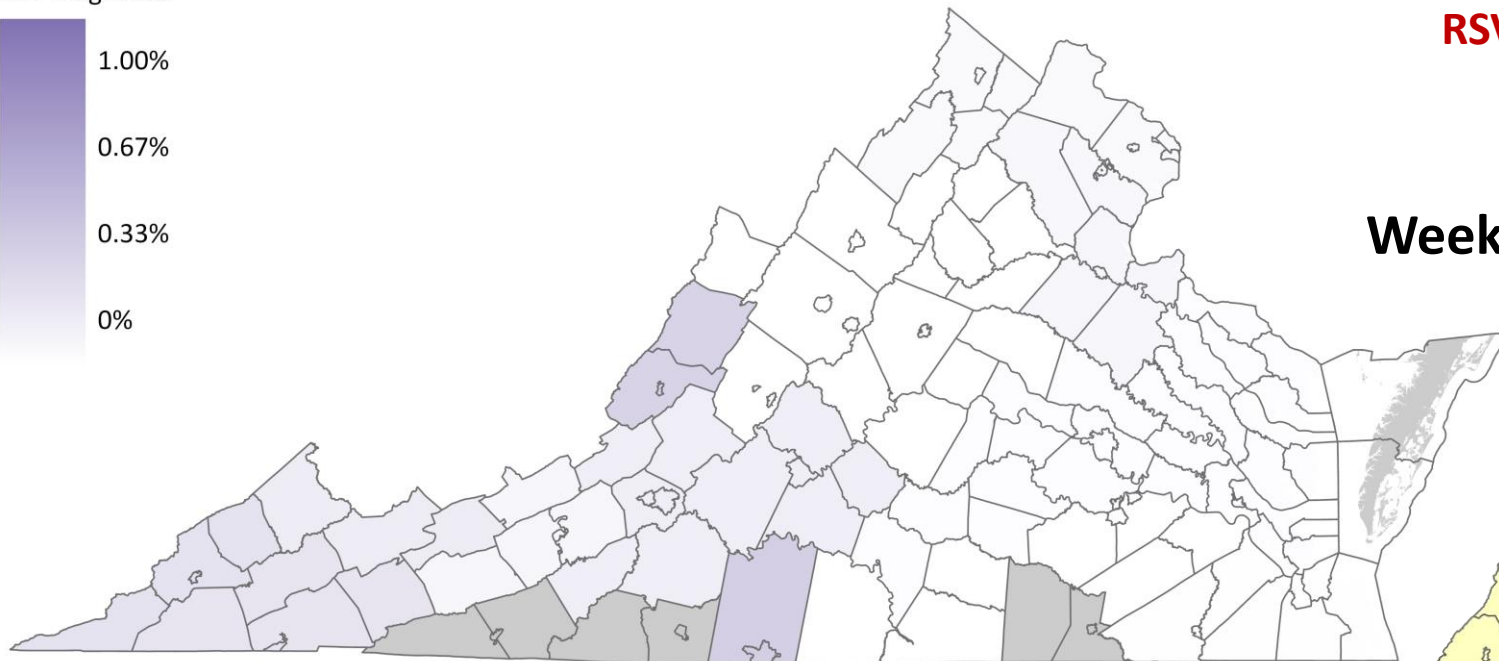
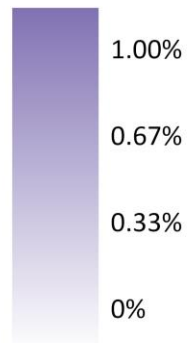
4/5/2024

# Emergency Department Diagnosis Rate – RSV

RSV diagnoses are low enough to necessitate a new color scale. They are highest near the Pittsylvania/Danville region and around Covington, but even these regions report < 0.5%.

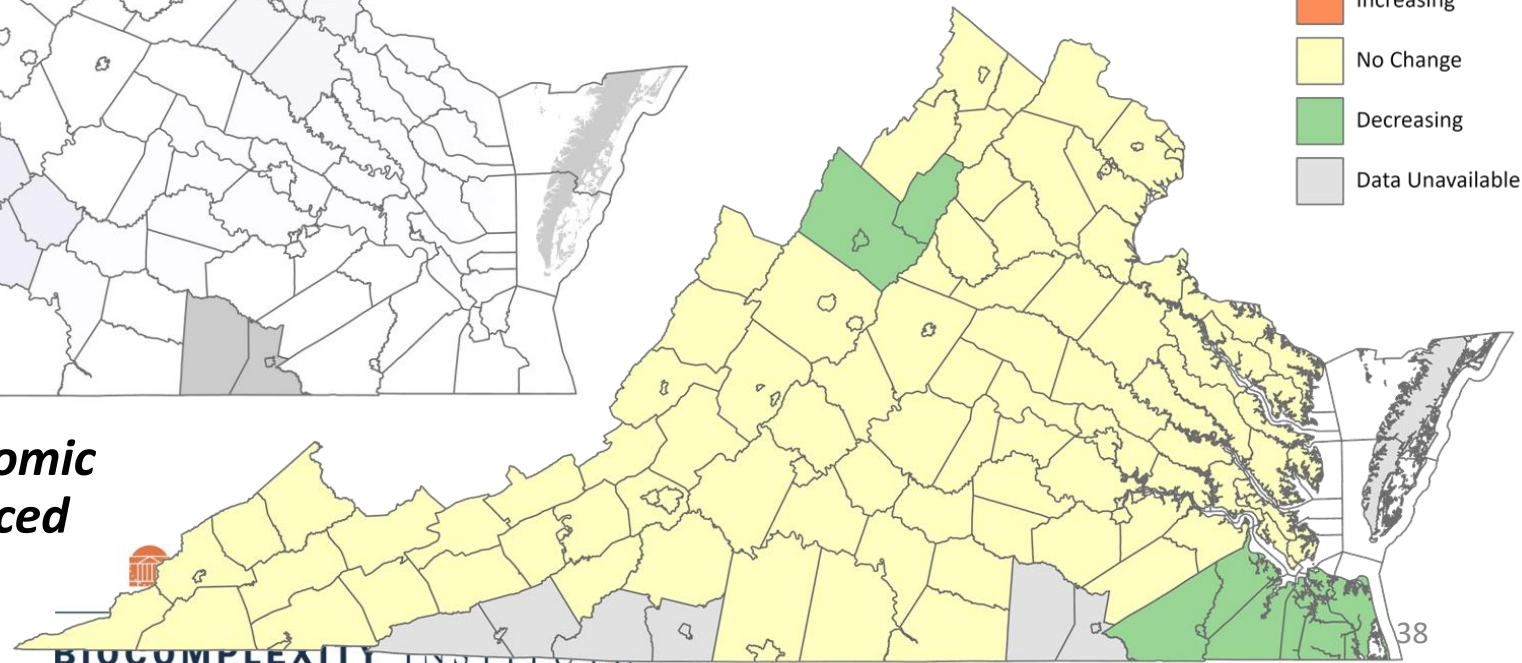
## ED Diagnosis Rate

RSV Diagnoses



Note color ramp stops at 1% for RSV as rates are very low compared to COVID-19 and Influenza.

## Weekly Trend of Diagnoses



*Derived from CDC National Syndromic Surveillance Program Data produced at the HSA level as of 2024-03-23.*

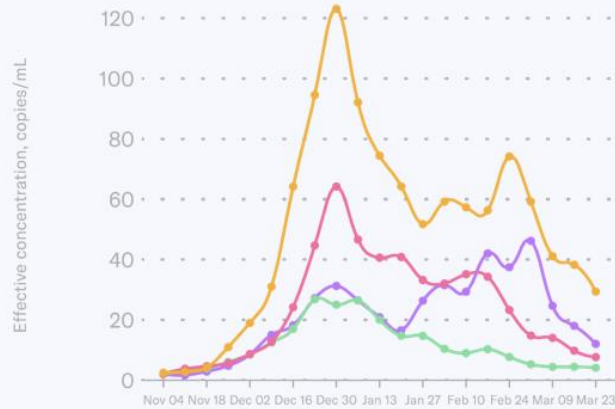
5-Apr-24

# Respiratory Illness Combined Update

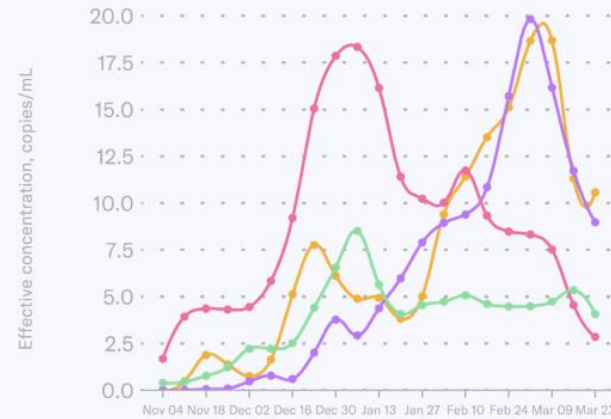
---

# Combined Respiratory Illness Viruses - Wastewater

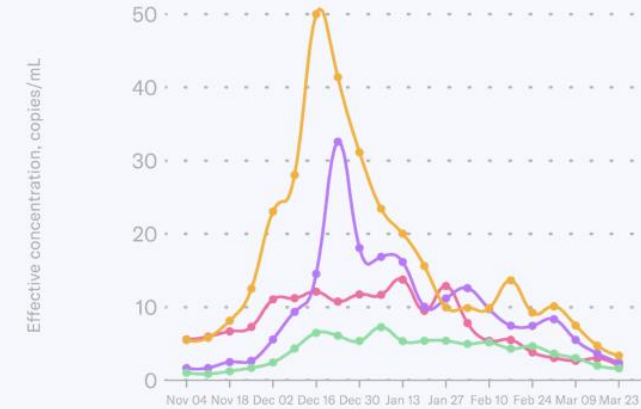
## Regional Flu and RSV Wastewater Concentrations



Influenza A



Influenza B



RSV



Biobot Analytics

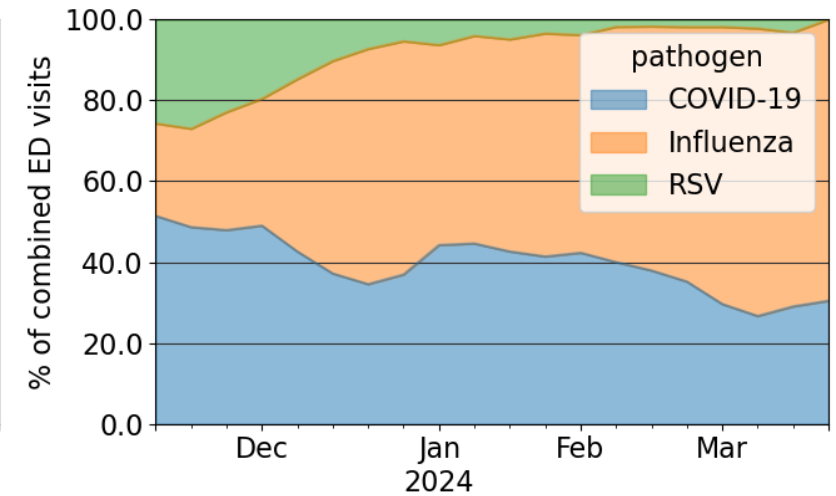
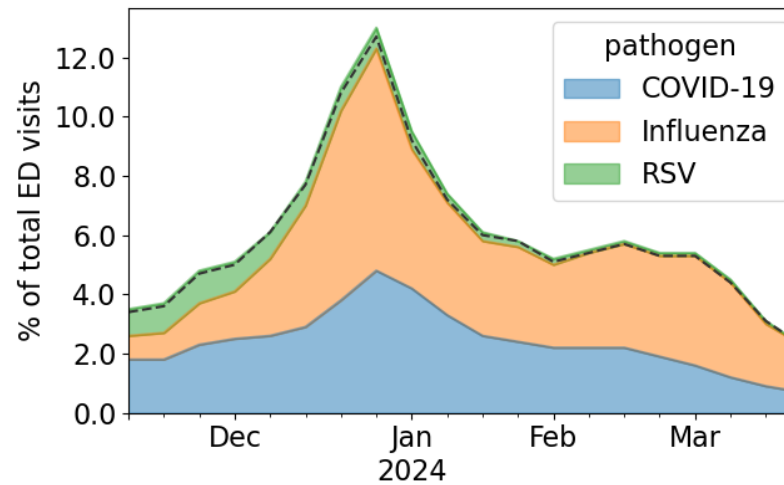
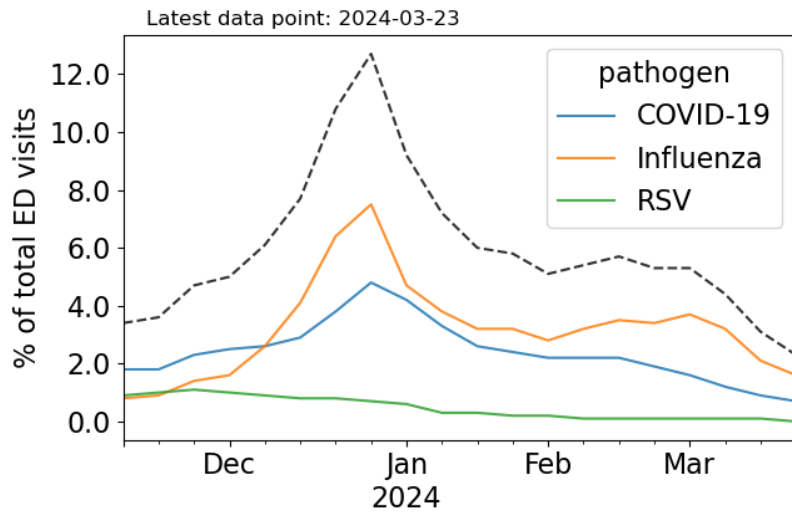
<https://biobot.io/data/>



BIOCOMPLEXITY INSTITUTE

# Combined Respiratory Illness Viruses – NSSP VA ED Visit

Virginia - COVID-19, Influenza, and RSV ED visits - Source: NSSP



Data as of March 23<sup>rd</sup>, 2024

# Key Takeaways

## **COVID-19 indicators have been in steady decline**

- Hospital admissions are higher than they were at this point last year, while ED visits with diagnosed COVID-19 are below and nearing an all-time low
- Wastewater viral activity levels have dropped significantly in recent weeks, with lows spread around Virginia
- Together this suggest continued declines easing into a low plateaus

## **Influenza has dropped significantly in VA and across the US**

## **RSV hospitalizations remain at minimal activity**



# Review of Total Presented Material

## Over 200 weeks of modeling, analytic, and research updates

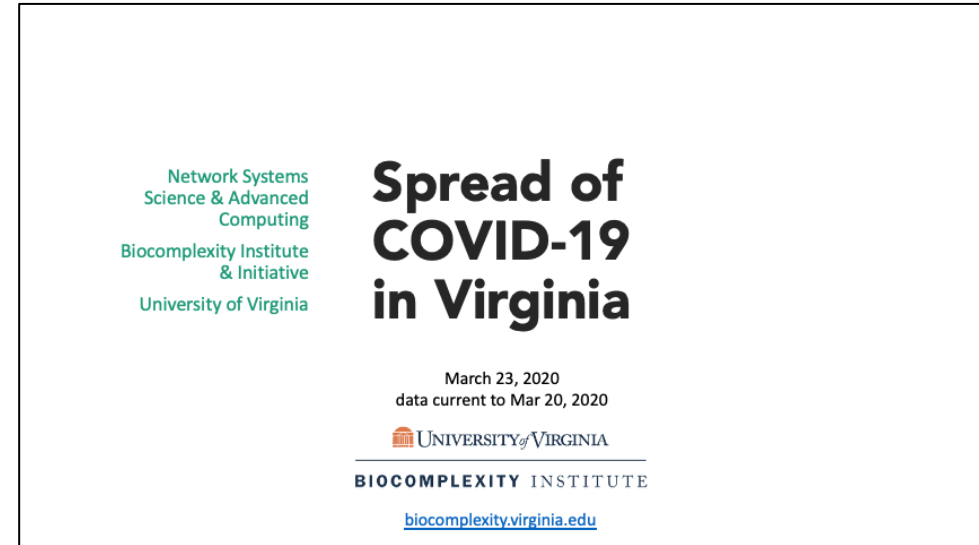
- 152 Spread / Analysis updates from March 2020-December 2022
- 33 Integrated Biosurveillance Research updates since January 2023
- 33 Genomic Research updates since January 2023
- 12+ ad-hoc Wastewater / Genomics updates
- 7 Metaculus updates
- 26 Summary presentations since January 2023

Total of 263 (+/-) slide presentations

Many presented twice or thrice in a week

Approximately 336 hours of presented material (one continuous fortnight)

Dozens of Publications to be detailed in reports



**The First One - March 23<sup>rd</sup>, 2020**

# Questions?

## Biocomplexity COVID-19 Response Team

### Points of Contact

Bryan Lewis

[brylew@virginia.edu](mailto:brylew@virginia.edu)

Srini Venkatramanan

[srini@virginia.edu](mailto:srini@virginia.edu)

Madhav Marathe

[marathe@virginia.edu](mailto:marathe@virginia.edu)

Chris Barrett

[ChrisBarrett@virginia.edu](mailto:ChrisBarrett@virginia.edu)

Aniruddha Adiga, Abhijin Adiga, Hannah Baek, Chris Barrett, Golda Barrow, Richard Beckman, Parantapa Bhattacharya, Jiangzhuo Chen, Clark Cucinell, Patrick Corbett, Allan Dickerman, Stephen Eubank, Stefan Hoops, Ben Hurt, Ron Kenyon, Brian Klahn, Bryan Lewis, Dustin Machi, Chunhong Mao, Achla Marathe, Madhav Marathe, Henning Mortveit, Mark Orr, Joseph Outten, Akhil Peddireddy, Przemyslaw Porebski, Erin Raymond, Jose Bayoan Santiago Calderon, James Schlitt, Samarth Swarup, Alex Telionis, Srinivasan Venkatramanan, Anil Vullikanti, James Walke, Andrew Warren, Amanda Wilson, Dawen Xie