Network Systems Science & Advanced Computing

Biocomplexity Institute & Initiative

University of Virginia

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

September 14th, 2023

(data current to Sept 2nd – Sept 12th)

Biocomplexity Institute Technical report: TR BI-2023-242

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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

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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

Activity levels have slowed and may be starting to plateau

- Case rates show signs of leveling off as do other indicators, while hospital admissions continue to grow though may be slowing
- Wastewater based indicators also show lower viral loads and CLI indicators also slow.

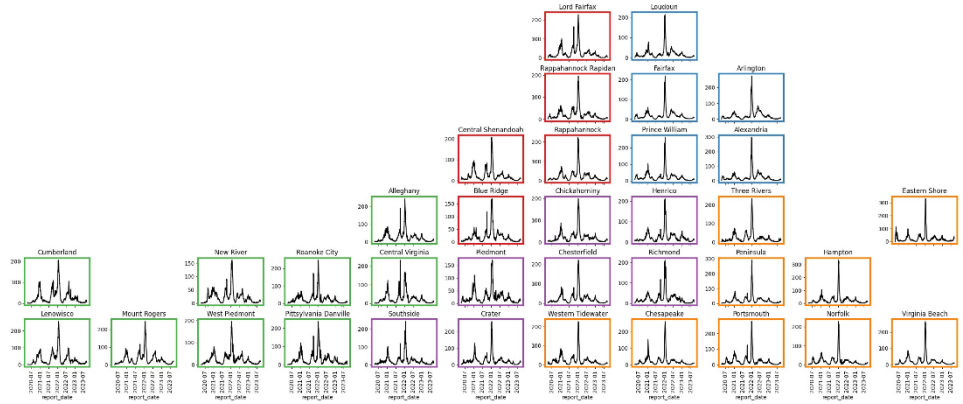
Genomic Surveillance maintains high diversity with no dominating variant

- Lineage BA.2.86 continues to be detected in wastewater and traveler surveillance
- Recent evidence softens concerns that BA.2.86 has enhanced infectivity and immune escape and suggests current vaccine may maintain effectiveness
- Sub-variants of XBB.1.[5,9,16]: EG.5, FL.1.5.1, HV.1 continue domestic spread

Current signs suggest a slowing and potential pause in growth

COVID-19 Surveillance

Case Rates (per 100k)



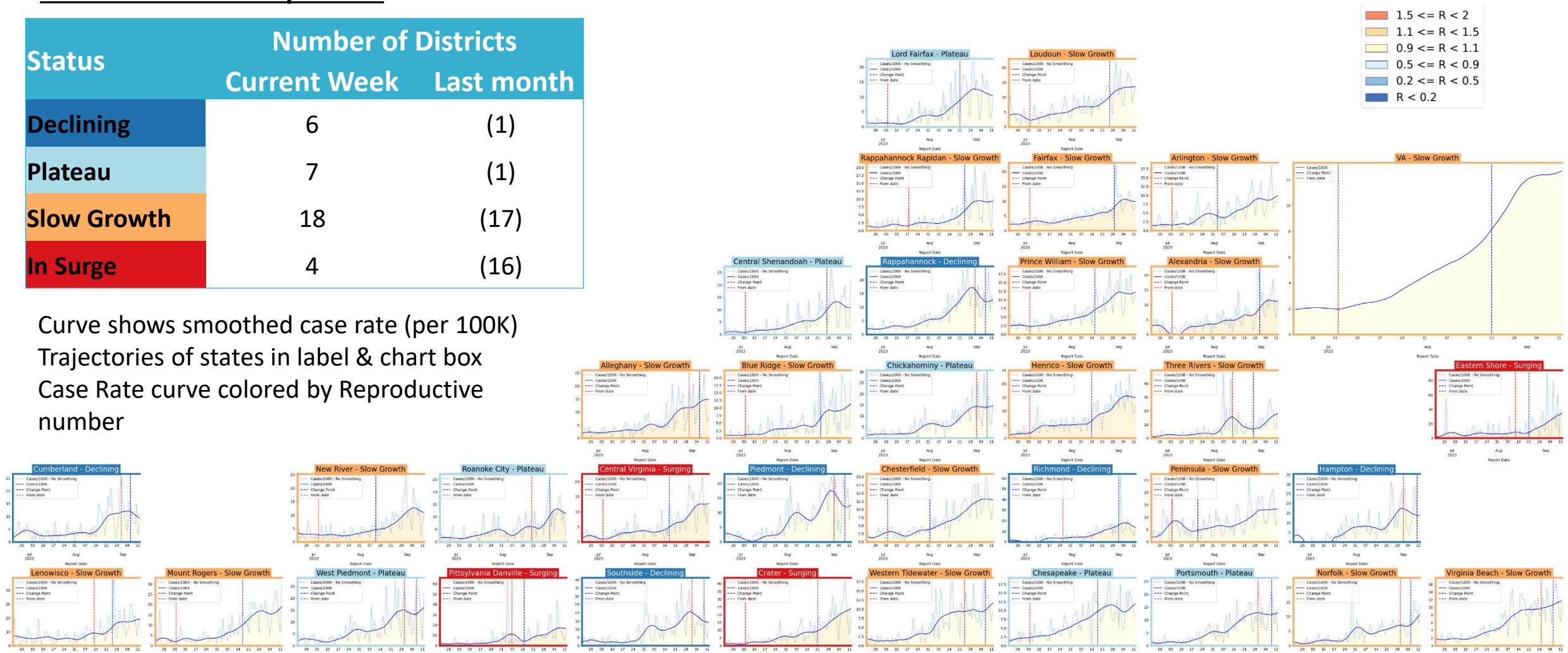
Whole pandemic

District Case Trajectories – last 10 weeks

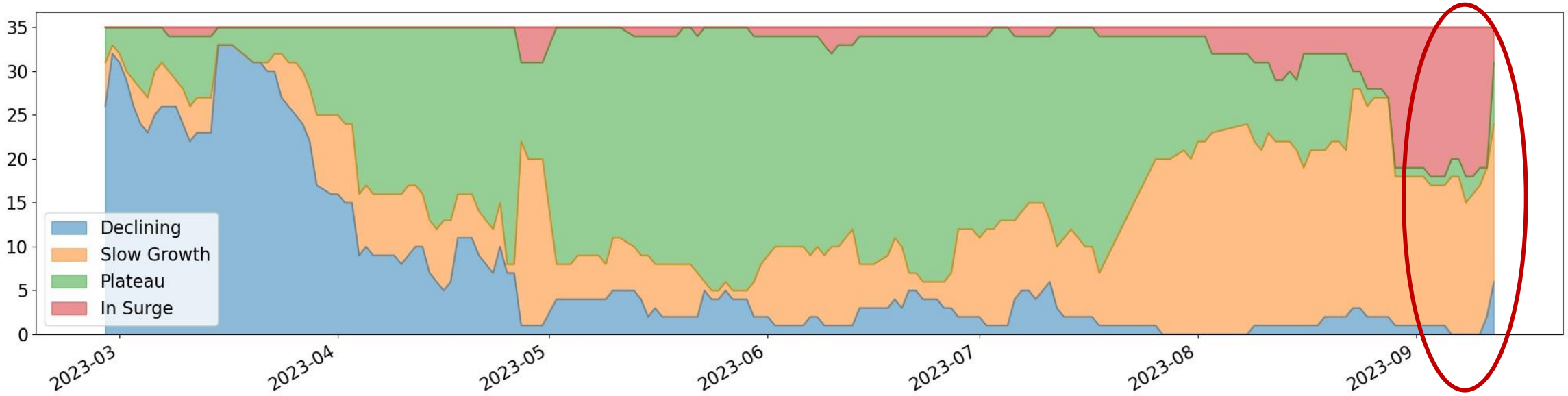
Rt estimates from EpiNow2

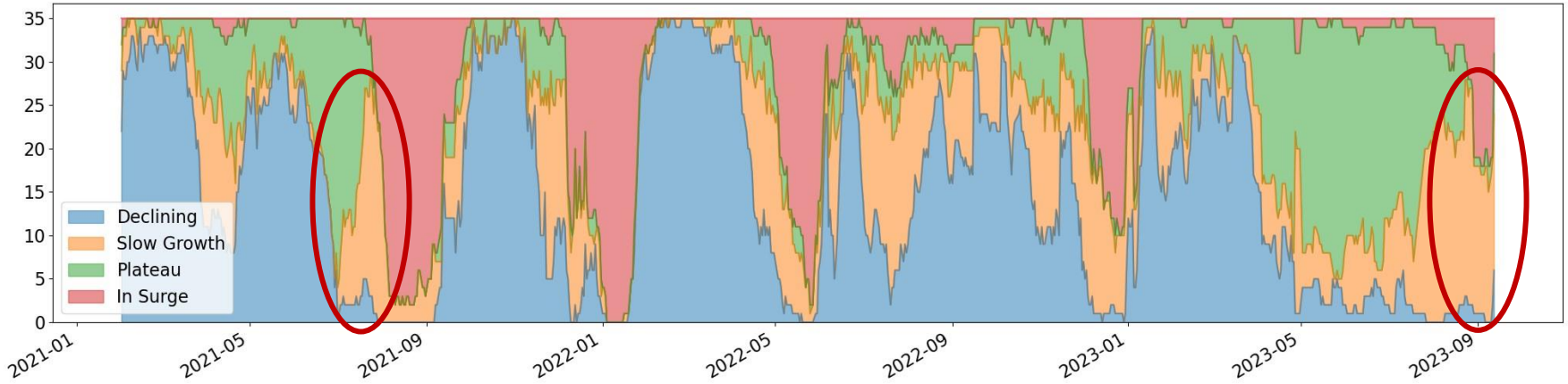
Status	Number of Districts	
	Current Week	Last month
Declining	6	(1)
Plateau	7	(1)
Slow Growth	18	(17)
In Surge	4	(16)

Curve shows smoothed case rate (per 100K)
Trajectories of states in label & chart box
Case Rate curve colored by Reproductive number



District Case Trajectories – Recent 6 months





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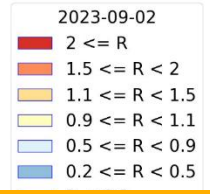
District Hospital Trajectories – last 10 weeks

Rt estimates from EpiNow2

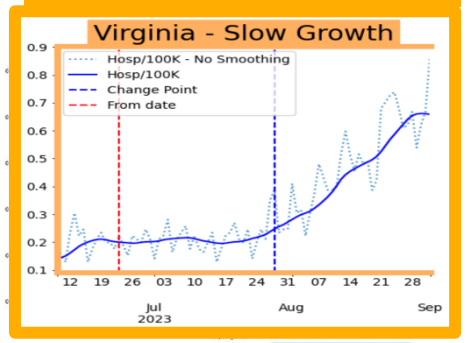
Status	Number of Districts	
	Current Week	Last week
Declining	0	(0)
Plateau	16	(12)
Slow Growth	17	(19)
In Surge	2	(4)

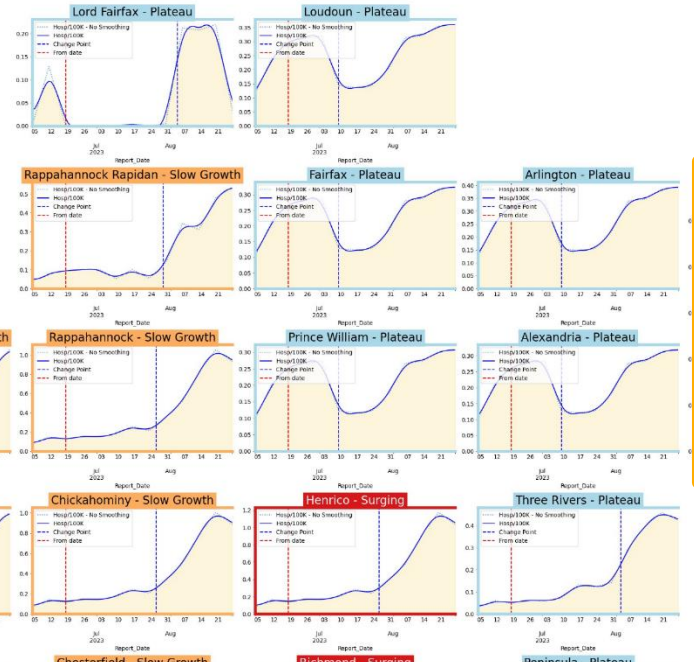
Hospitalization by county inferred from Facility data mapped to counties through Hospital Referral Regions.

As of Sept 2nd



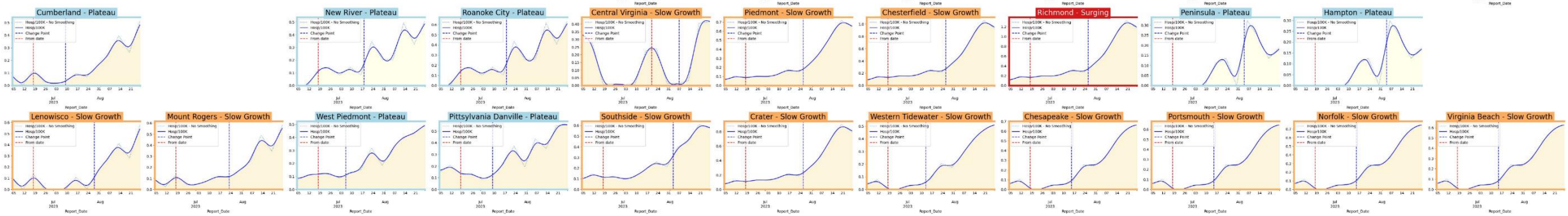
State level Time Series





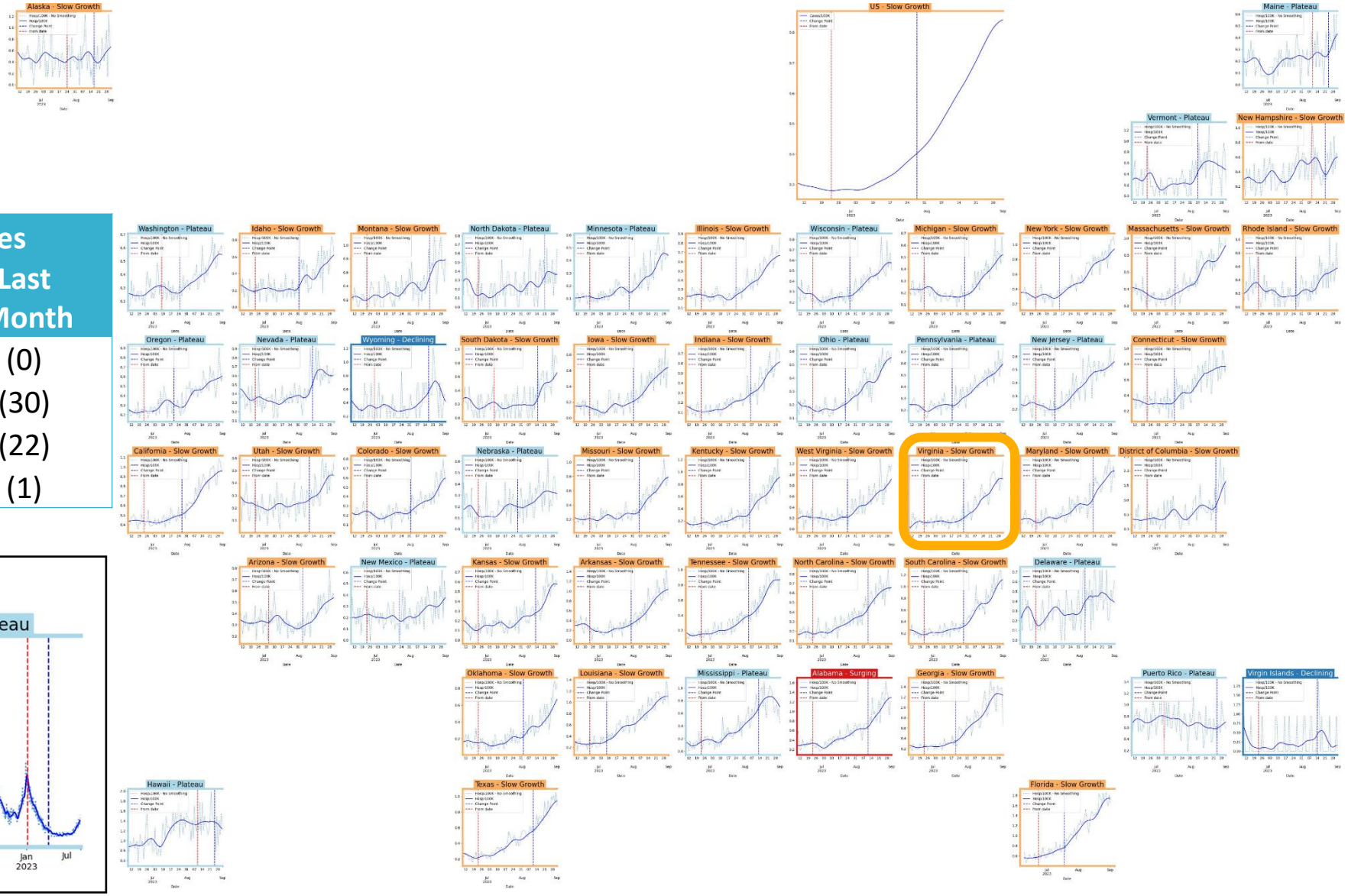
Curve shows smoothed hospitalization rate (per 100K) by district

Hosp rate curve colored by R_e number

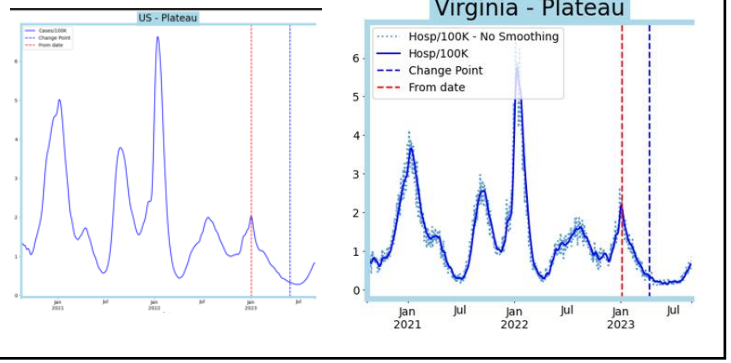


United States Hospitalizations

Status	Number of States	
	Current Week	Last Month
Declining	2	(0)
Plateau	17	(30)
Slow Growth	33	(22)
In Surge	1	(1)

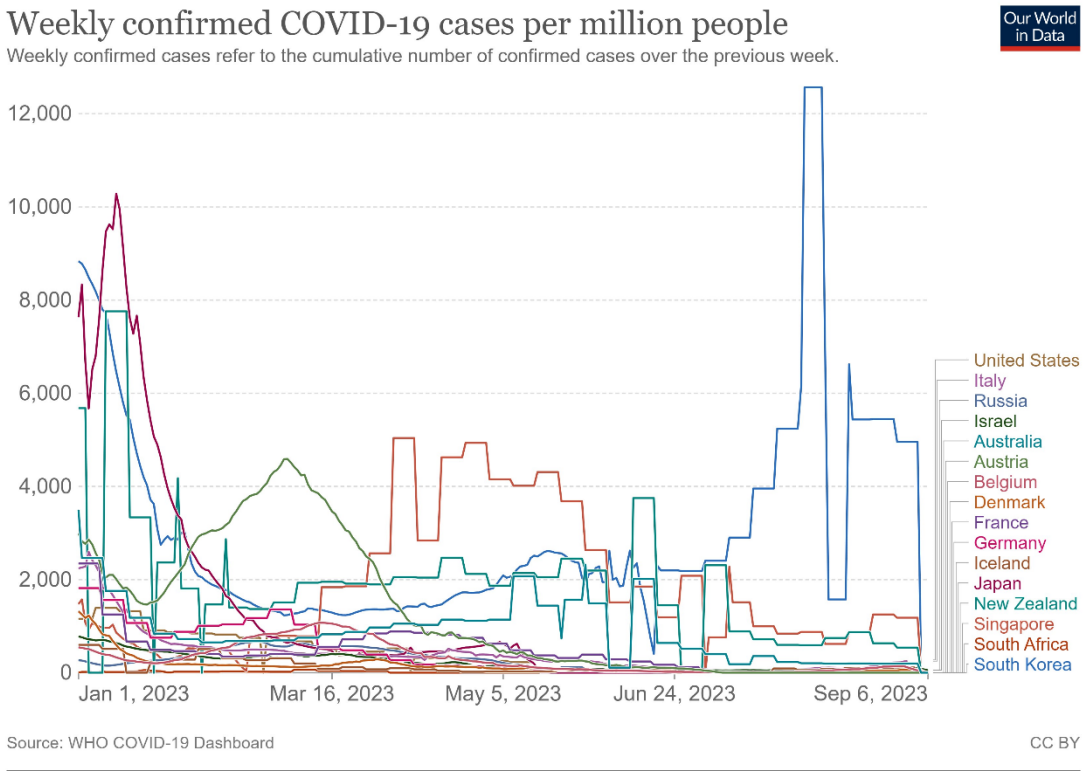


Whole Pandemic

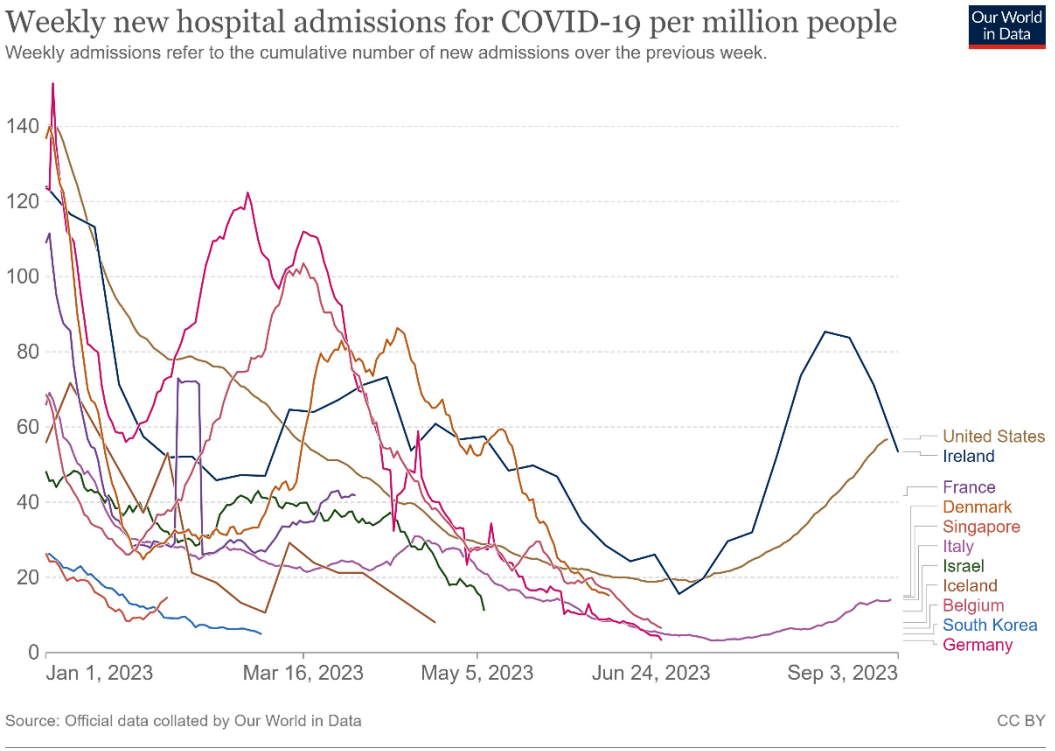


Around the World – Various trajectories

Confirmed cases



Hospitalizations



Our World in Data [Our World in Data]

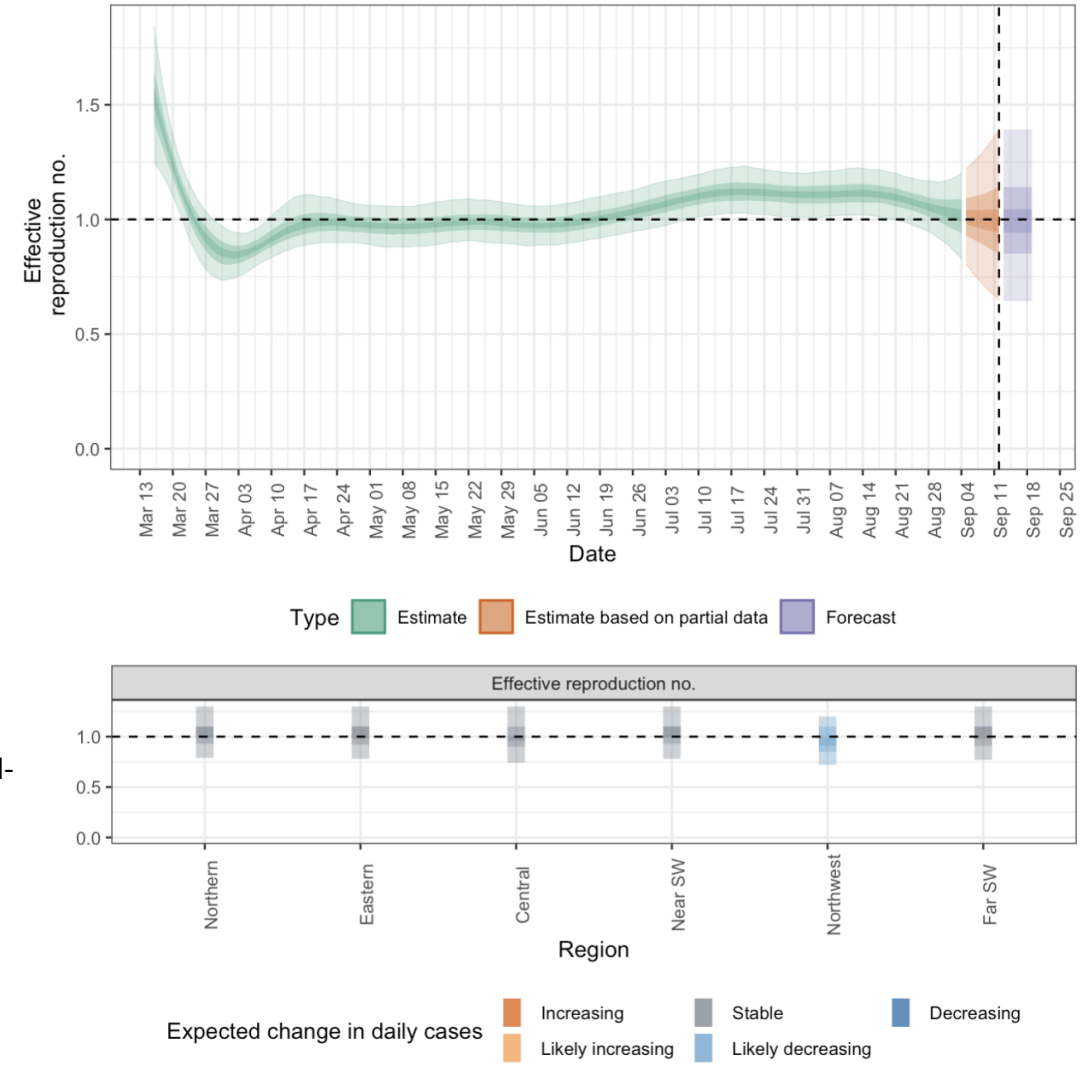
COVID-19 Growth Metrics

Estimating Daily Reproductive Number –
VDH report dates – EpiNow2 estimation

Reproductive Estimate Summary as of September 12, 2023

Region	Reproductive number estimate	Confidence interval	Trend forecast
State-wide cases	1.0	0.65 - 1.4	Stable
State-wide hosp	1.1	1.0 - 1.1	Increasing
Central	0.99	0.74 - 1.3	Stable
Eastern	1.0	0.78 - 1.3	Stable
Far SW	1.0	0.77 - 1.3	Stable
Near SW	1.0	0.78 - 1.3	Stable
Northern	1.0	0.84 - 1.4	Stable
Northwest	0.96	0.82 - 1.6	Likely decreasing

Re from VDH Cases (last 6 months)



Methodology

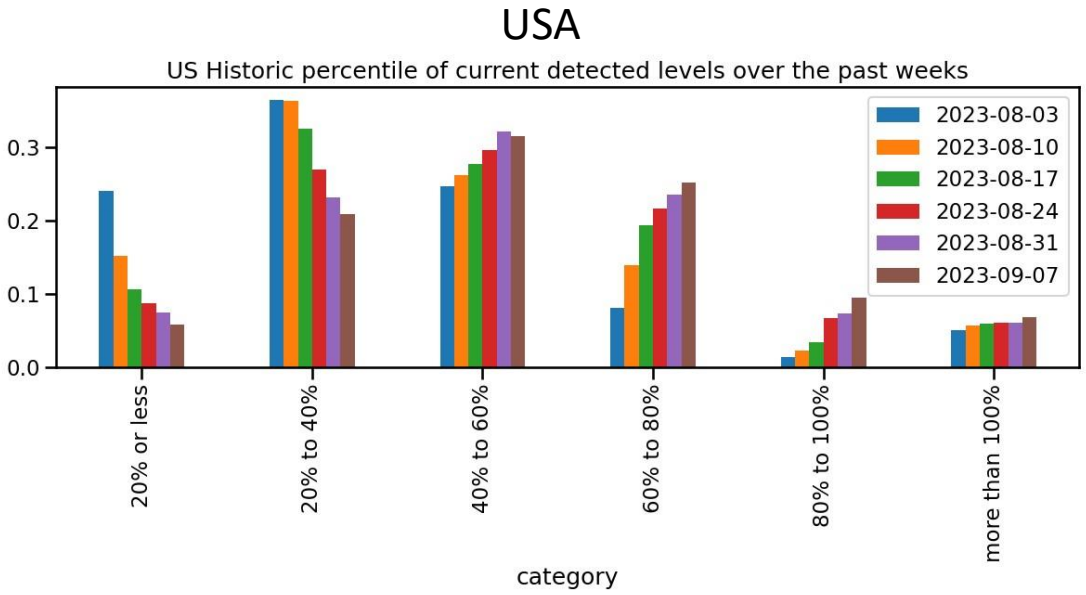
- Sam Abbott, Joel Hellewell, Katharine Sherratt, Katelyn Gostic, Joe Hickson, Hamada S. Badr, Michael DeWitt, Robin Thompson, EpiForecasts, Sebastian Funk (2020). **EpiNow2**: Estimate Real-Time Case Counts and Time-Varying Epidemiological Parameters. doi:10.5281/zenodo.3957489.
- Serial interval updates with COVID-19 disease model built into EpiNow2
- Uses confirmation date but report date biases are better accounted for
- Note: most recent data point for hospitalizations is 10 days prior to that of cases (HHS hospitalization through 9/2/23 vs. VDH case data through 9/12/23)

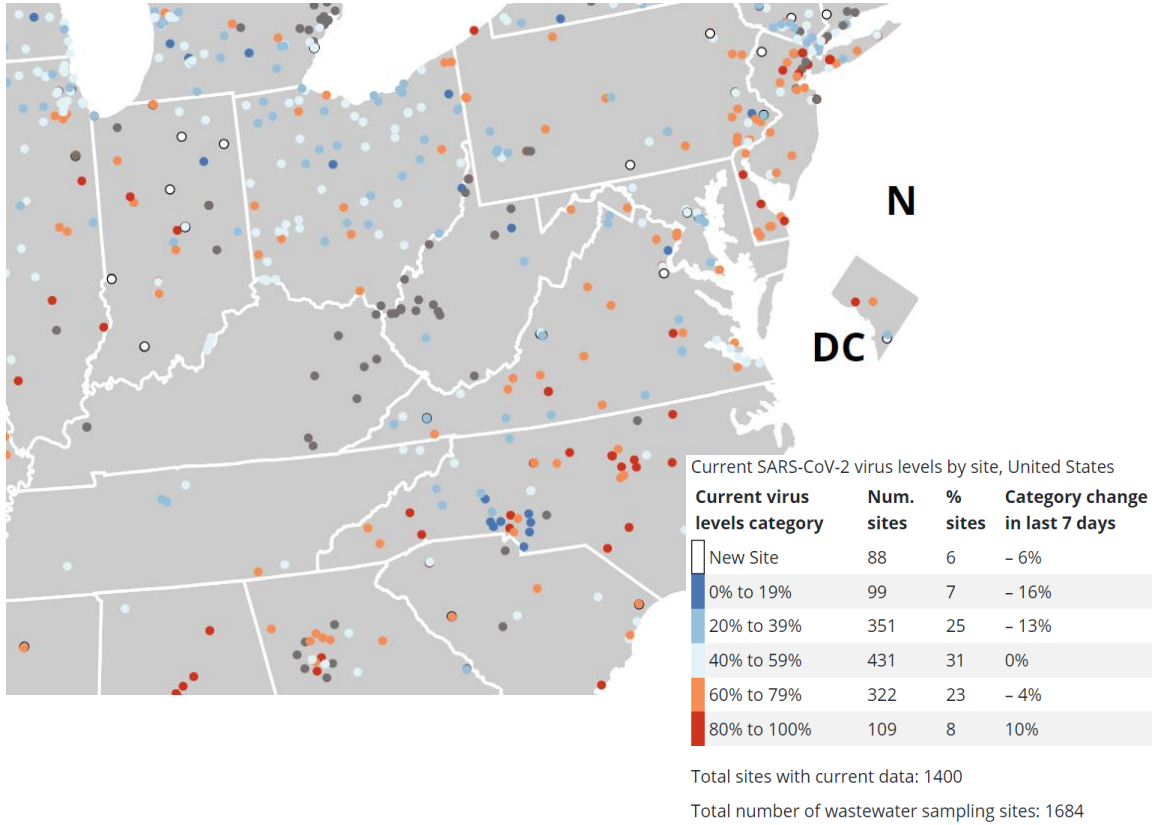
EpiNow2 home: https://epiforecasts.io/EpiNow2/

Wastewater Monitoring

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

- Nationwide and in VA, sites have shifted from lower trend categories to higher trend categories



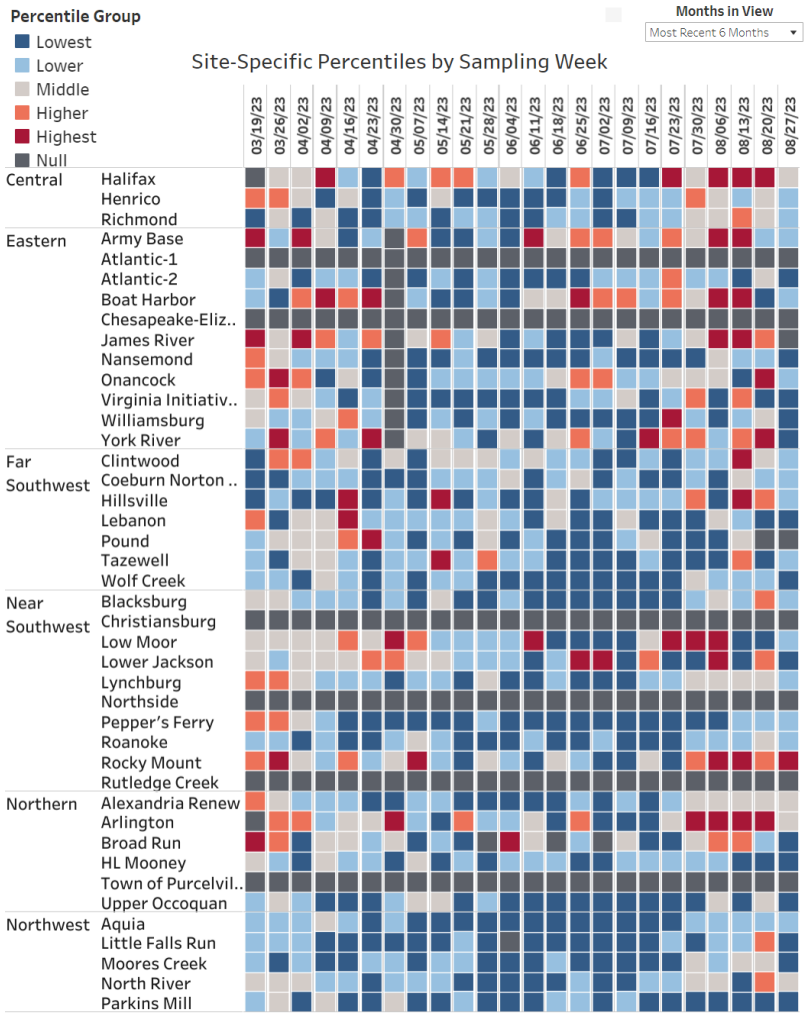


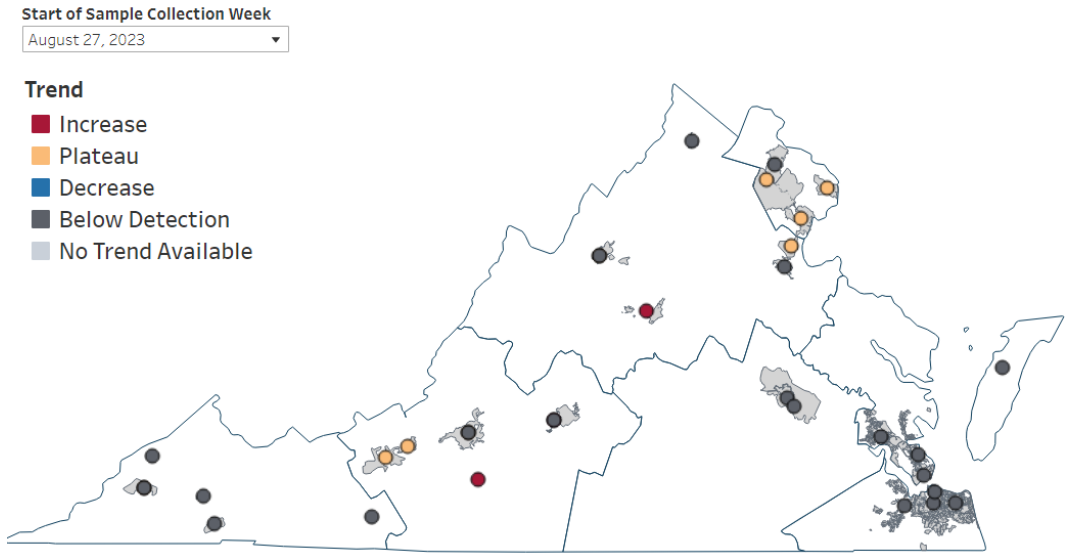
Data Source: [CDC Data Tracker]

Wastewater Monitoring – VA Sites

Wastewater provides a coarse early warning of COVID-19 levels in communities

- Some VA sites (esp. Eastern) are starting to shift to higher quintiles in wastewater percentile groups





From: https://www.vdh.virginia.gov/coronavirus/see-the-numbers/covid-19-data-insights/sars-cov-2-in-wastewater/#surveillance-trend

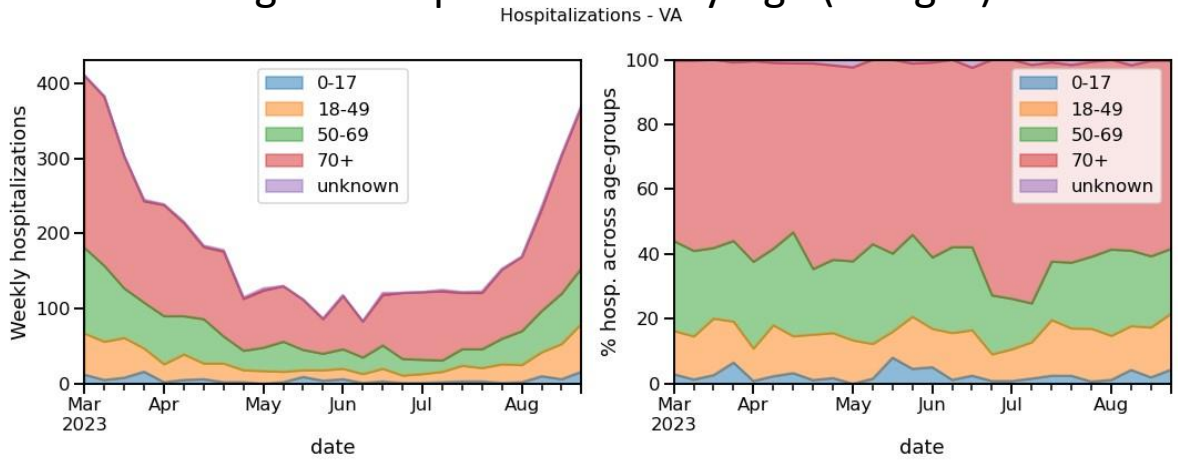
Hospitalizations in VA by Age

Age distribution in hospitals showing slight shift towards younger age groups

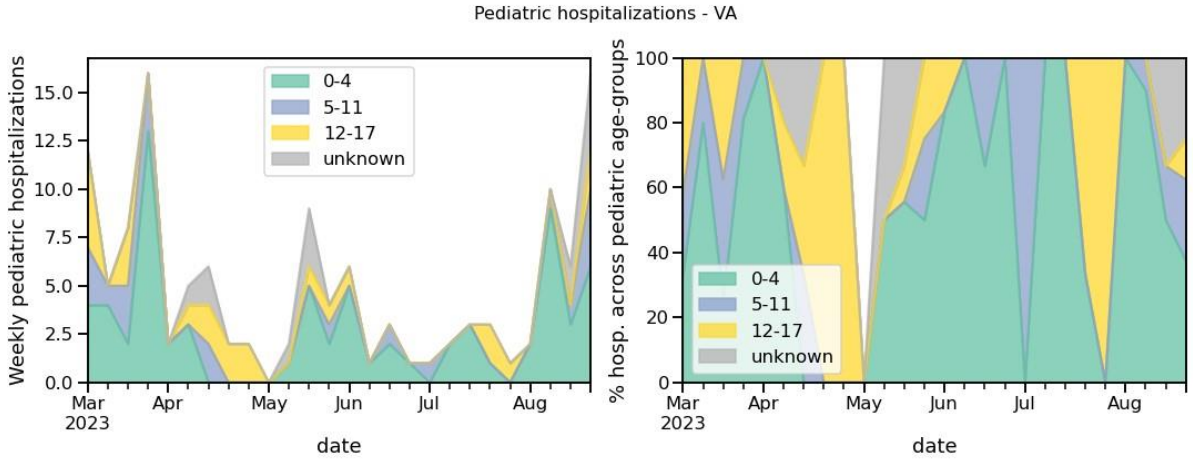
- Overall hospitalizations increasing across all age groups
- Increase in pediatric hospitalizations (0-4 age group), near highest level in last 6 months

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

Virginia Hospitalizations by Age (all ages)



Pediatric Hospitalizations by Age (0-17yo)

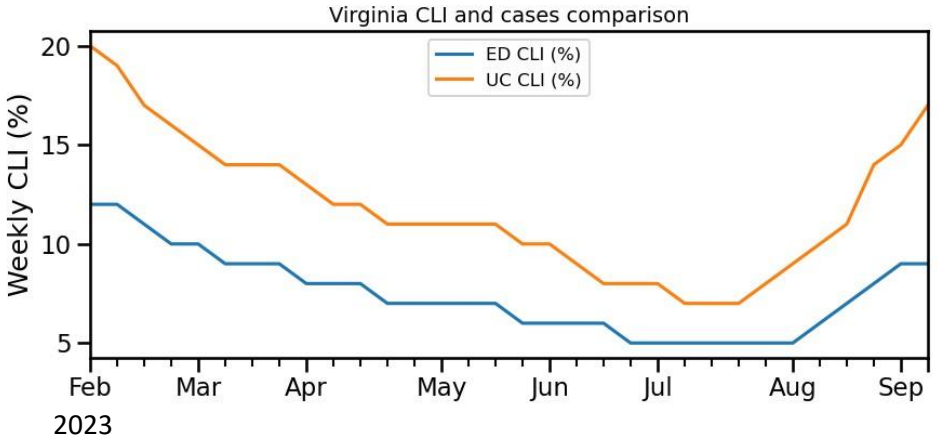


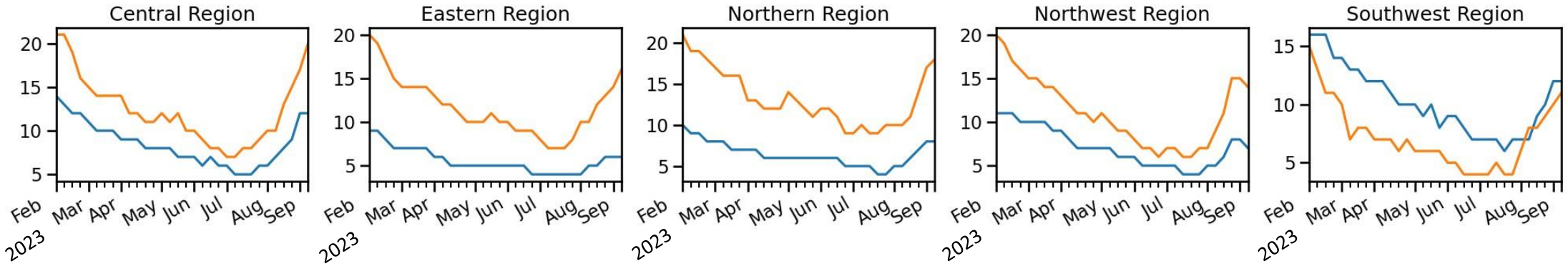
Data Source: Delphi and HHS

COVID-like Illness Activity

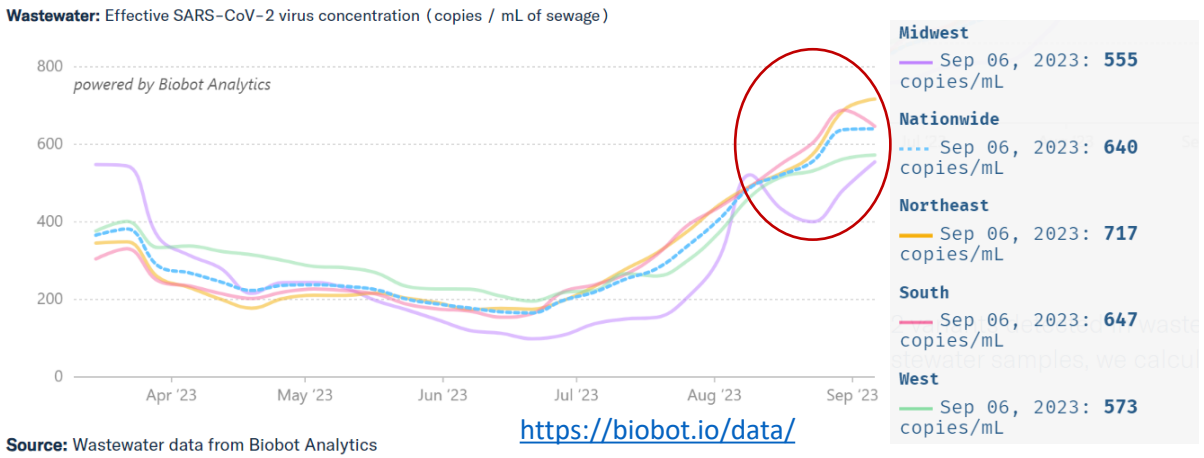
COVID-like Illness (CLI) gives a measure of COVID transmission in the community

- Emergency Dept (ED) based CLI is more correlated with case reporting
- Urgent Care (UC) is a leading indicator but may be influenced by testing for other URIs
- **CLI continues to grow, rapidly in many regions**
- **Levels now similar to those last seen in late winter**

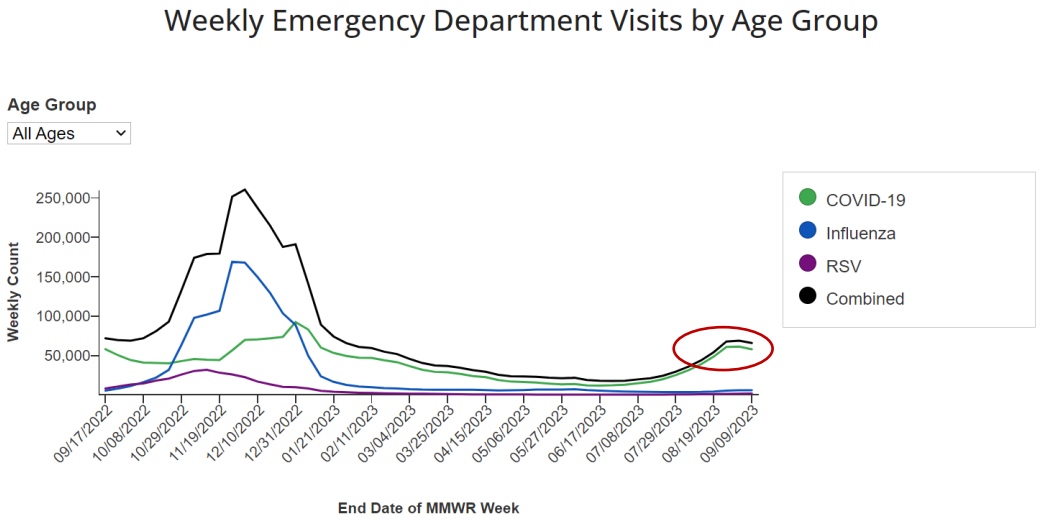




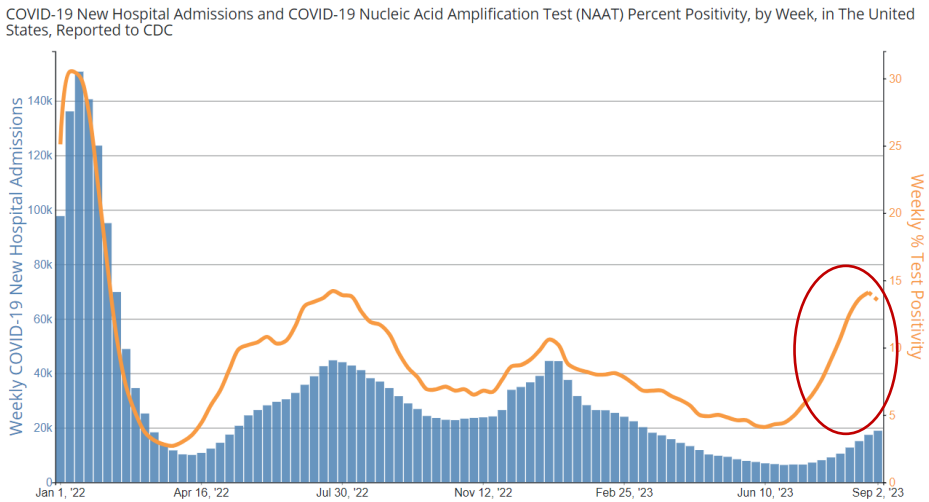
Wastewater, ED visits, and Test positivity



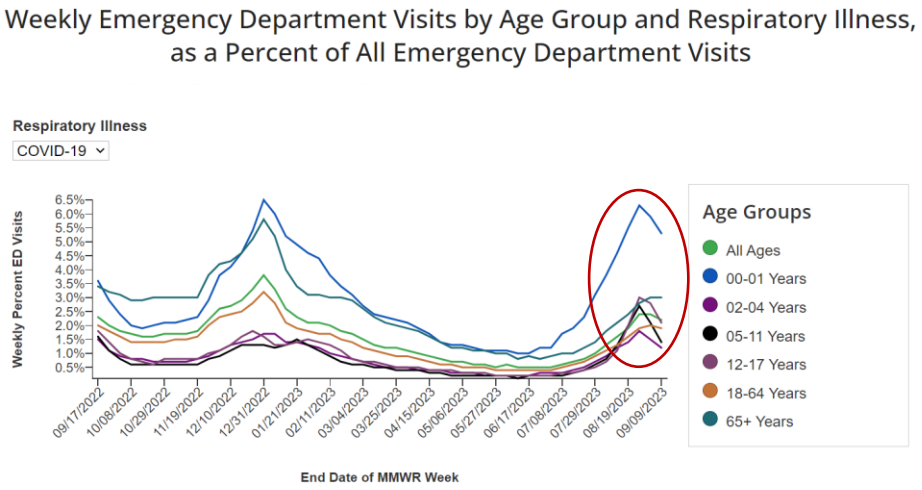
https://biobot.io/data/



- WW signal plateauing, with Midwest rebounding into growth
- National testing volumes remain low (<50k/week) while positivity and admissions double
- ED visits for COVID also show signs of leveling off



https://covid.cdc.gov/covid-data-tracker/#trends_weeklyhospitaladmissions_testpositivity_00



https://www.cdc.gov/ncird/surveillance/respiratory-illnesses/index.html

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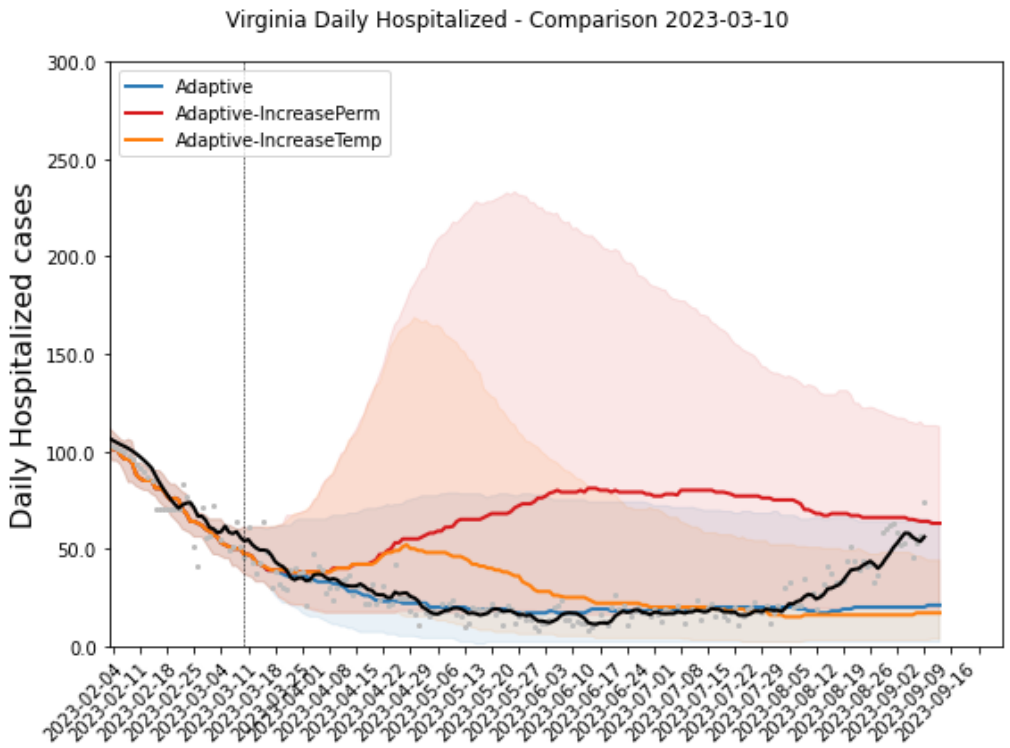
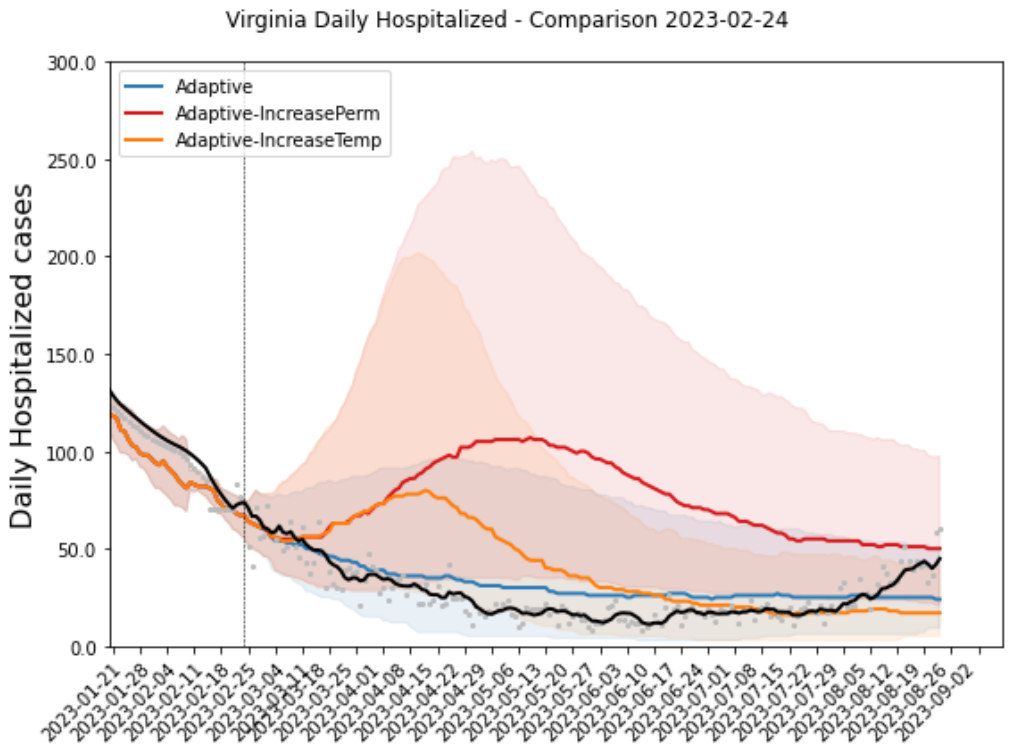
Past projections – Hospitalizations

Projections from mid-March no longer match observations as growth exceeds previous slow uptick. Previous projections had no scenarios based on changes in late summer.

Previous round – 27 weeks ago



Previous round – 29 weeks ago



Projections were for only 6 months

COVID-19 Spatial Epidemiology

ZIP Code level case rate per 100K since last meeting

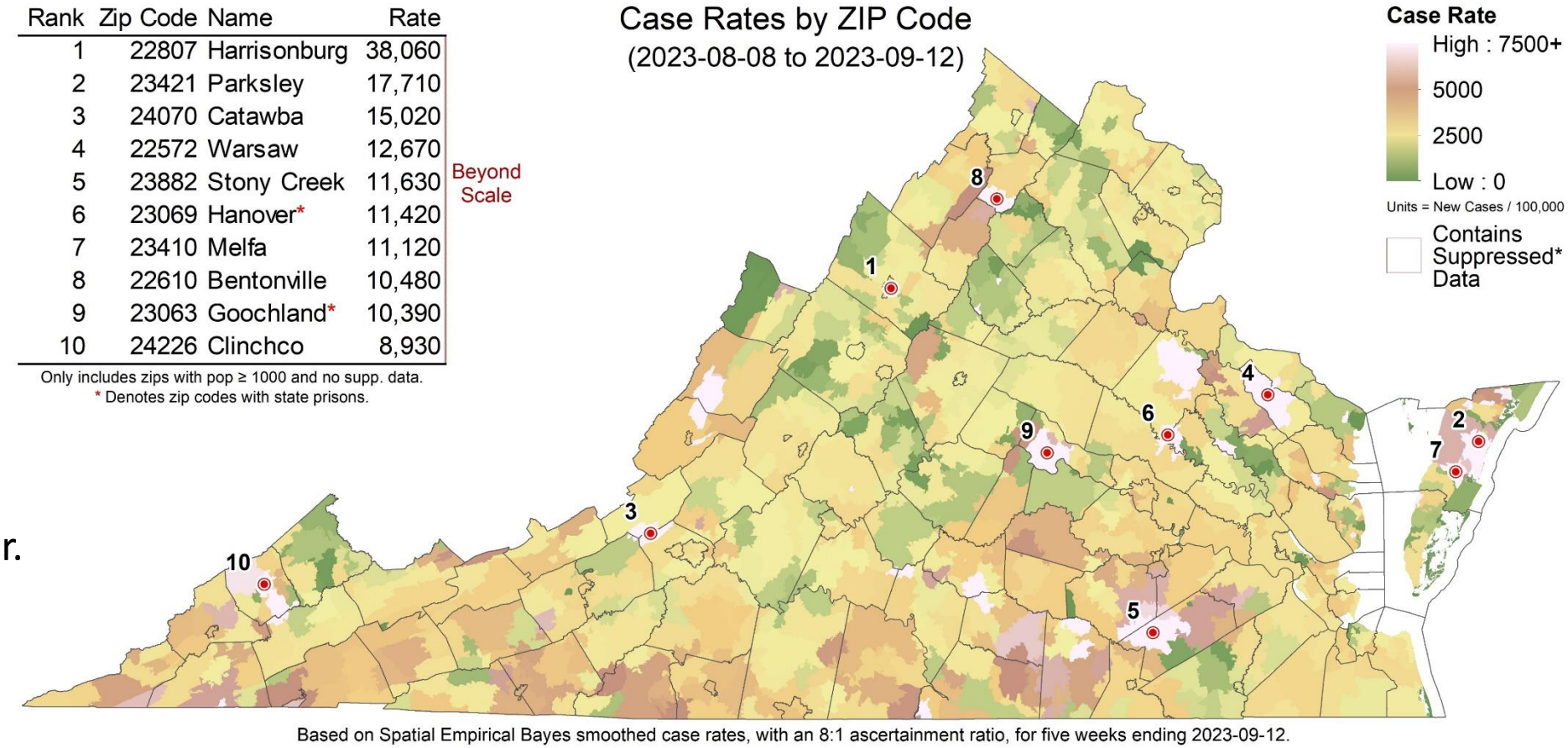
New cases per 100k in the last five weeks

- Statewide COVID-19 case rates have grown significantly since last report.
- Divide rates by five to calculate average weekly incidence.
- Harrisonburg data may be confounded by the changing population denominator as JMU started the new semester.
- Hanover and Goochland represent the prison-containing ZIP codes in this week's top 10.

Rank	Zip Code	Name	Rate
1	22807	Harrisonburg	38,060
2	23421	Parksley	17,710
3	24070	Catawba	15,020
4	22572	Warsaw	12,670
5	23882	Stony Creek	11,630
6	23069	Hanover*	11,420
7	23410	Melfa	11,120
8	22610	Bentonville	10,480
9	23063	Goochland*	10,390
10	24226	Clinchco	8,930

Beyond Scale

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



Based on Spatial Empirical Bayes smoothed case rates, with an 8:1 ascertainment ratio, for five weeks ending 2023-09-12.

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Risk of Exposure by Group Size and HCW prevalence

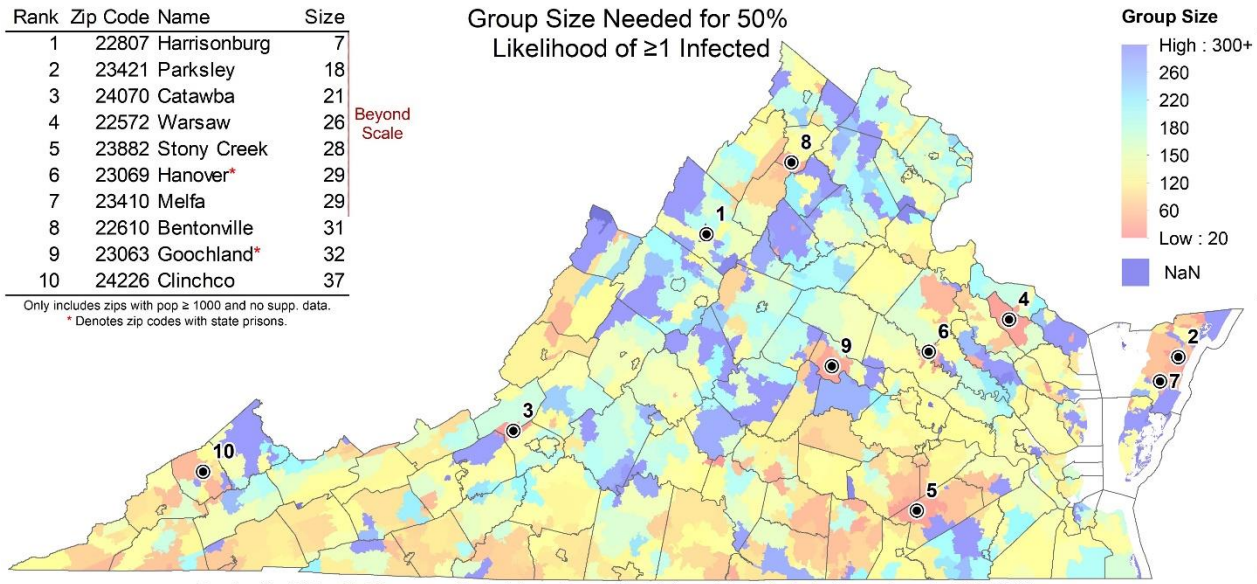
Case prevalence since last meeting (5 weeks) by zip code used to calculate risk of encountering someone infected in a gathering of randomly selected people

- **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 18 in Parksley, there is a 50% chance someone will be infected).
- **HCW ratio**: Case rate among health care workers (HCW) in the last five weeks using patient facing health care workers as the numerator / population's case prevalence. High HCW rates are found in orbit of Roanoke.

Rank	Zip Code	Name	Size
1	22807	Harrisonburg	7
2	23421	Parksley	18
3	24070	Catawba	21
4	22572	Warsaw	26
5	23882	Stony Creek	28
6	23069	Hanover*	29
7	23410	Melfa	29
8	22610	Bentonville	31
9	23063	Goochland*	32
10	24226	Clinchco	37

Beyond Scale

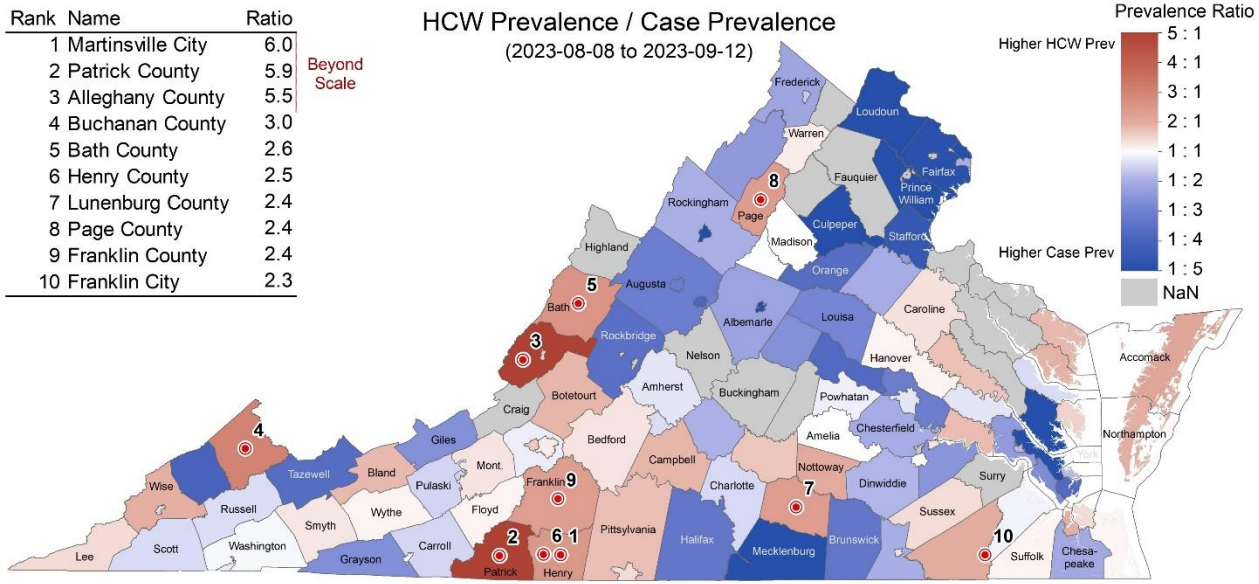
Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.



Based on Spatial Empirical Bayes smoothed point prevalence, with an 8:1 ascertainment ratio, for five weeks ending 2023-09-12.
Note: New color scale.

Rank	Name	Ratio
1	Martinsville City	6.0
2	Patrick County	5.9
3	Alleghany County	5.5
4	Buchanan County	3.0
5	Bath County	2.6
6	Henry County	2.5
7	Lunenburg County	2.4
8	Page County	2.4
9	Franklin County	2.4
10	Franklin City	2.3

Beyond Scale



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

Current Hot-Spots

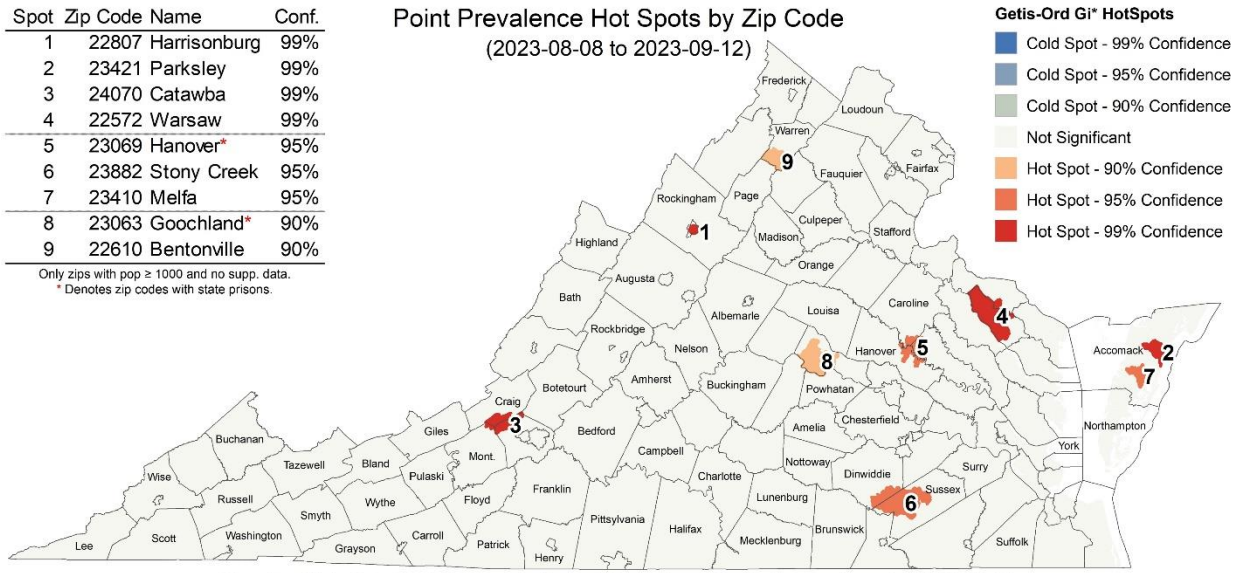
Case rates that are significantly different from neighboring areas or model projections

- **Spatial**: Getis-Ord Gi* based hot spots compare clusters of zip codes with five-week (since last meeting) case prevalence higher than nearby zip codes to identify larger areas with statistically significant deviations.
- **Temporal**: The cumulative case rate (per 100K) projected in March compared to those observed by county, which highlights temporal fluctuations that differ from the model's projections.
- Spatial hotspots were again found sporadically across Virginia. Model overpredictions were seen in Southside and Crater, and slightly in New River. Cases in Lenowisco, Pitt-Dan, and Eastern Shore were underpredicted.

Spatial Hotspots

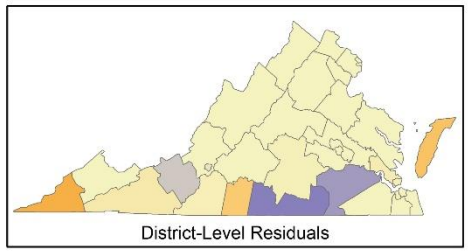
Spot	Zip Code	Name	Conf.
1	22807	Harrisonburg	99%
2	23421	Parksley	99%
3	24070	Catawba	99%
4	22572	Warsaw	99%
5	23069	Hanover*	95%
6	23882	Stony Creek	95%
7	23410	Melfa	95%
8	23063	Goochland*	90%
9	22610	Bentonville	90%

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



Based on Global Empirical Bayes smoothed point prevalence for the five weeks ending 2023-09-12.

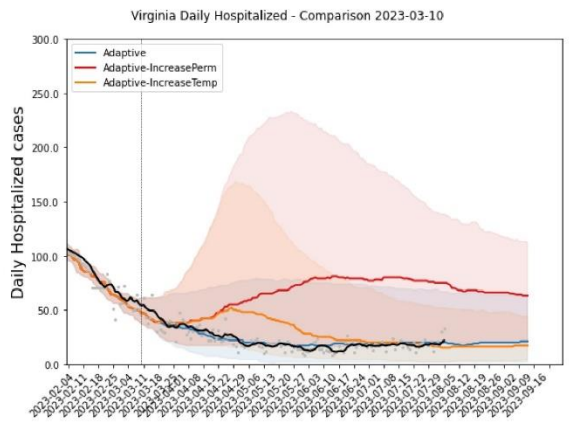
Clustered Temporal Hotspots



Health District Level Moran's I = 0.088994, Z-Score = 2.002757, P-Value = 0.045203
Residual Autocorrelation DETECTED

Hospitalization Scenario Trajectory Tracking

Which scenario from March 10 did each county track closest?

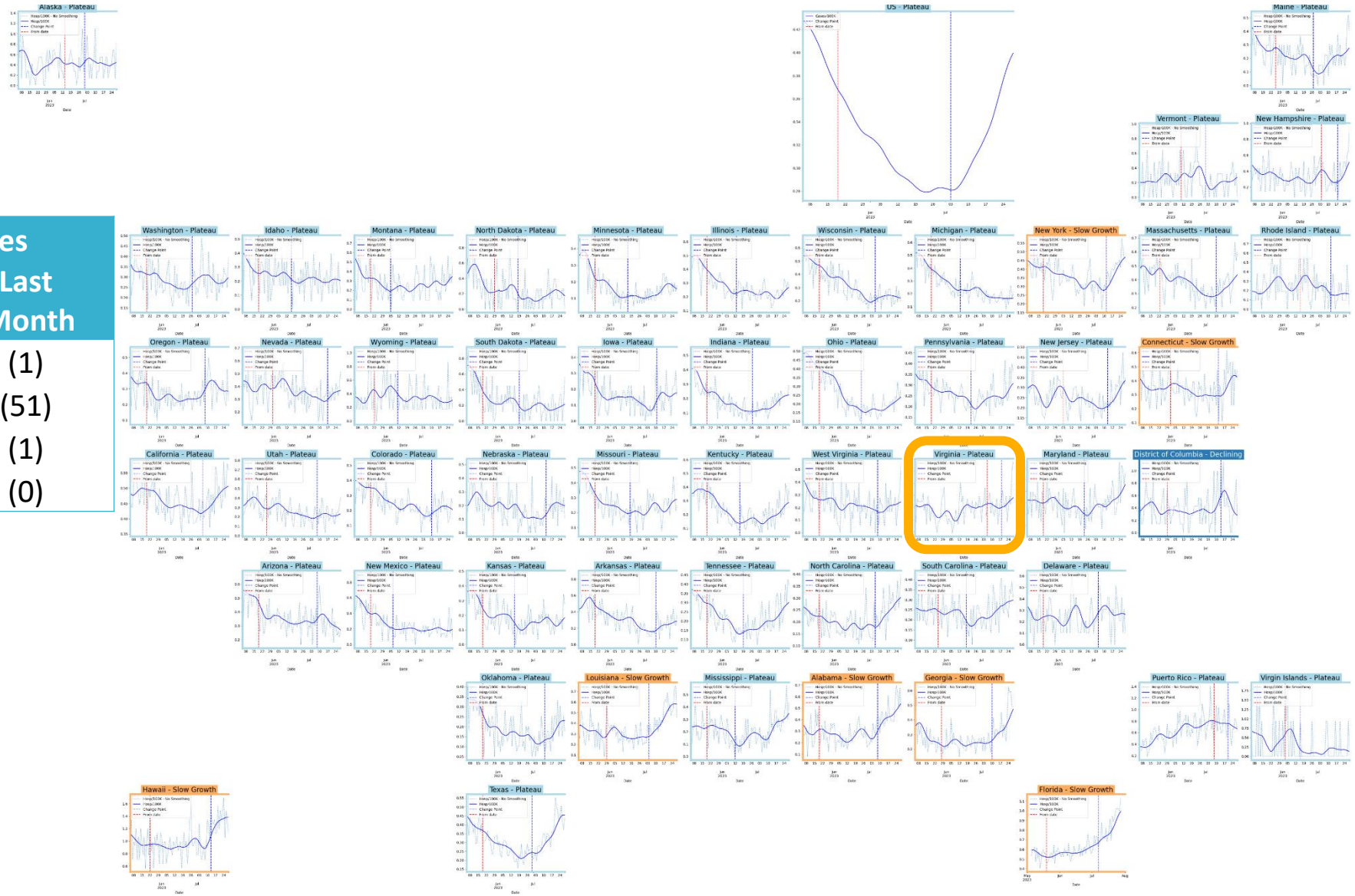


- A band of counties along the North Carolina boarder tracked Increased-Temp most strongly.
- The northern Shenandoah Valley and areas near Bristol are still tracking Increase-Perm.
- Other areas of the Commonwealth are unchanged, mostly tracking Adaptive or tied with Adaptive.

COVID-19 Broader Context

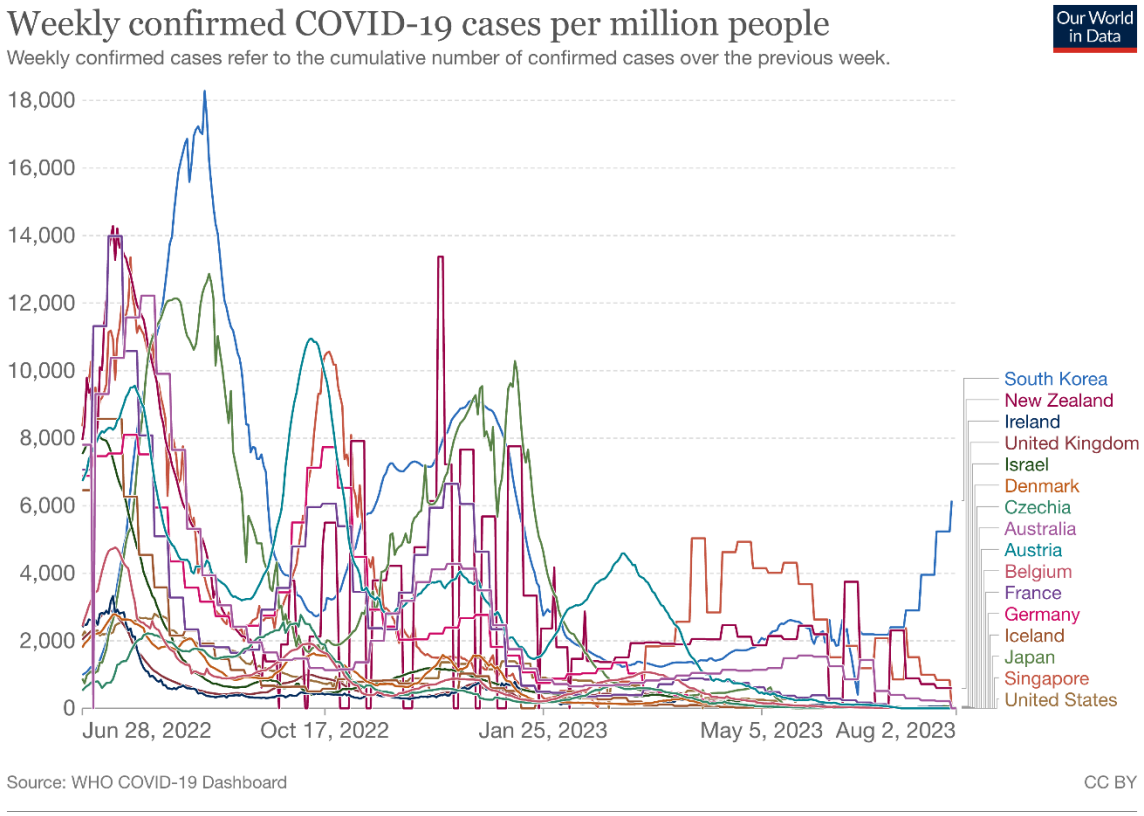
United States Hospitalizations

Status	Number of States	
	Current Week	Last Month
Declining	1	(1)
Plateau	45	(51)
Slow Growth	7	(1)
In Surge	0	(0)

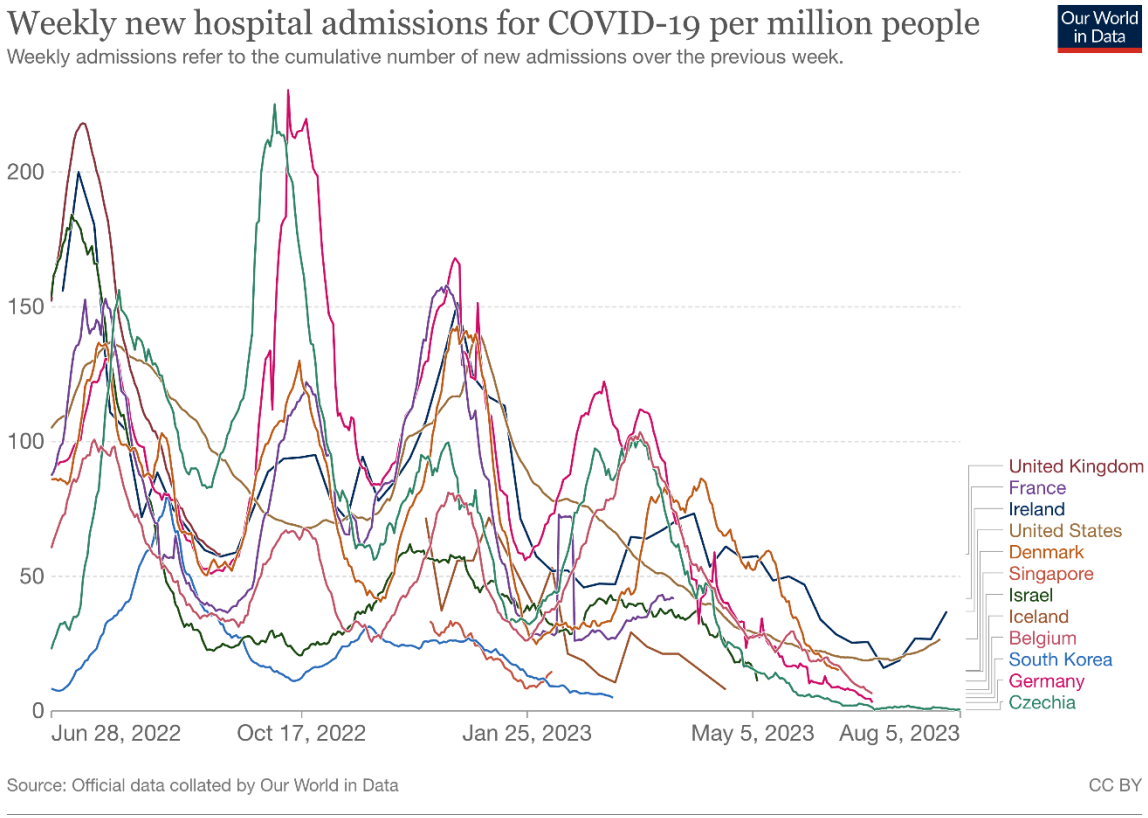


Around the World – Various trajectories

Confirmed cases



Hospitalizations



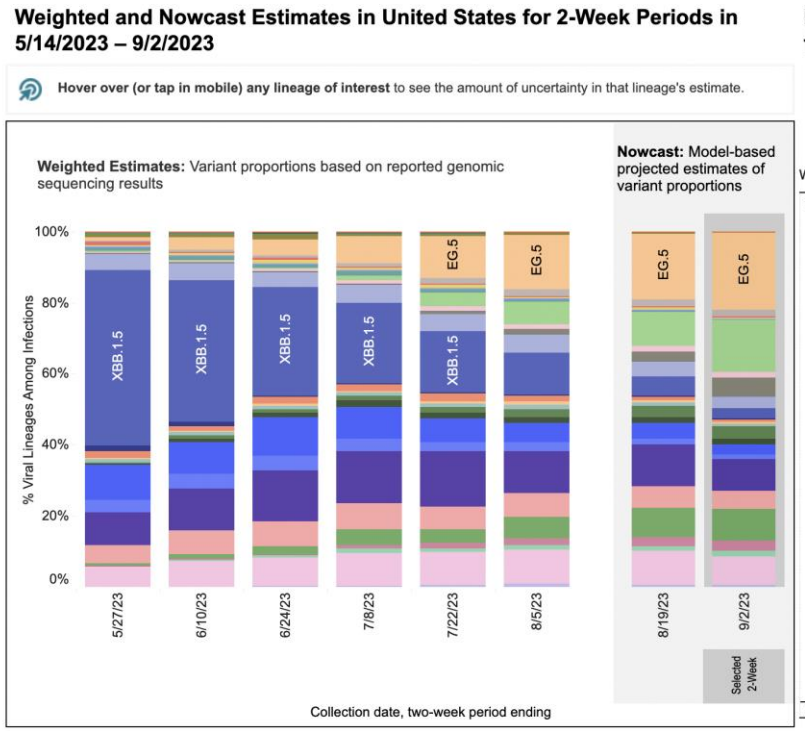
Our World in Data [Our World in Data]

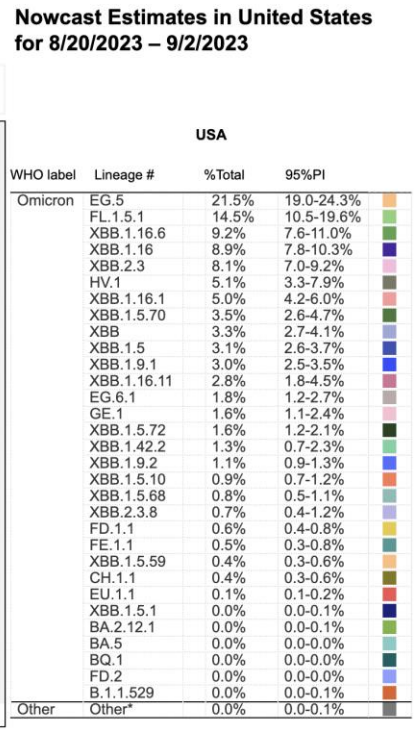
COVID-19 Genomic Update

SARS-CoV2 Variants of Concern

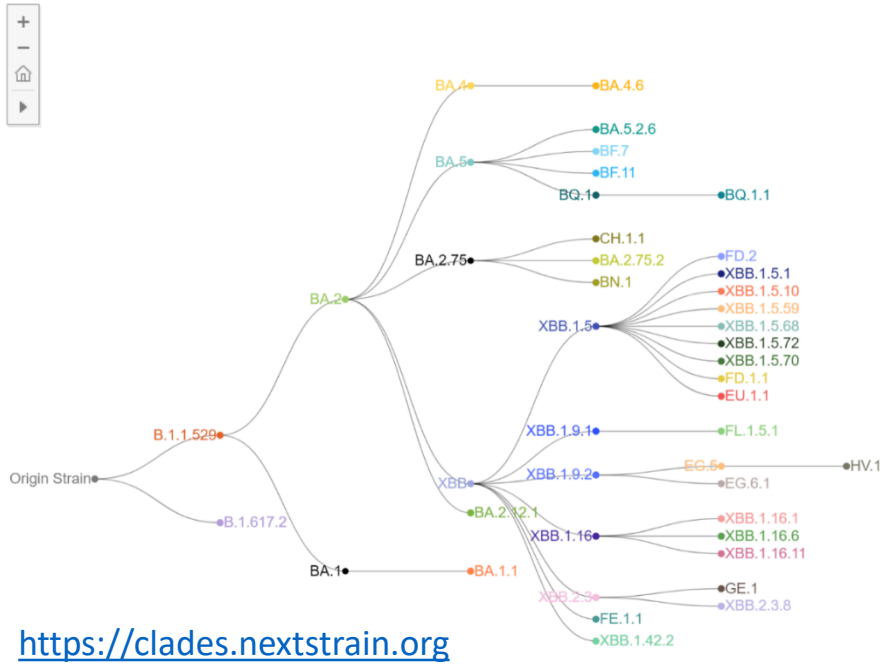
Emerging variants have potential to continue to alter the future trajectories of pandemic and have implications for future control

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





WHO label	Lineage #	%Total	95%PI
Omicron	EG.5	21.5%	19.0-24.3%
	FL.1.5.1	14.5%	10.5-19.6%
	XBB.1.16.6	9.2%	7.6-11.0%
	XBB.1.16	8.9%	7.8-10.3%
	XBB.2.3	8.1%	7.0-9.2%
	HV.1	5.1%	3.3-7.9%
	XBB.1.16.1	5.0%	4.2-6.0%
	XBB.1.5.70	3.5%	2.6-4.7%
	XBB	3.3%	2.7-4.1%
	XBB.1.5	3.1%	2.6-3.7%
	XBB.1.9.1	3.0%	2.5-3.5%
	XBB.1.16.11	2.8%	1.8-4.5%
	EG.6.1	1.8%	1.2-2.7%
	GE.1	1.6%	1.1-2.4%
	XBB.1.5.72	1.6%	1.2-2.1%
	XBB.1.42.2	1.3%	0.7-2.3%
	XBB.1.9.2	1.1%	0.9-1.3%
	XBB.1.5.10	0.9%	0.7-1.2%
	XBB.1.5.68	0.8%	0.5-1.1%
	XBB.2.3.8	0.7%	0.4-1.2%
	FD.1.1	0.6%	0.4-0.8%
	FE.1.1	0.5%	0.3-0.8%
	XBB.1.5.59	0.4%	0.3-0.6%
	CH.1.1	0.4%	0.3-0.6%
	EU.1.1	0.1%	0.1-0.2%
	XBB.1.5.1	0.0%	0.0-0.1%
	BA.2.12.1	0.0%	0.0-0.1%
	BA.5	0.0%	0.0-0.0%
	BQ.1	0.0%	0.0-0.0%
	FD.2	0.0%	0.0-0.0%
	B.1.1.529	0.0%	0.0-0.1%
Other	Other*	0.0%	0.0-0.1%



https://clades.nextstrain.org

Omicron Updates*

- USA level variant estimates are shown
- HHS Regions insufficient data for NowCast
- New lineage EG.5 up to 21.5% from 20%
- New lineage FL.1.5.1 up to 14.5% from 13.3%
- Most circulating variants are sublineages of XBB.1.9, XBB.1.16, and XBB.1.5

*percentages are CDC NowCast Estimates

SARS-CoV2 Variants of Concern

BA.2.86 detected
Ohio wastewater
NYC wastewater
VA traveler surveillance

SARS CoV-2 Sublineage BA.2.86 has potential to be a significant variant

- **Viral Genomics**: BA.2.86 is a newly designated variant of SARS-CoV-2 that has a number of additional mutations compared with previously detected Omicron variants. Specifically, the genetic sequence of BA.2.86 has changes that represent over 30 amino acid differences compared with BA.2, which was the dominant Omicron lineage in early 2022. BA.2.86 also has >35 amino acid changes compared with the more recently circulating XBB.1.5, which was dominant through most of 2023. **This number of genetic differences is roughly of the same magnitude as seen between the initial Omicron variant (BA.1) and previous variants, such as Delta (B.1.617.2).**

- **Immune Impacts**: The large number of mutations in this variant raises concerns of greater escape from existing immunity from vaccines and previous infections compared with other recent variants. For example, one analysis of mutations suggests the difference may be as large as or greater than that between BA.2 and XBB.1.5, which circulated nearly a year apart. However, virus samples are not yet broadly available for more reliable laboratory testing of antibodies, and it is too soon to know the real-world impacts on immunity. **Nearly all the U.S. population has antibodies to SARS-CoV-2 from vaccination, previous infection, or both, and it is likely that these antibodies will continue to provide some protection against severe disease from this variant. This is an area of ongoing scientific investigation.**

- **Therapeutics**: **Examination of the mutation profile of BA.2.86 suggests that currently available treatments like Paxlovid, Veklury, and Lagevrio will be effective against this variant.** Monitoring is ongoing and CDC will update this document as human data on the impact of this variant on therapeutics become available.

https://www.cdc.gov/respiratory-viruses/whats-new/covid-19-variant.html

Likely effects of mutations relative to BA.2

These are **only estimates** of mutation effects from deep mutational scanning experiments.

- **ins16MPLF**: antibody escape (NTD supersite)
- R21T
- S50L
- del69-70
- V127F
- **delY144**: antibody escape (NTD supersite)
- **F157S**: antibody escape (NTD supersite)
- **R158G**: antibody escape (NTD supersite)
- delN211
- L212I
- L216F
- **H245N**: antibody escape (NTD supersite)
- **A264D**: antibody escape (NTD supersite)
- I332V
- D339H
- **K356T**: antibody escape, adds N-glycosylation site
- **R403K**: improves ACE2 affinity, antibody escape
- **V445H**: antibody escape
- **G446S**: antibody escape
- **N450D**: antibody escape
- **L452W**: antibody escape
- **N460K**: improves ACE2 affinity, antibody escape
- N481K
- **delV483**: reduces ACE2 affinity, antibody escape
- **A484K**: antibody escape
- **F486P**: reduces ACE2 affinity, antibody escape
- **R493Q**: improves ACE2 affinity
- E554K
- A570V
- P621S
- I670V*
- H681R
- S939F
- **P1143L**: increases spike-mediated entry in cell culture

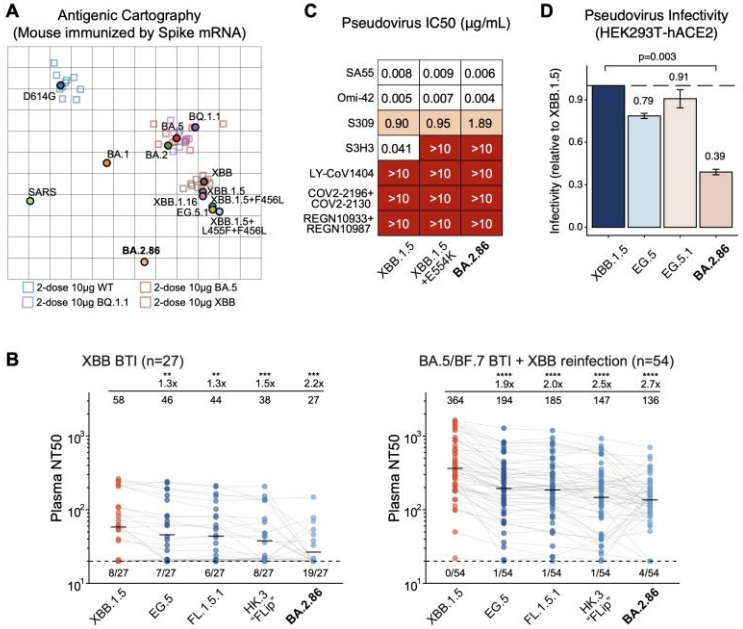
Estimates of effects of mutations from RBD deep mutational scanning by Tyler Starr, full-spike deep mutational scanning of BA.2 and XBB.1.5 by Bernadeta Dadonaite (Bloom lab), the Bloom lab RBD escape calculator informed by data from Yunlong Cao, and definition of the NTD supersite by Matthew McCallum & David Veesler. Experiments were performed in various genetic backgrounds and so there could be unmodeled epistasis. The * indicates mutations only in some sequences of the new variant.

https://slides.com/jbloom/new_2nd_gen_ba2_variant#/5

SARS-CoV2 Variants of Concern

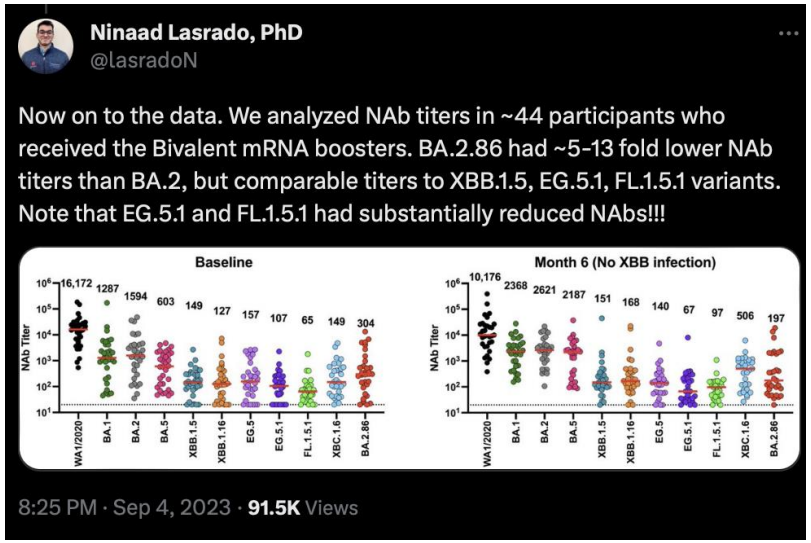
SARS CoV-2 Sublineage BA.2.86 additional studies indicate mixed bag on baseline infectivity and immune evasion, hope for vax based immunity

Low infectivity in some cell lines and high infectivity in others

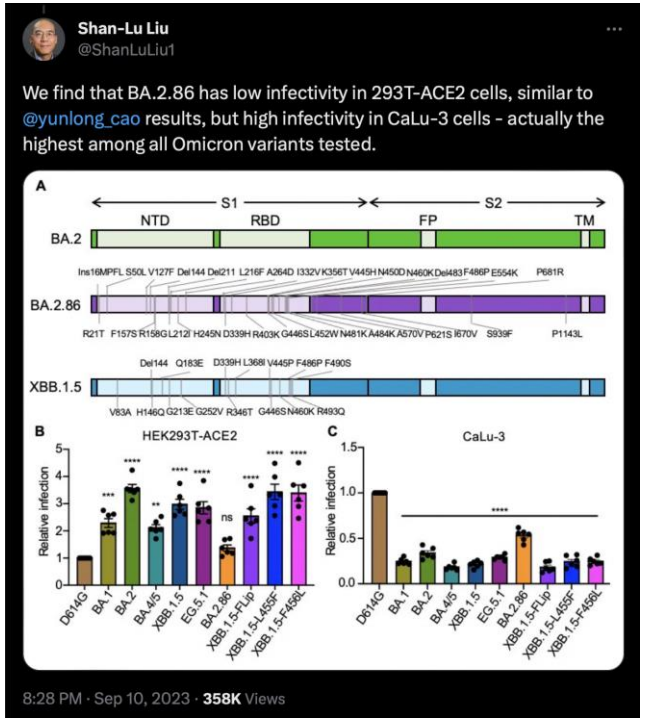


In sum, it appears that BA.2.86 has traded its infectivity for higher immune evasion during long-term host-viral evolution.

https://www.biorxiv.org/content/10.1101/2023.09.01.555815v1.full.pdf



https://twitter.com/lasradoN/status/1698854743483863318
https://twitter.com/BarouchLab/status/1698850719959544271



https://twitter.com/ShanLuLiu1/status/1701029792571592936

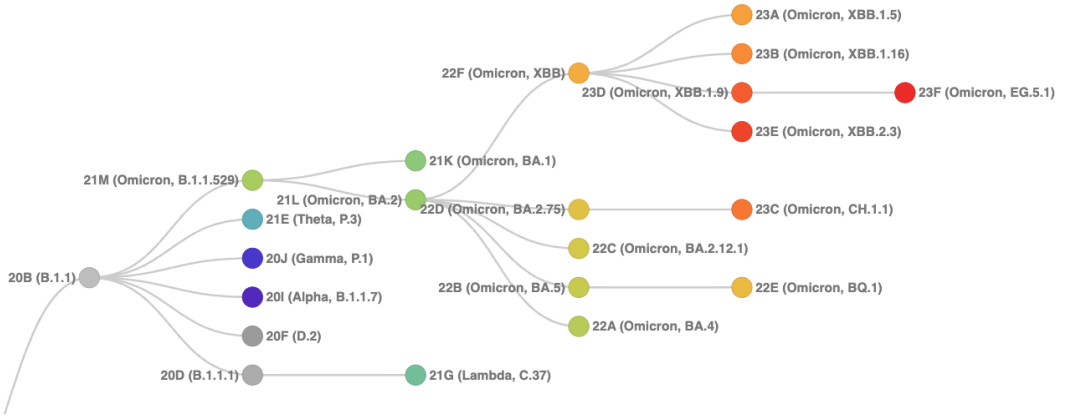
BA.2.86 evades immune response more than BA.2, but similar levels to current circulating variants.

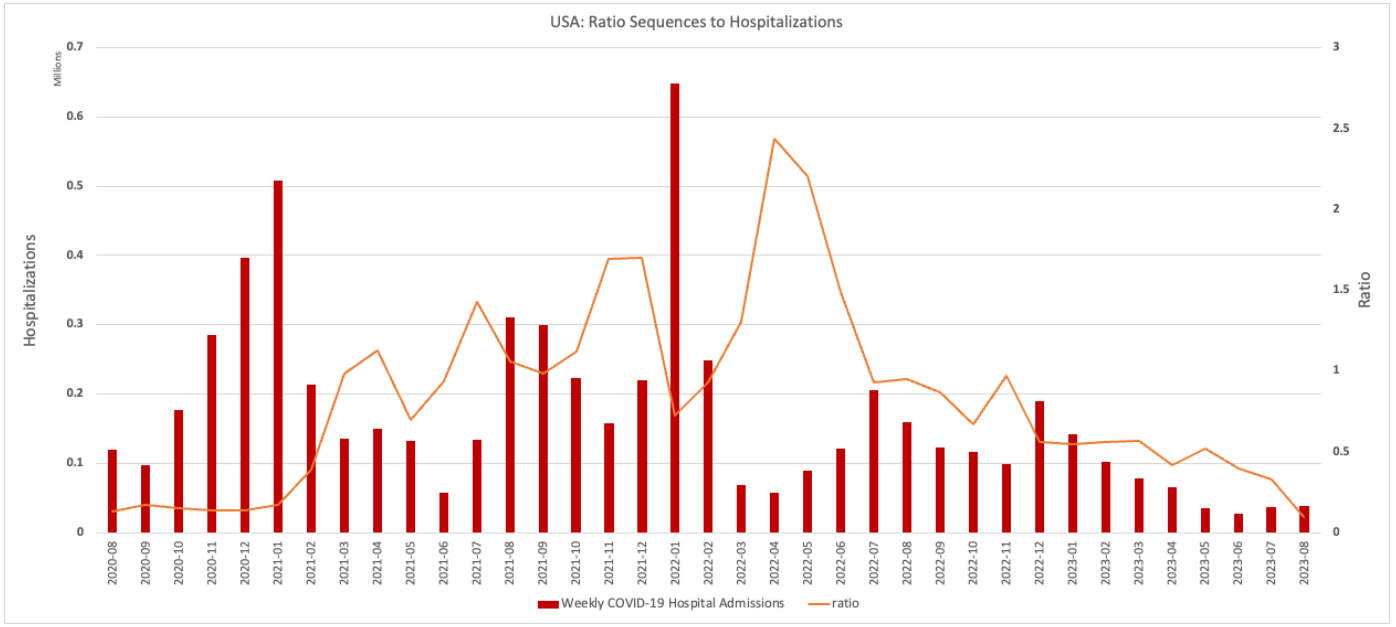
Responses are raised for those with XBB infection, suggesting that XBB.1.5 based vaccines will provide reasonable cross-immunity against BA.2.86

SARS-CoV2 Sequencing

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

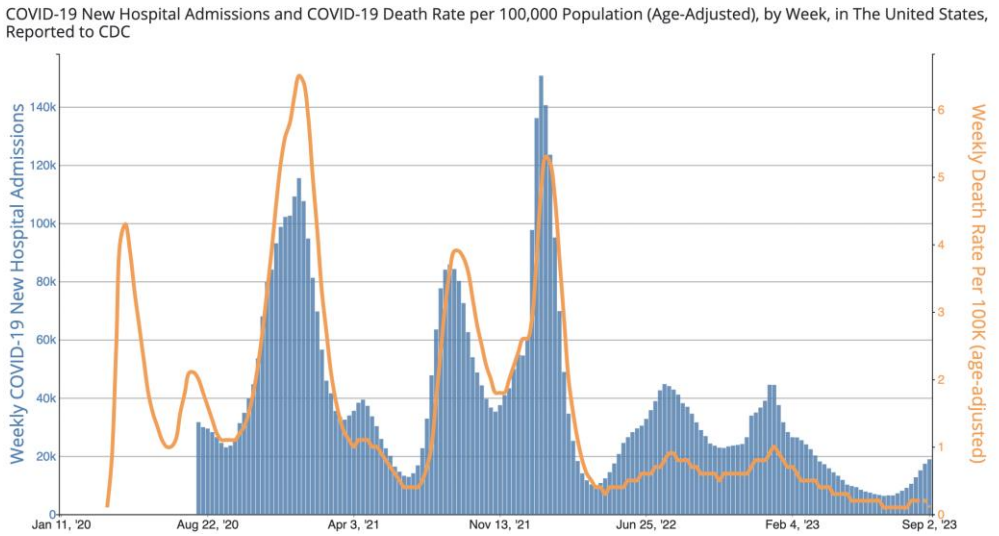
- Current proportion of cases being sequenced is on a downward trend nationally.
- Leveraging additional resources such as wastewater sequencing and adopting into existing infrastructure will be an important supplement





United States

https://clades.nextstrain.org



https://cov-spectrum.org/explore/United%20States/AllSamples/Past6M/sequencing-coverage

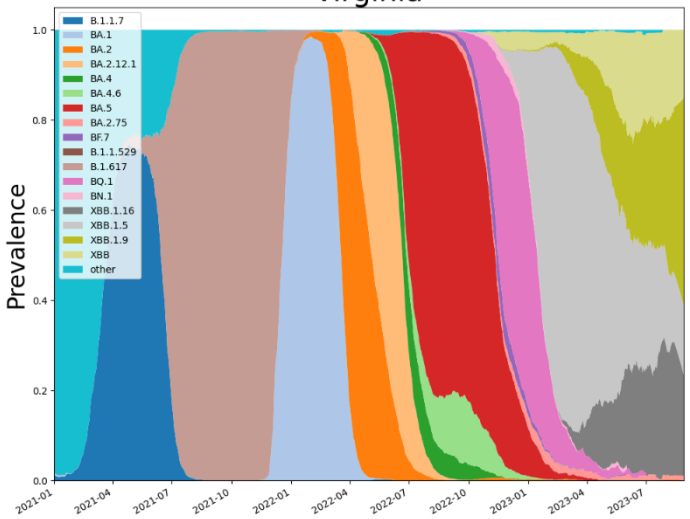
https://covid.cdc.gov/covid-data-tracker/#trends_weeklyhospitaladmissions_weeklydeathrateaa_00

SARS-CoV2 Omicron Sub-Variants

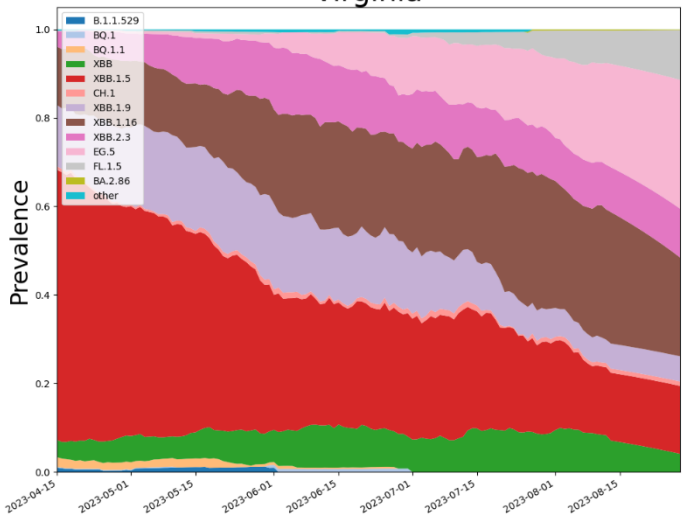
covSPECTRUM
Enabled by data from GISAID

As detected in whole Genomes in public repositories

Virginia

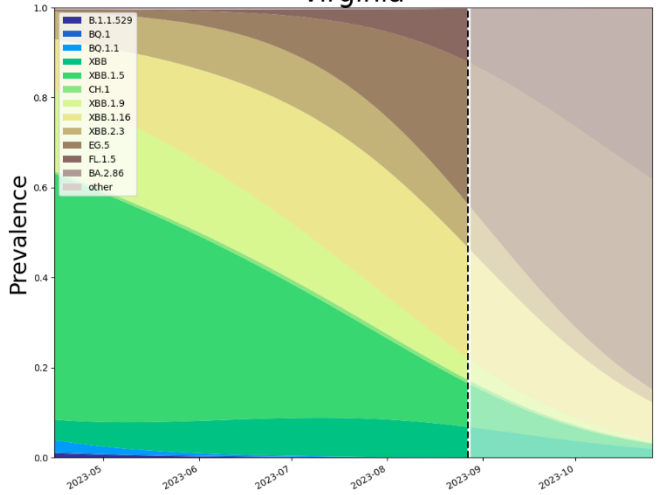


Virginia

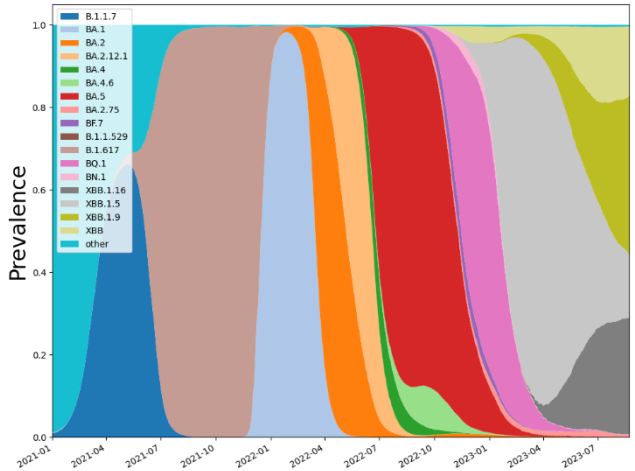


VoC Polynomial Fit Projections

Virginia



United States



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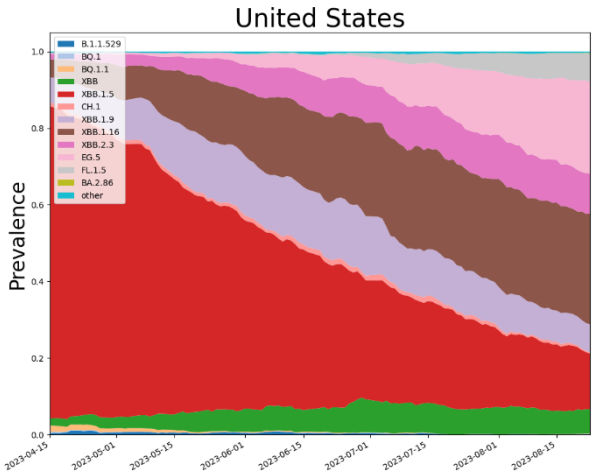
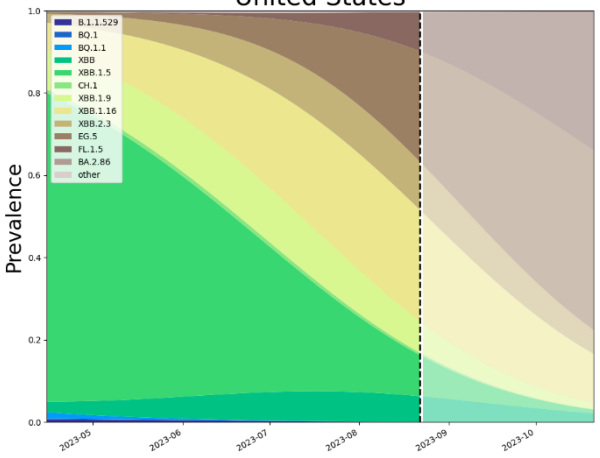


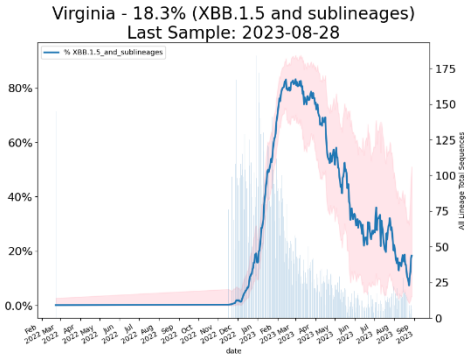
United States



Note: Everything from dotted line forward is a projection.

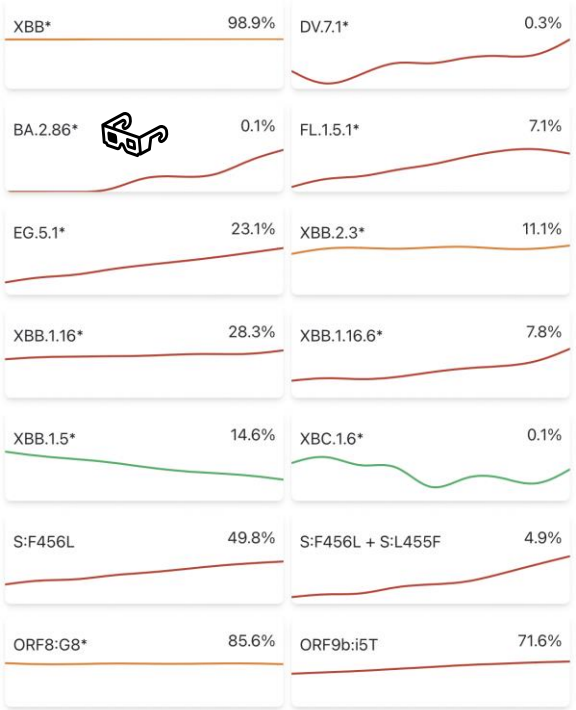
BIOCOMPLEXITY INSTITUTE

SARS-CoV2 Omicron Sub-Variants



[COV-spectrum](#)

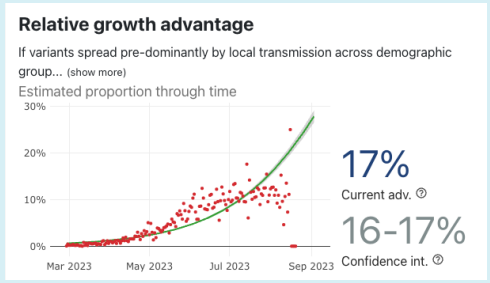
"Editor's choice"
Variants to watch

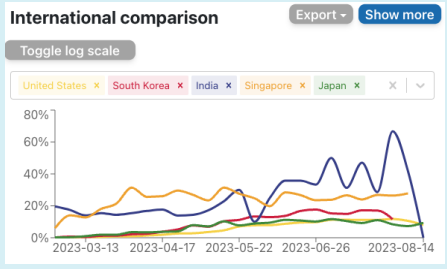


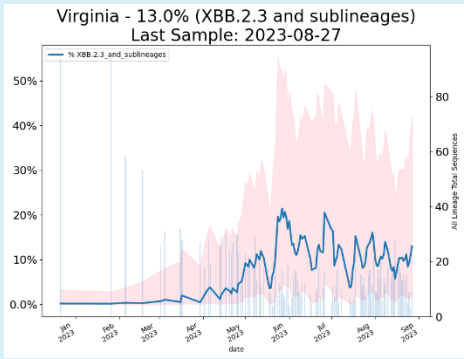
Enabled by data from GISAID

15-Sep-23

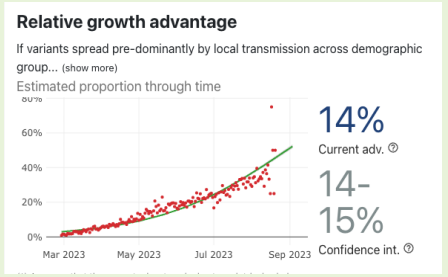
XBB.2.3*

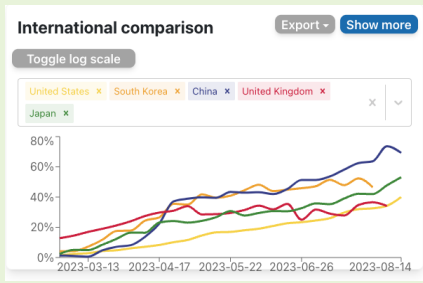


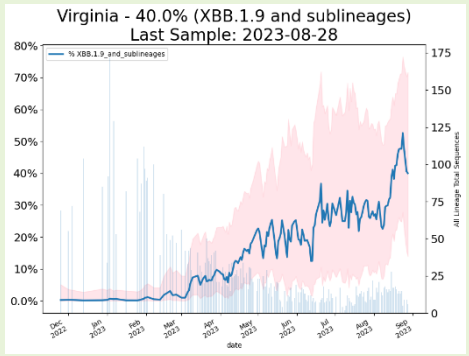




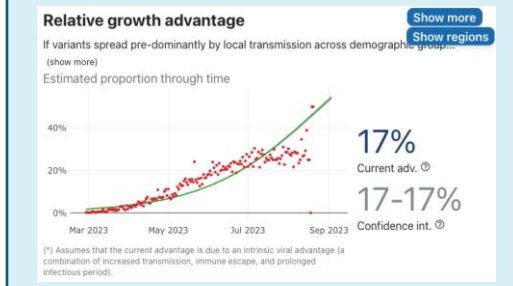
XBB.1.9*

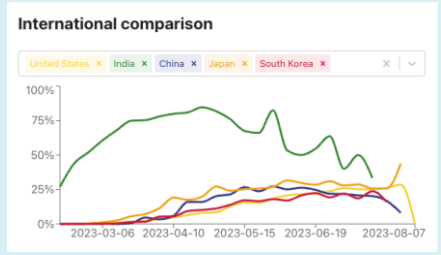


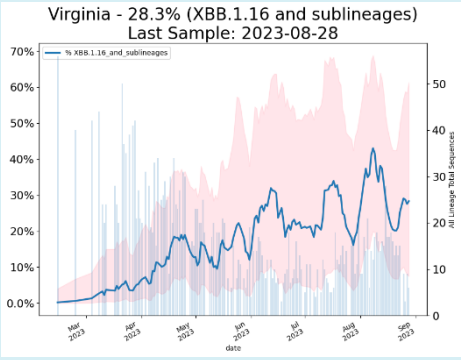




XBB.1.16*

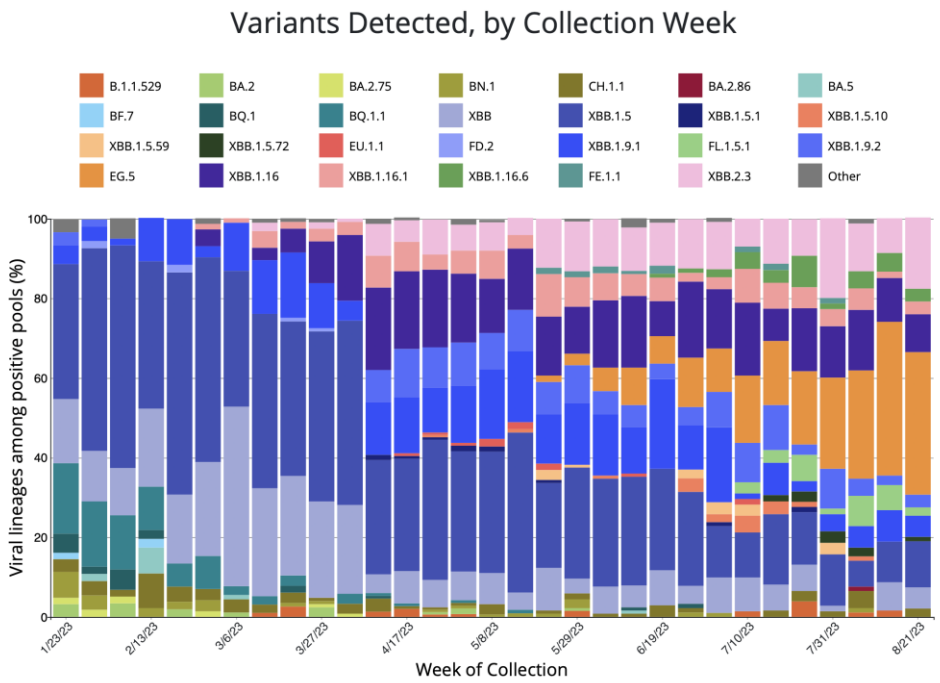


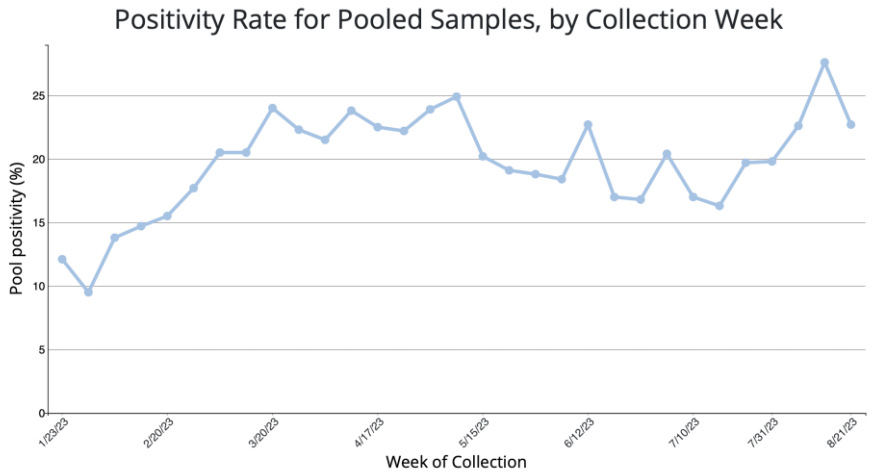


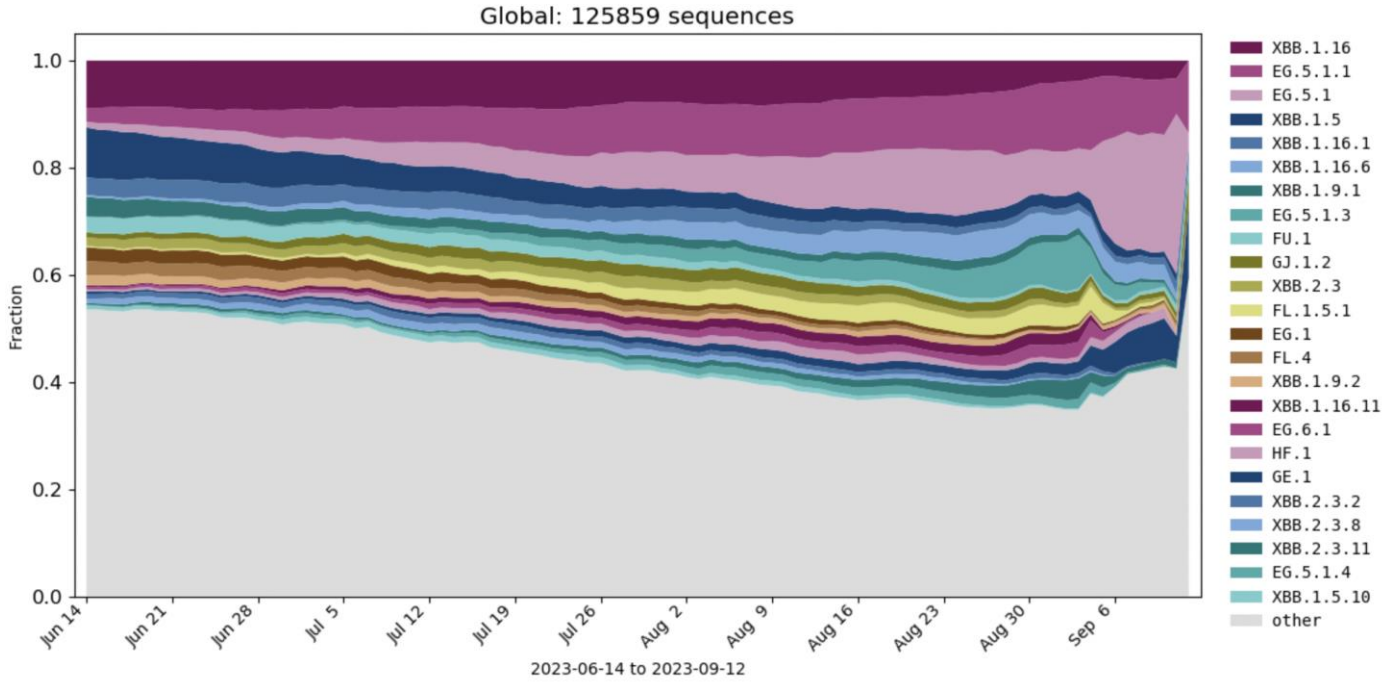


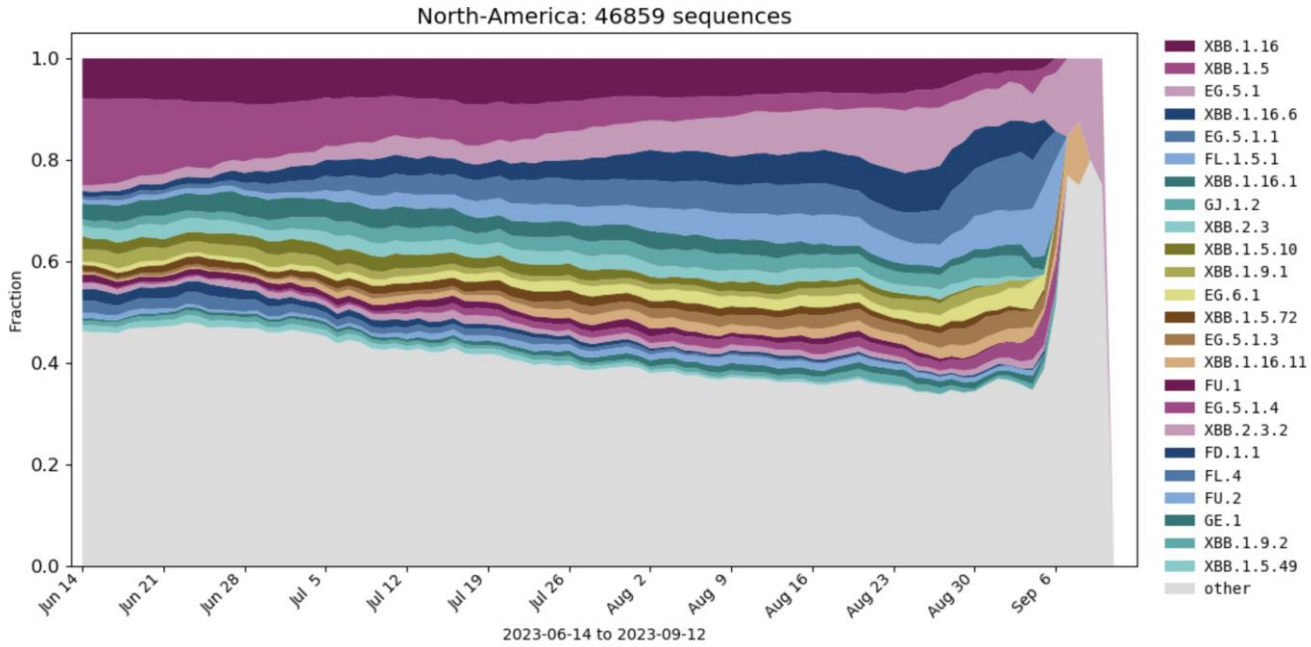
Global SARS-CoV2 Variant Status

Traveller Surveillance









https://cov.lanl.gov/components/sequence/COV/sparks.comp
https://covid.cdc.gov/covid-data-tracker/#traveler-genomic-surveillance

Pandemic pubs – Variant emergence - Alpha

[19 August 2021]

Goal:

- Exploring the heterogeneous spreading of an emerging variant (B.1.1.7 from Kent, UK) through phylogeography of ~17,000 genome sequences
- Correlation with interregional mobility and ongoing non-pharmaceutical interventions

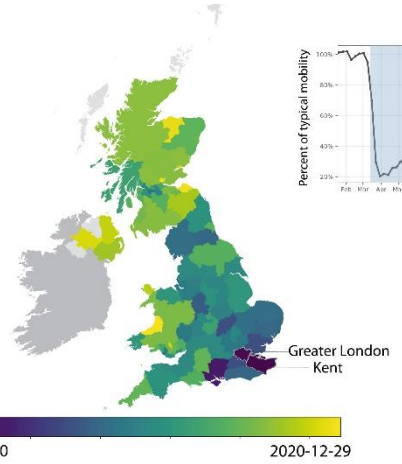
Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence

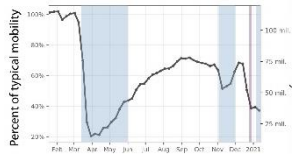
MORITZ U. G. KRAEMER, VERITY HILL, [...], AND OLIVER G. PYBUS +22 authors Authors Info & Affiliations

SCIENCE • 19 Aug 2021 • Vol 373, Issue 6557 • pp. 889-895 • DOI: 10.1126/science.abj0113

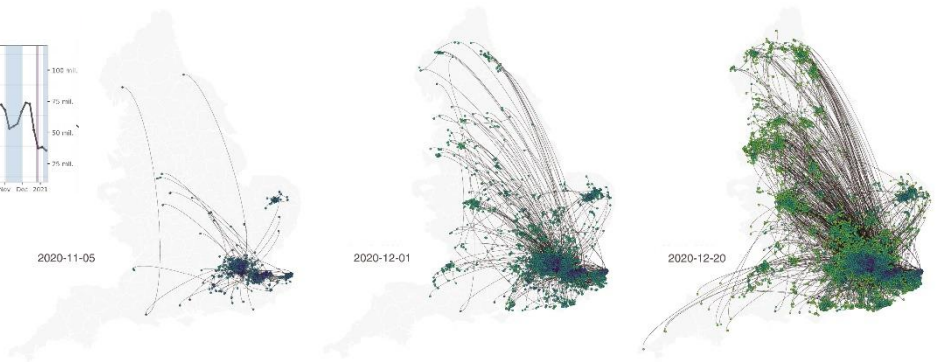
https://www.science.org/doi/full/10.1126/science.abj0113

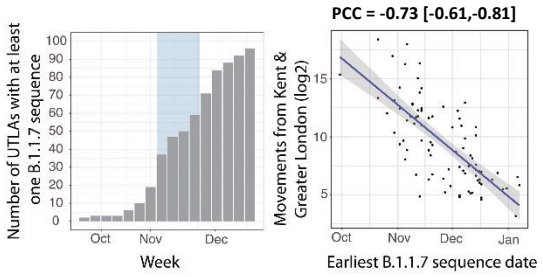
High correlation in earliest arrival time and total mobility from source



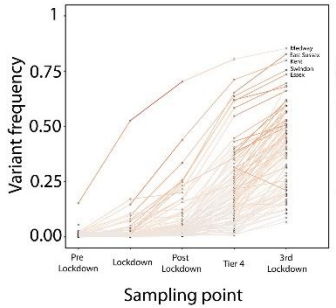


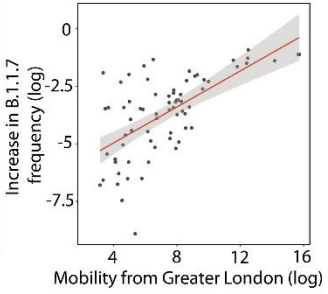
Different phases of spatial dynamics

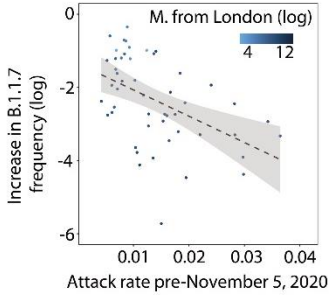




Increase in frequency of B.1.1.7 positive correlated with mobility from source; Negatively correlated with prior attack rate;







Findings

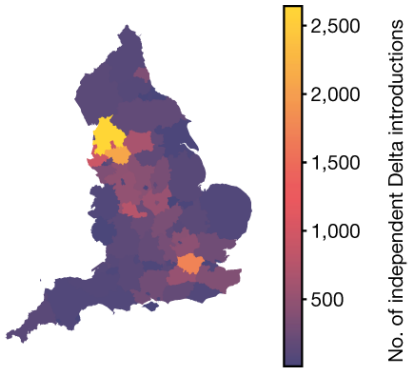
- External mobility responsible for seeding as well as increased growth rate
- Early long-distance dispersal was limited by lockdowns; Could not establish role of NPI in later lineage exportations
- Prior infection attack rate (residual immunity) found to impact growth rate

Pandemic pubs – Variant importation - Delta

[11 August 2022]

Goal:

- Exploring various factors underlying the importation and subsequent spread of Delta variant
- Study involving ~53K genomes in England, ~93K genomes from rest of the world



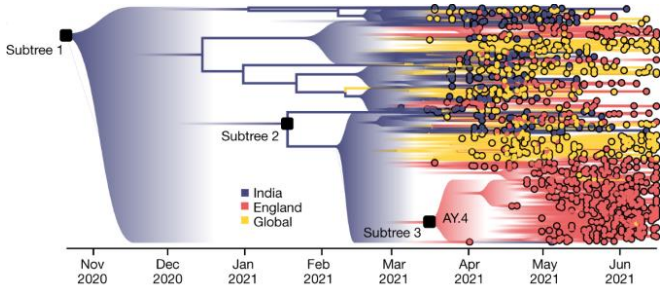
Article | Open Access | Published: 11 August 2022

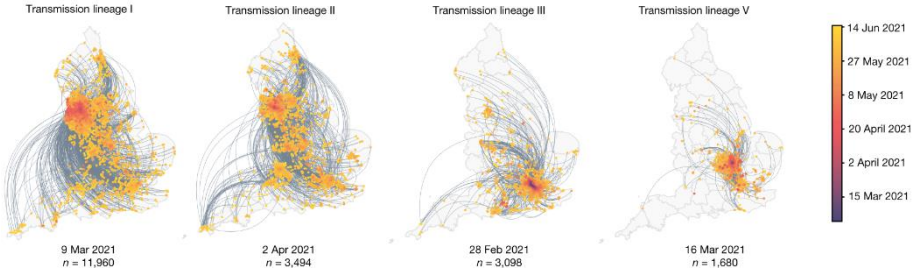
Context-specific emergence and growth of the SARS-CoV-2 Delta variant

John T. McCrone, Verity Hill, Sumali Bajaj, Rosario Evans Pena, Ben C. Lambert, Rhys Inward, Samir Bhatt, Erik Volz, Christopher Ruis, Simon Dellicour, Guy Baele, Alexander E. Zarebski, Adam Sadilek, Neo Wu, Aaron Schneider, Xiang Ji, Jayna Raghwani, Ben Jackson, Rachel Colquhoun, Áine O'Toole, Thomas P. Peacock, Kate Twohig, Simon Thelwall, Gavin Dabrera, The COVID-19 Genomics UK (COG-UK) Consortium, … Moritz U. G. Kraemer + Show authors

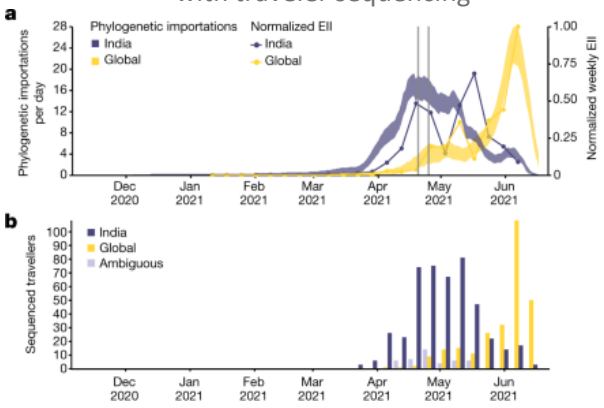
Nature **610**, 154–160 (2022) | Cite this article

https://www.nature.com/articles/s41586-022-05200-3

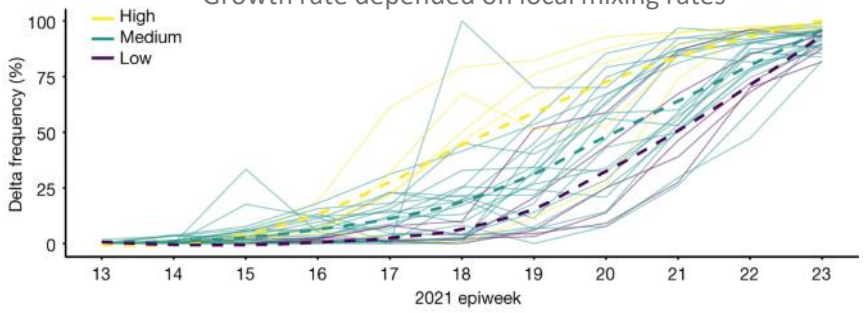




Estimated phylogenetic importations line up with traveler sequencing



Growth rate depended on local mixing rates



Findings

- Delta was introduced more than 1000 times and spread due to NPI relaxations
- Inter-regional travel led to multiple (up to 2000) lineage introductions from elsewhere
- Increased levels of local mixing were associated with faster relative spread of Delta

Pandemic pubs – Variant importation - Omicron

[20 July 2023]

Genomic assessment of invasion dynamics of SARS-CoV-2 Omicron BA.1

JOSEPH L.-H. TSUI, JOHN T. MCCRONE, BEN LAMBERT, SUMALI BAJAJ, RHYS P. D. INWARD, PAOLO BOSETTI, ROSARIO EVANS PENA, HOURIIYAH TEGALLY, VERITY HILL, [...], AND MORITZ U. G. KRAEMER +31 authors Authors Info & Affiliations

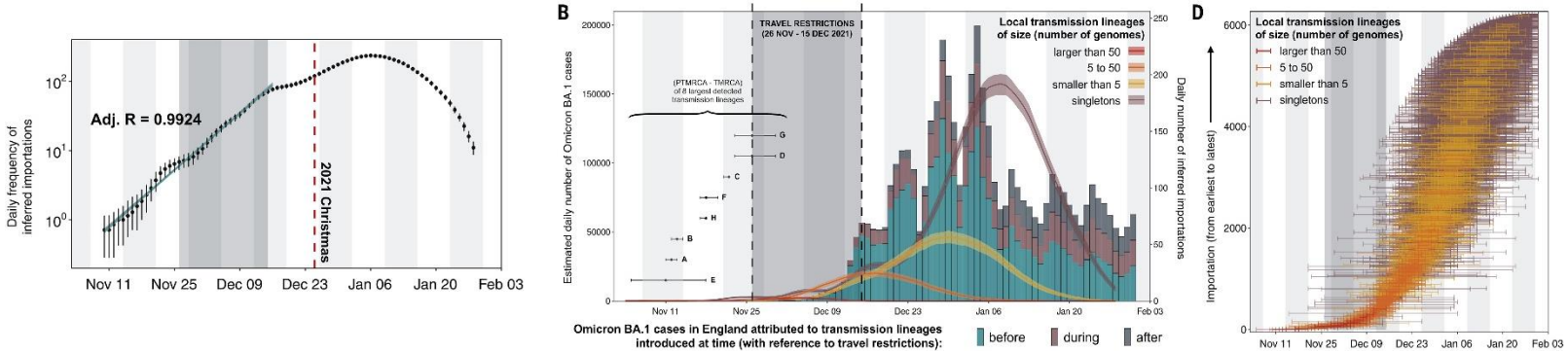
SCIENCE • 20 Jul 2023 • Vol 381, Issue 6655 • pp. 336-343 • DOI: 10.1126/science.adg6605

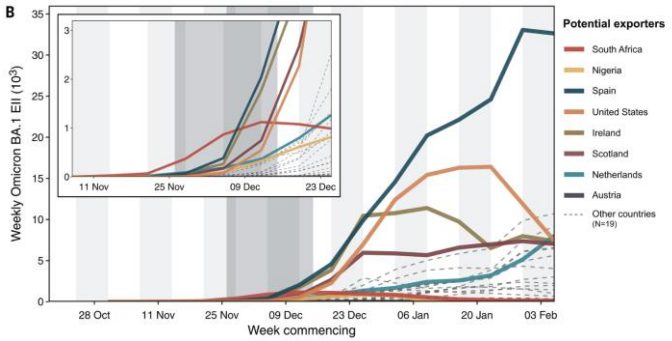
https://www.science.org/doi/10.1126/science.adg6605

Goal:

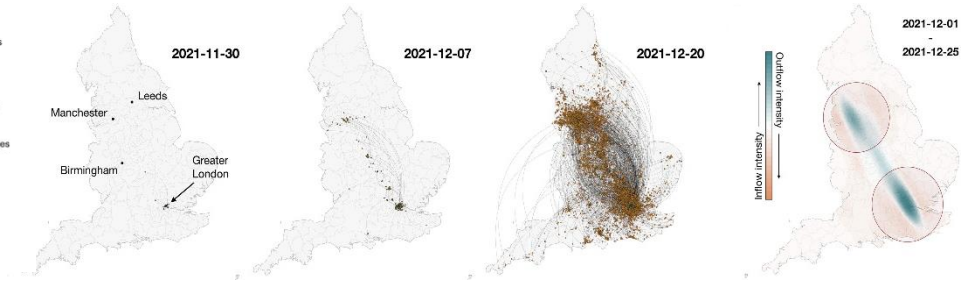
- Studying the importation and spread dynamics of Omicron BA.1 variant with immune evasion using ~115K genomes
- Understanding the role of international restrictions and multi-scale nature of variant spread

Most critical importations occurred before travel restrictions





Different stages of importation



Findings

- More than 6000 introductions of Omicron into England; locally transmitting before first report by SA
- Importation continued despite targeted travel restriction; However, most local cases mostly caused by early importations.
- Two stage process of initiation and dispersal of variants using human geography and hierarchical travel network

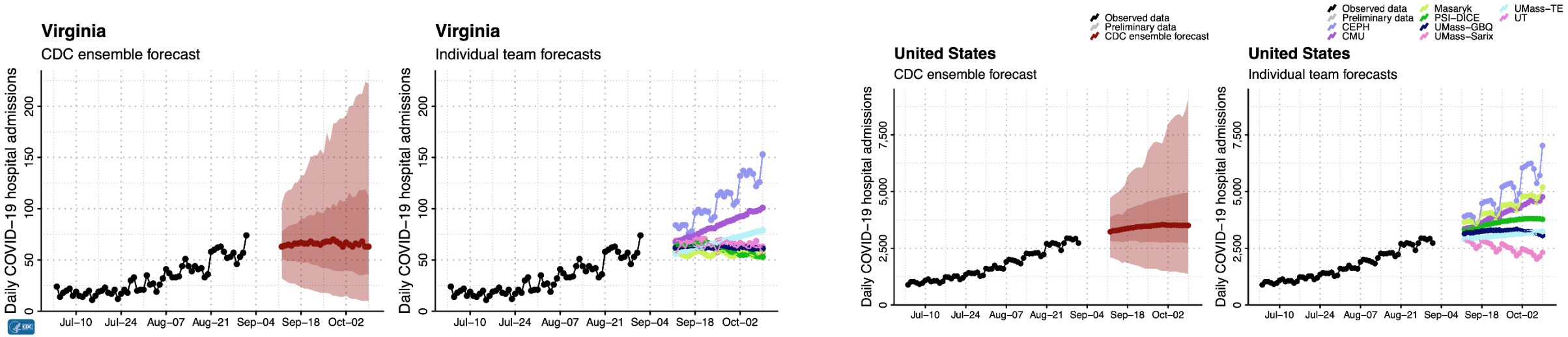
National Modeling Hub Updates

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)



Scenario Modeling Hub – Influenza (Round 4)

Collaboration of multiple academic teams to provide national and state-by-state level projections for 6 aligned scenarios

- Round just recently completed
- Round Designed to explore a season dominated by H3 vs. H1 with different levels of seasonal flu vaccination coverage

Scenario Dimensions:

Influenza type A/H3 vs. A/H1:

- H3 higher hospitalization rates with vax efficacy weaker in older groups

- H1 lower hospitalization rates and efficacy even across age groups

Vaccination levels (compared to 2021-22 season):

Low (20% less) vs.
Business as Usual (same) vs.
Higher (20% more)

https://fluscenariomodelinghub.org/viz.html

	Season dominated by influenza A/H3N2, indexed on age distribution of 2017-18 season. **VE = 40% against medically attended illnesses and hospitalizations, VE drops in older age groups**	**Season dominated by influenza A/H1N1, indexed on age distribution of 2019-20 season.** **VE = 40% against medically attended illnesses and hospitalizations, similar VE across all age groups**
Higher than Usual Vaccine Coverage • Vaccine coverage is **20% higher than in the 2021-22** flu season in all age groups and jurisdictions. (20% is a relative change, ie a 50% coverage for age group *a* and jurisdiction *j* in 2021-22 translates to a 50%*1.20=60% coverage for 2023-24). Overall, the US coverage is about 60% in this scenario.	**Scenario A**	**Scenario B**
Business as Usual Vaccine Coverage • Vaccine coverage is **the same as in the 2021-22** flu season in all age groups and jurisdictions. Overall, the US coverage is about 50% in this scenario.	**Scenario C**	**Scenario D**
Low Vaccine Coverage • Vaccine coverage is **20% lower than in the 2021-22** flu season in all age groups and jurisdictions. Overall, the US coverage is about 40% in this scenario.	**Scenario E**	**Scenario F**

Scenario Modeling Hub – COVID-19 (Round 17)

Collaboration of multiple academic teams to provide national and state-by-state level projections for 6 aligned scenarios

https://covid19scenariomodelinghub.org/viz.html

- Preliminary Results
- Round Designed to explore different seasonal vaccination levels and the impact of Immune Escape

Scenario Dimensions:

Immune Escape (IE):

Slower IE (20%/yr) vs.
Faster IE (50%/yr)

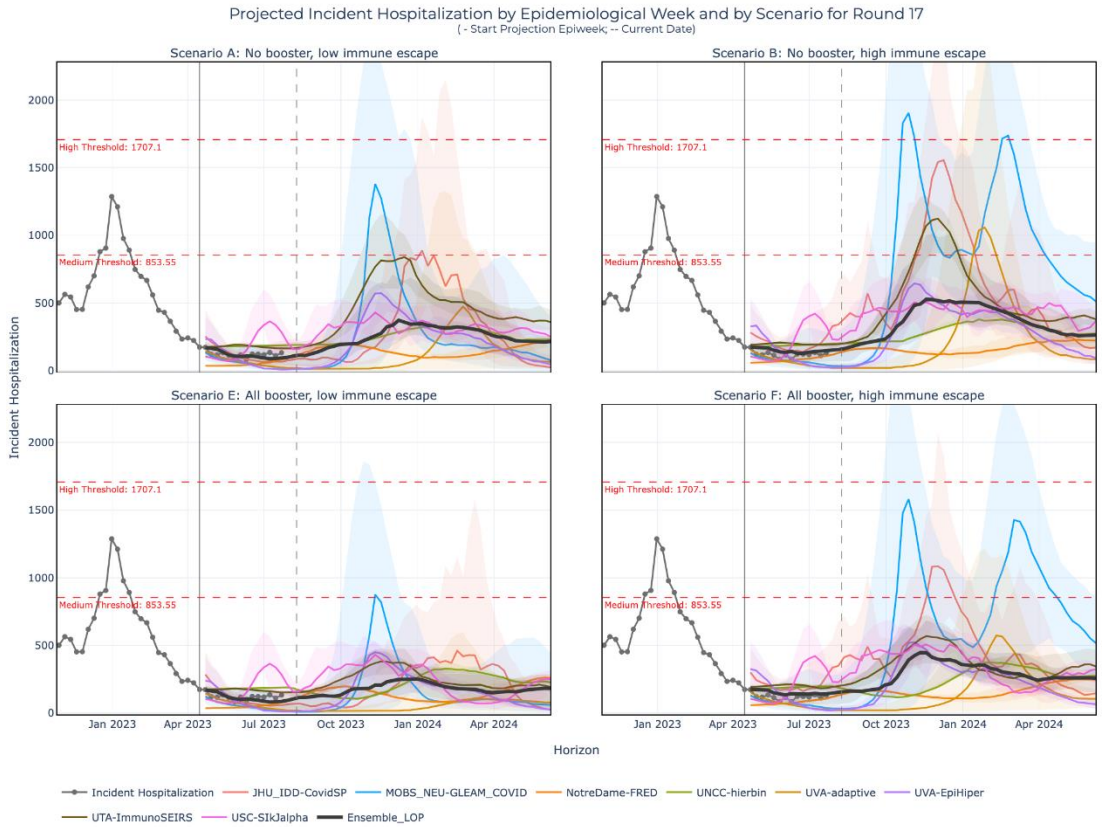
Vaccination levels:

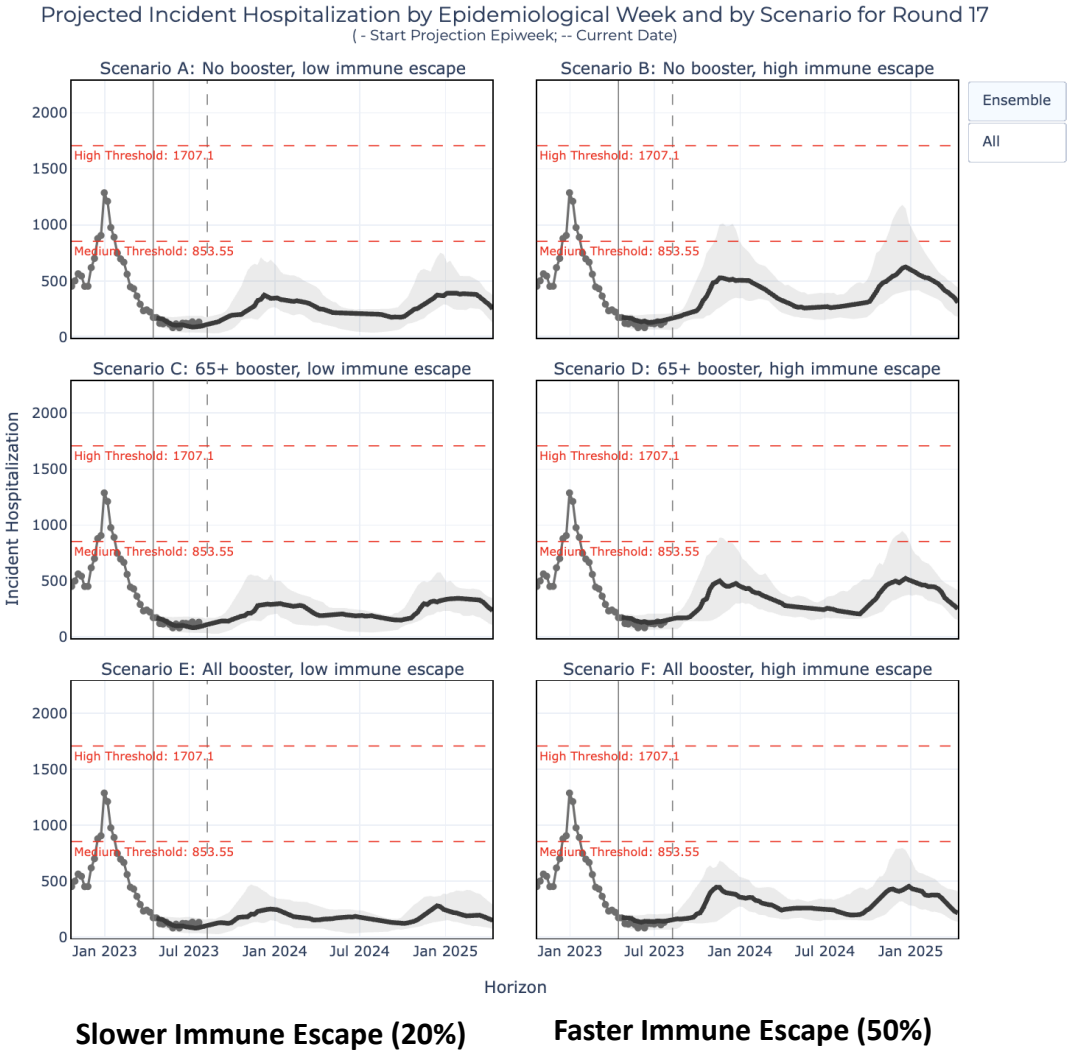
None vs.
Vulnerable and 65 + vs.
Broader population of eligible

	Low immune escape • Immune escape occurs at a constant rate of **20% per year**	**High immune escape** • Immune escape occurs at a constant rate of **50% per year**
No vaccine recommendation • Uptake negligible or continues at very slow levels based on existing 2022 booster trends	Scenario A	Scenario B
Reformulated annual vaccination recommended for 65+ and immunocompromised • Reformulated vaccine has **65% VE against variants circulating on June 15** • Vaccine becomes **available September 1** • Uptake in 65+ same as first booster dose recommended in September 2021 • Uptake in individuals under 65 negligible or continues to trickle based on 2022 booster trends	Scenario C	Scenario D
Reformulated annual vaccination recommended for all currently eligible groups • Reformulated vaccine has **65% VE against variants circulating on June 15** • Vaccine becomes **available September 1** • 65+ uptake same as first booster dose recommended in September 2021 • Coverage in individuals under 65+ saturates at levels of the 2021 booster (approximately 34% nationally)	Scenario E	Scenario F

SMH – COVID-19 (Round 17) – Virginia Results

- To date, immune escape evolution has been slow. Booster campaign size remains unknown.
- Significant variation in Fall-Winter 2023 outlook across models

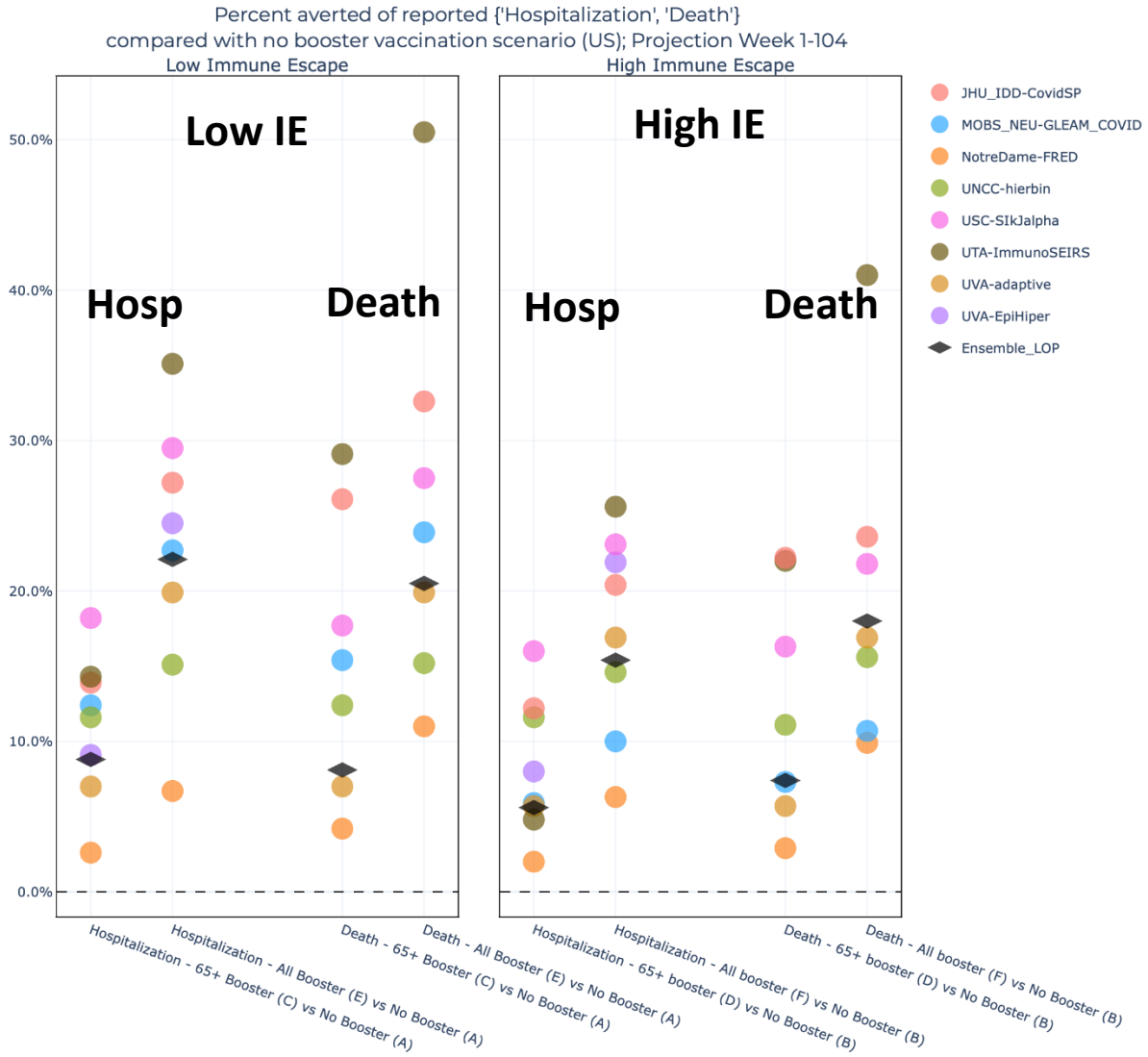




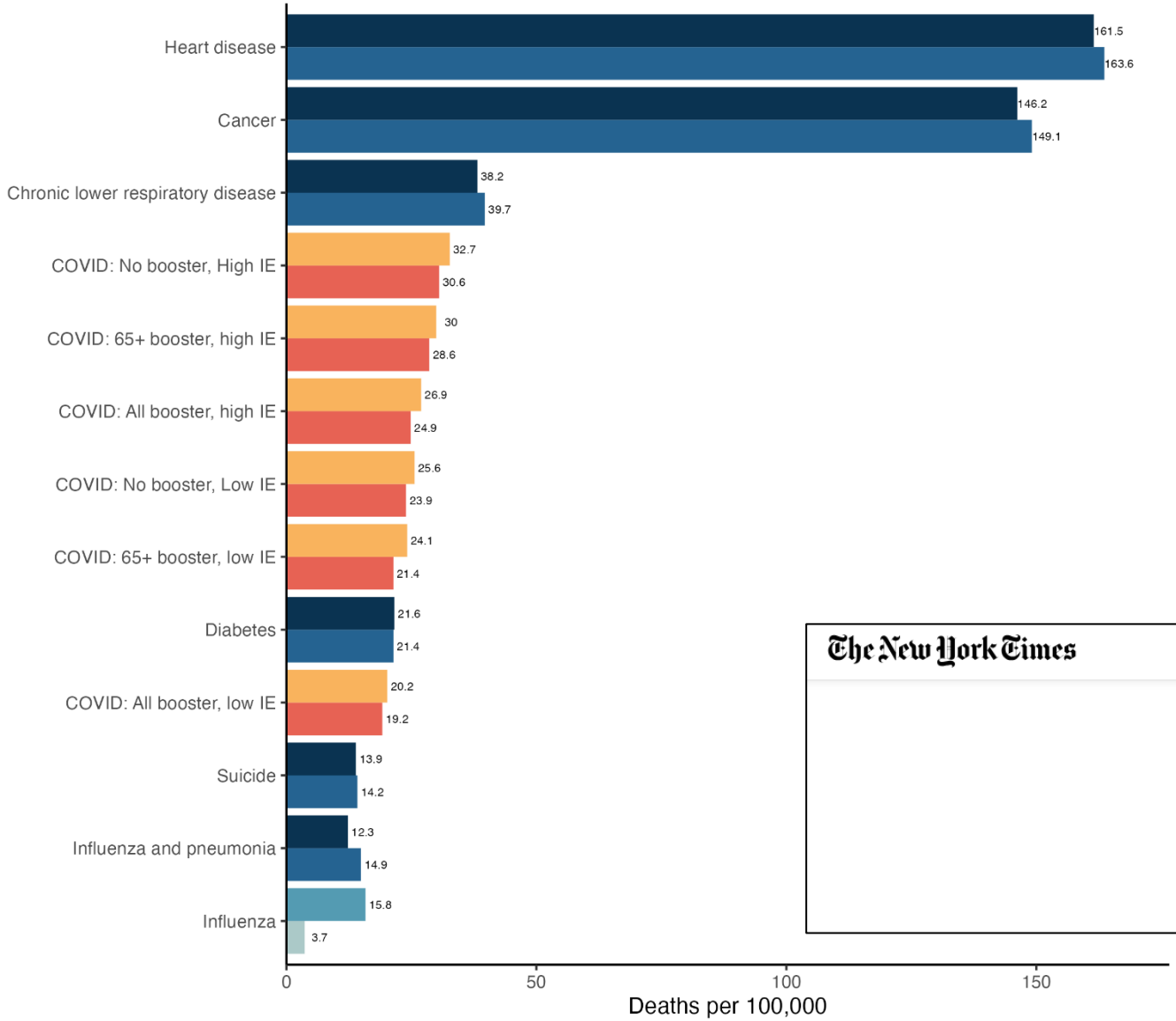
Slower Immune Escape (20%) **Faster Immune Escape (50%)**

SMH – COVID-19 (Round 17) – Results – Booster Impact

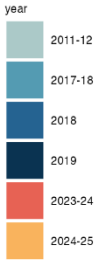
- Models estimate potential reduction in hospitalizations ranging from 2% - 18% for a 65+ only campaign to 5% - 35% for a whole population campaign
- Reductions in deaths are similar with ensemble estimates of 8% reduction for 65+ campaign and 22% reduction for whole population campaign
- For high immune escape scenarios, the reductions are smaller and more pronounced for deaths than hospitalizations



SMH – COVID-19 (Round 17) – Broader context



Across scenarios, COVID-19 is likely to be among the top 10 causes of mortality in the United States



The New York Times

HEALTH | Amid Signs of a Covid Uptick, Researchers Brace for the 'New Normal'

The range of estimated deaths would place Covid somewhere between liver disease and diabetes for causes of death. "Even in that most optimistic scenario, we're getting into the range of mortality that we see for top 10 causes of death in the United States," Dr. Lessler said.

Key Takeaways

- Upticks in cases and hospitalizations hint at a late summer wave
- Hospitalizations have increased ~12% in recent week from prolonged plateau
- Other indicators from wastewater, ED visits show sustained growth through July
- Genomic surveillance hinting at the possible role of EG.5

- Literature review: Recent publications using wastewater surveillance
- National modeling updates

Questions?

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