Network Systems Science & Advanced Computing

Biocomplexity Institute & Initiative

University of Virginia

Estimation of COVID-19 Impact in Virginia

February 2nd, 2022 (2-2-22)

(data current to Jan 30th – Feb 1st)

Biocomplexity Institute Technical report: TR 2022-007

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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 COVID-19 mitigations in Virginia
- **Approach:**
  - Calibrate explanatory mechanistic model to observed cases
  - Project based on scenarios for next 4 months
  - Consider a range of possible mitigation effects in "what-if" scenarios
- **Outcomes:**
  - Ill, Confirmed, Hospitalized, ICU, Ventilated, Death
  - Geographic spread over time, case counts, healthcare burdens

Key Takeaways

Projecting future cases precisely is impossible and unnecessary.
Even without perfect projections, we can confidently draw conclusions:

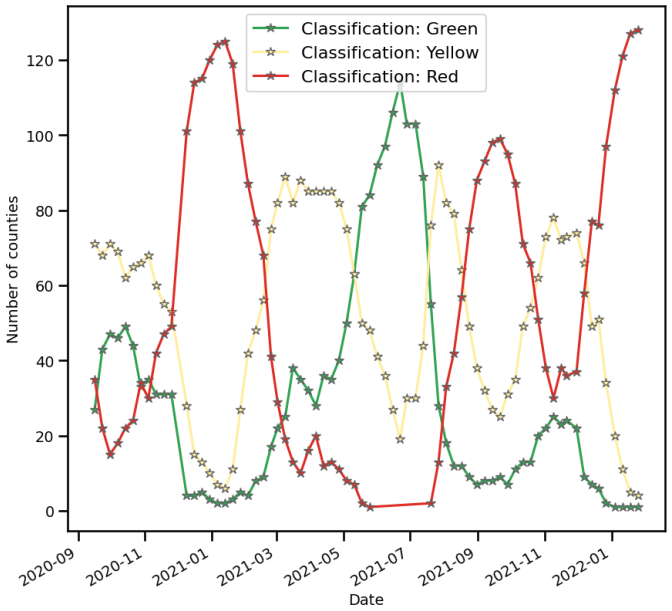
- **Case rates and hospitalizations seem to be leveling off and projections suggest we are nearing the peak**
- VA 7-day mean daily case rate is sharply down to 99/100K from 141/100K
  - US is also considerably down to 132/100K (from 194/100K)
- Projections anticipate continued declines:
  - Potential emerging BA2 subvariant of Omicron could slow and create a “small plateau” in coming weeks
  - Rapidity decline and final level of decline depends on degree of protection to Omicron garnered by previous Omicron infection
- Punxsutawney Phil prognosticates 6 more weeks of Winter
- Recent model updates:
  - Further refined model to be multi-variant model structure further refined to better capture different tiers of immunity and the immune evasion of the Omicron variant

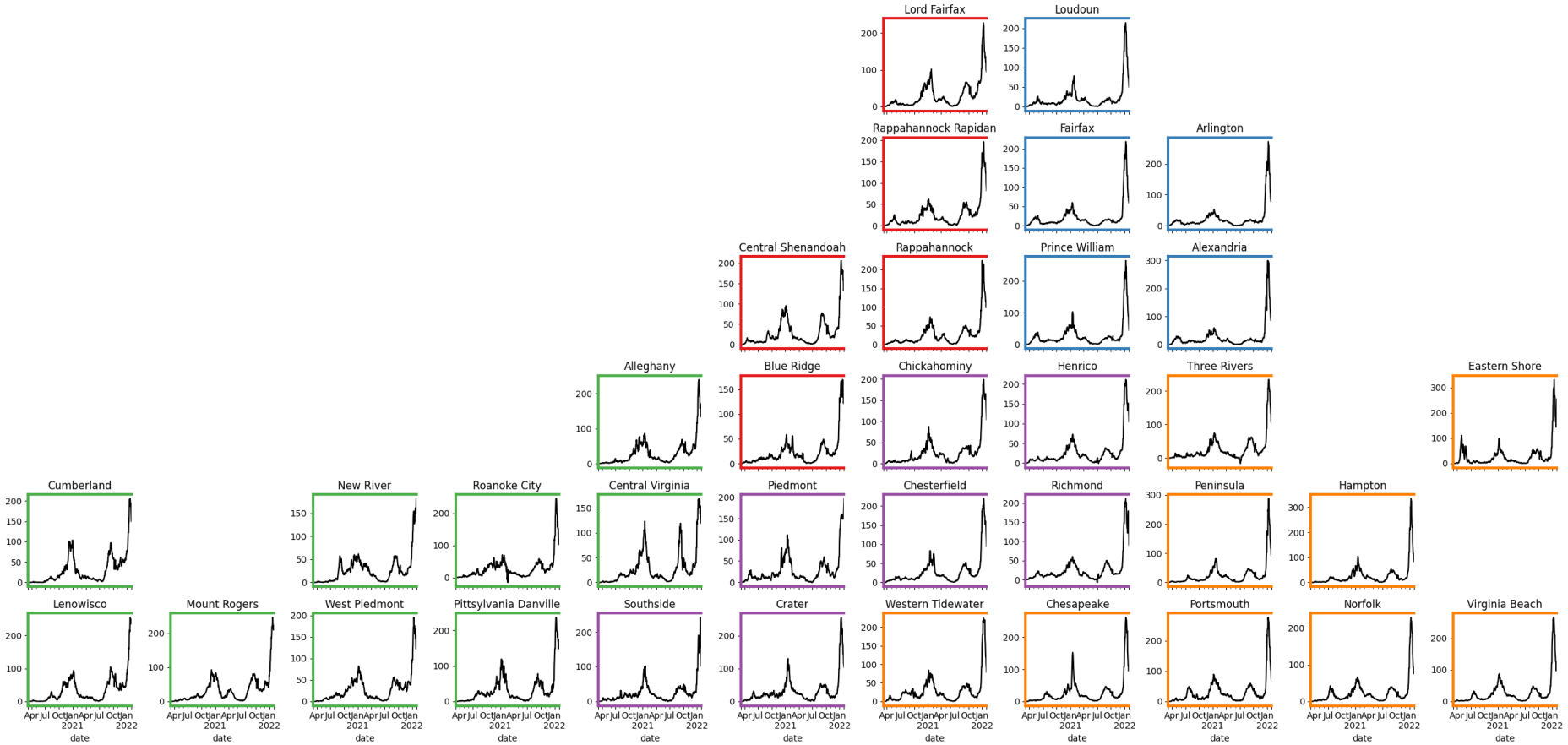
The situation continues to change. Models continue to be updated regularly.

Situation Assessment

Case Rates (per 100k) and Test Positivity

Data source: https://data.cms.gov/covid-19/covid-19-nursing-home-data





County level RT-PCR test positivity

Green: <5.0% (or <20 tests in past 14 days)

Yellow: 5.0%-10.0% (or <500 tests and <2000 tests/100k and >10% positivity over 14 days)

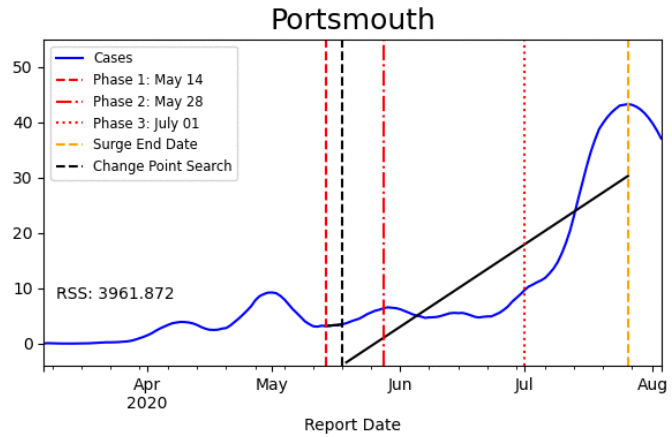
Red: >10.0% (and not "Green" or "Yellow")

District Trajectories

Goal: Define epochs of a Health District's COVID-19 incidence to characterize the current trajectory

Method: Find recent peak and use hockey stick fit to find inflection point afterwards, then use this period's slope to define the trajectory

Hockey stick fit

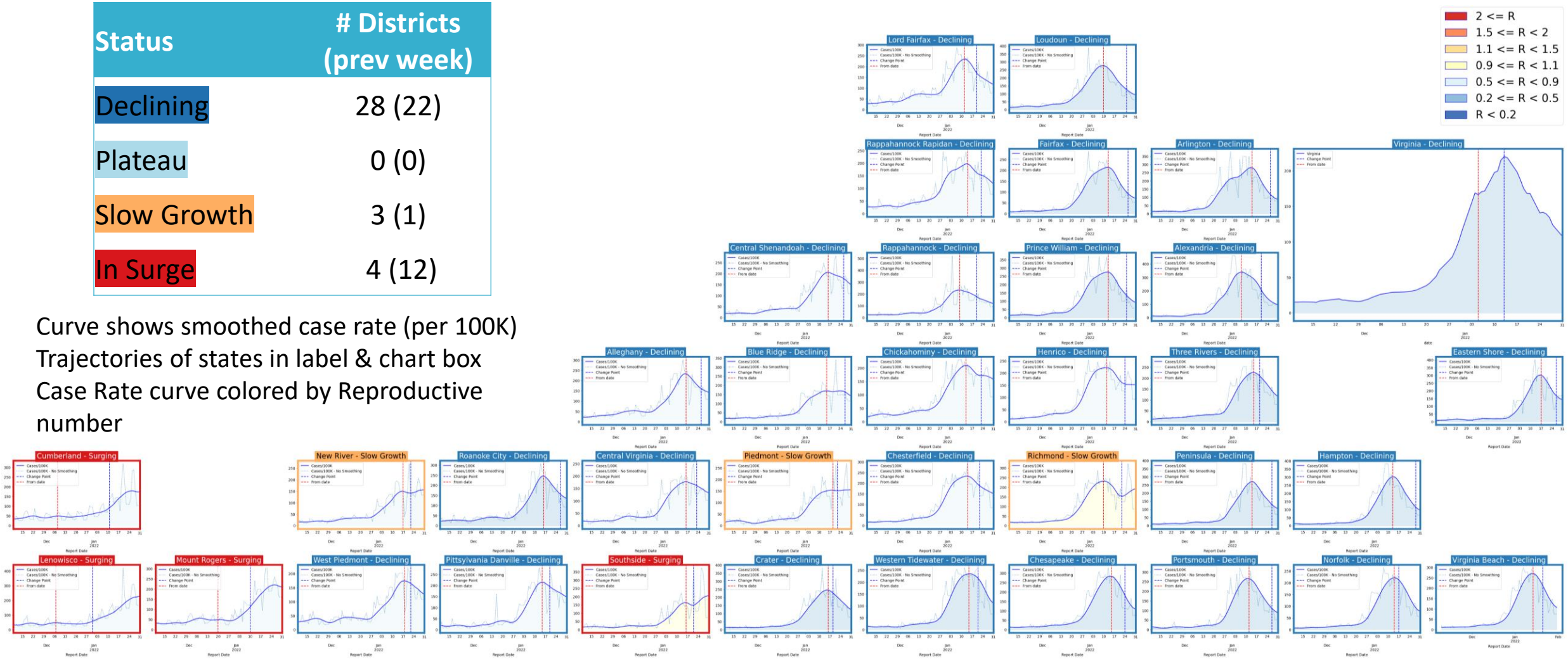


Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	28 (22)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	0 (0)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	3 (1)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	4 (12)

District Trajectories – last 10 weeks

Status	# Districts (prev week)
Declining	28 (22)
Plateau	0 (0)
Slow Growth	3 (1)
In Surge	4 (12)

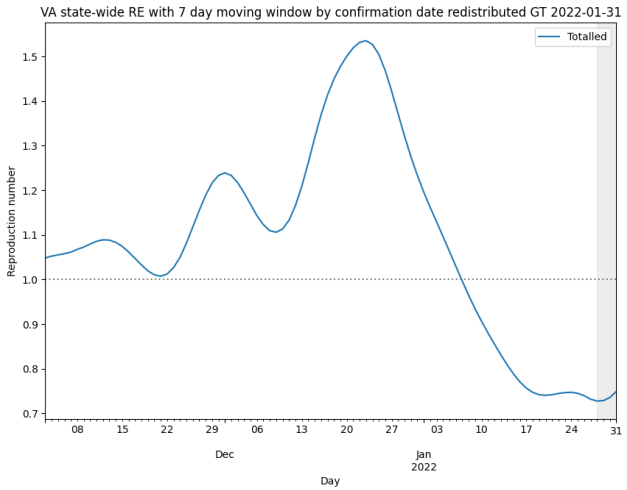
Curve shows smoothed case rate (per 100K)
Trajectories of states in label & chart box
Case Rate curve colored by Reproductive number

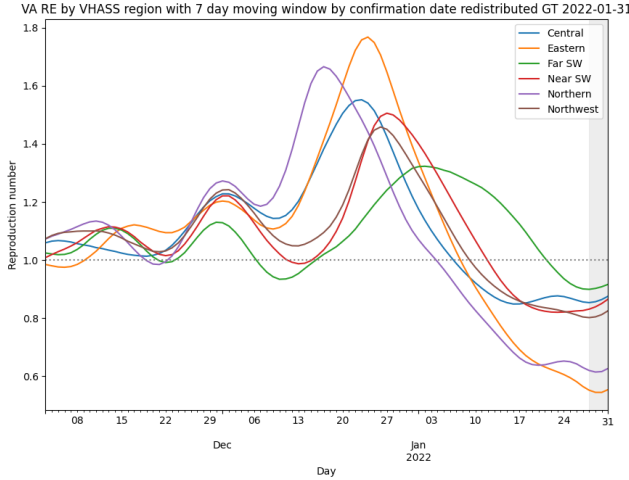


Estimating Daily Reproductive Number –
Redistributed gap

Jan 31st Estimates

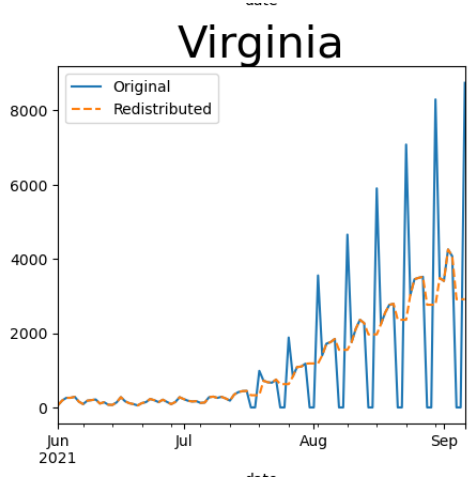
Region	Date Confirmed R_e	Date Confirmed Diff Last Week
State-wide	0.749	0.002
Central	0.876	0.048
Eastern	0.553	-0.132
Far SW	0.914	-0.121
Near SW	0.867	-0.012
Northern	0.627	0.089
Northwest	0.826	-0.085





Skipping Weekend Reports & holidays biases estimates

Redistributed "big" report day to fill in gaps, and then estimate R from "smoothed" time series



Methodology

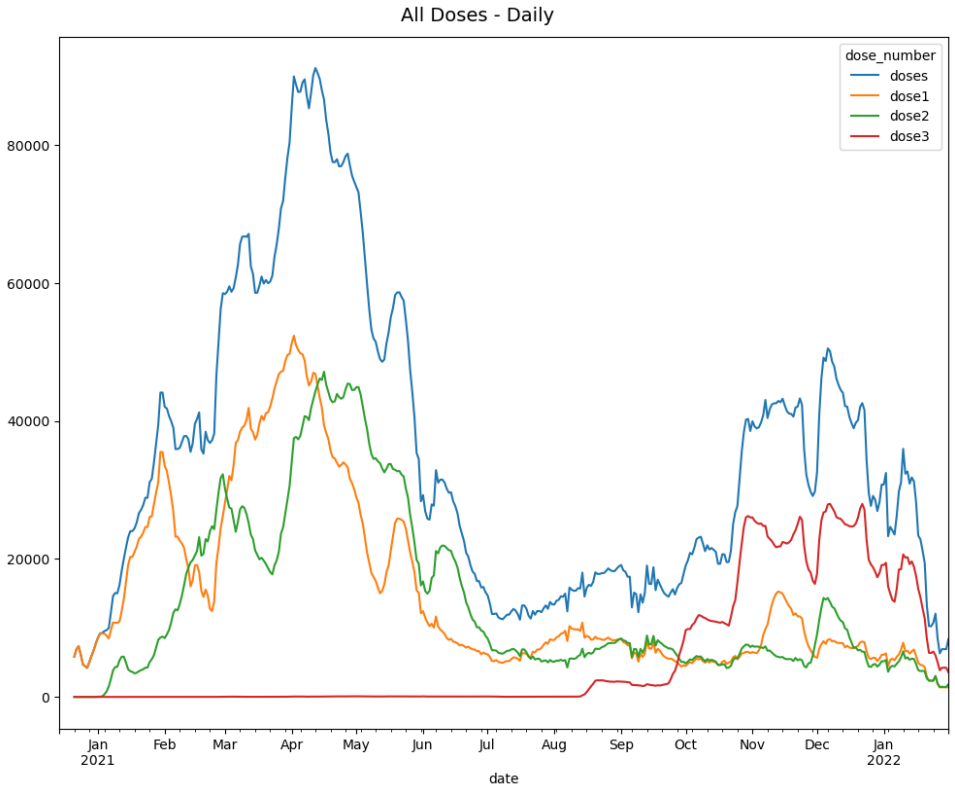
- Wallinga-Teunis method (EpiEstim[1]) for cases by **confirmation date**
- Serial interval: updated to discrete distribution from observations (mean=4.3, Flaxman et al, Nature 2020)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

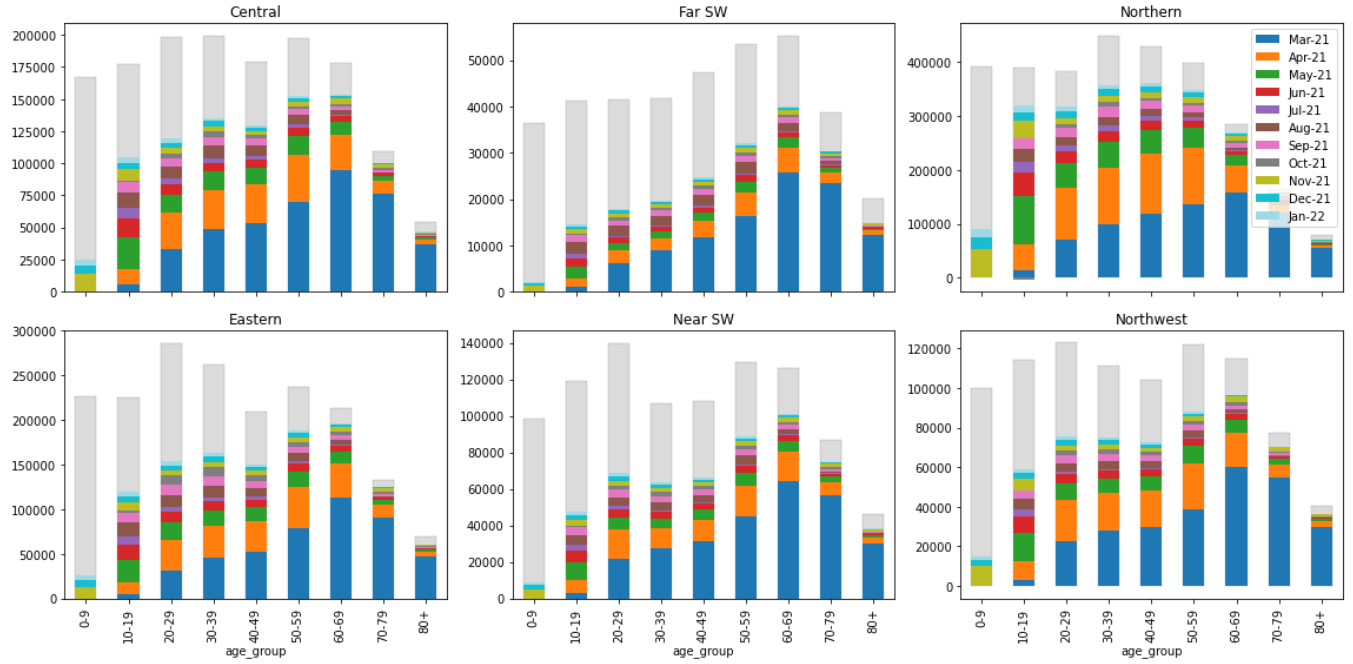
1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, https://doi.org/10.1093/aje/kwt133

Vaccination Administration in Virginia

Vaccine Doses administered:

- Doses administered rates approach levels first experienced when vaccines were first available
- Considerable reduction in vaccination rate experienced since mid-January
- Third dose administration outpaces 1st



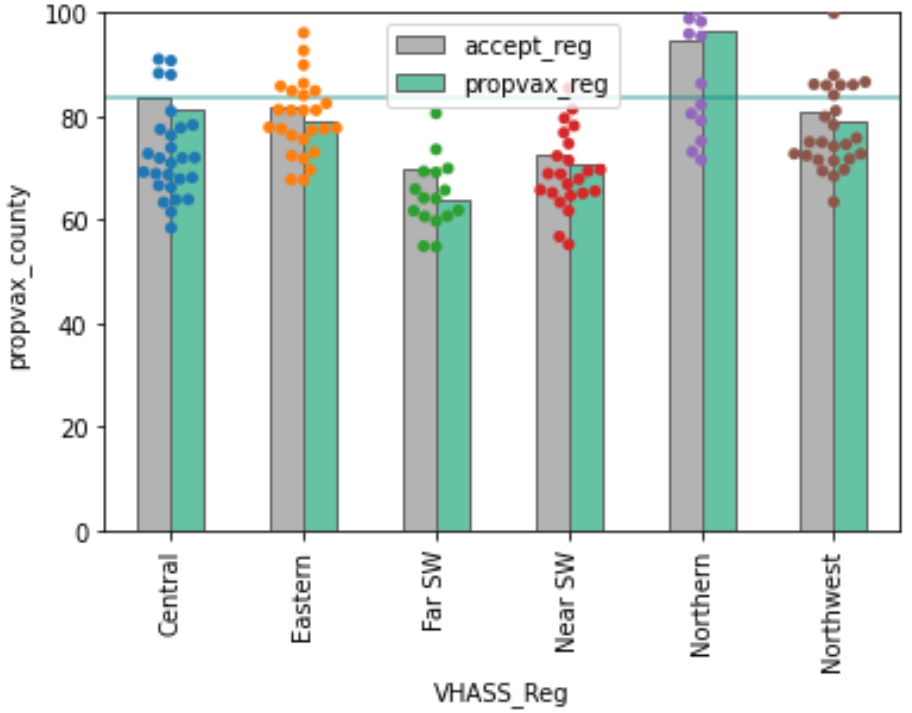


Vaccination Acceptance by Region

Corrections to surveys:

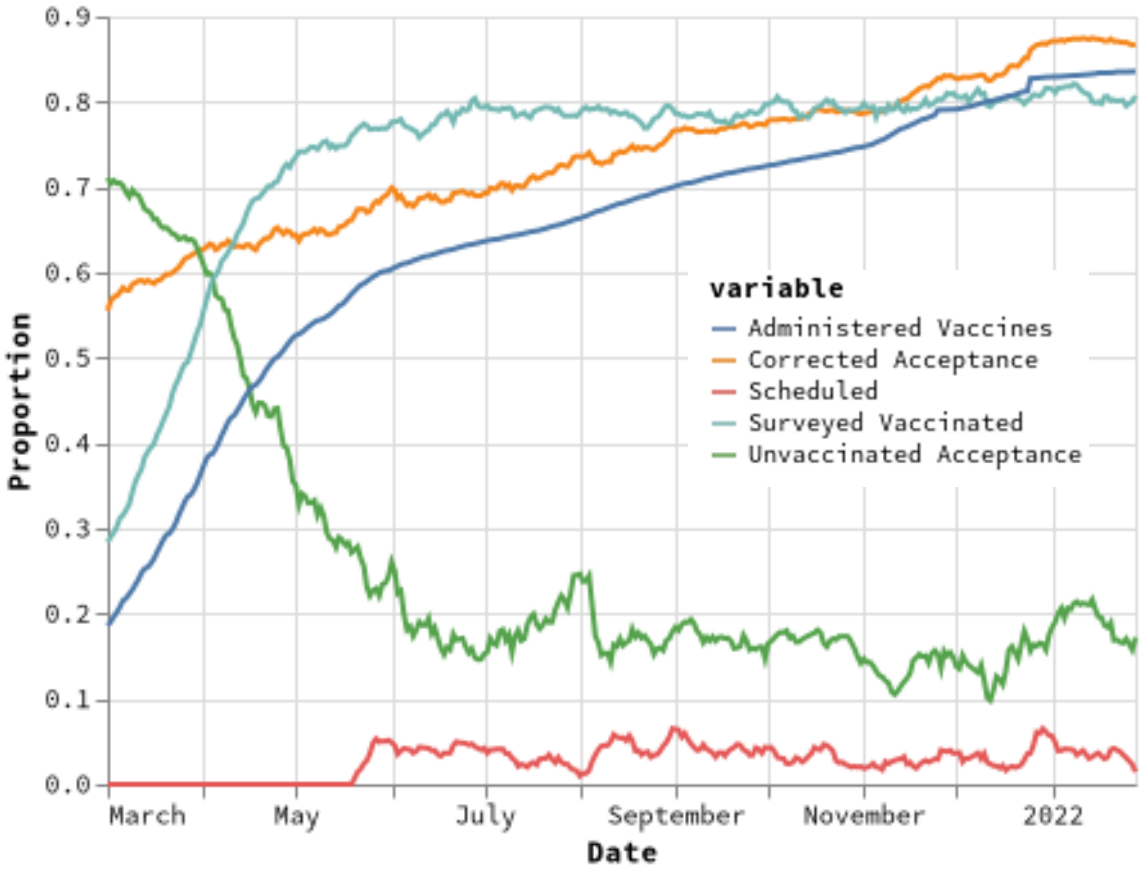
- Facebook administered survey is timely and broad, but biased by who accesses Facebook and answers the survey
- Correction approach:
  - Calculate an over-reporting fraction based on reported vaccinations compared to VDH administration data
  - Cross-validate coarse corrections against HPS survey at the state level and corrected in same manner

Region	COVIDcast accepting corrected	VDH proportion pop vaccinated
Central	84%	81%
Eastern	83%	79%
Far SW	68%	64%
Near SW	75%	71%
Northern	98%	96%
Northwest	83%	79%
Virginia	**87%**	**84%**



Grey Bar: Survey measured and corrected acceptance
Green Bar: Proportion of eligible population administered a vaccine
Dots: Proportion administered at least one dose for each county

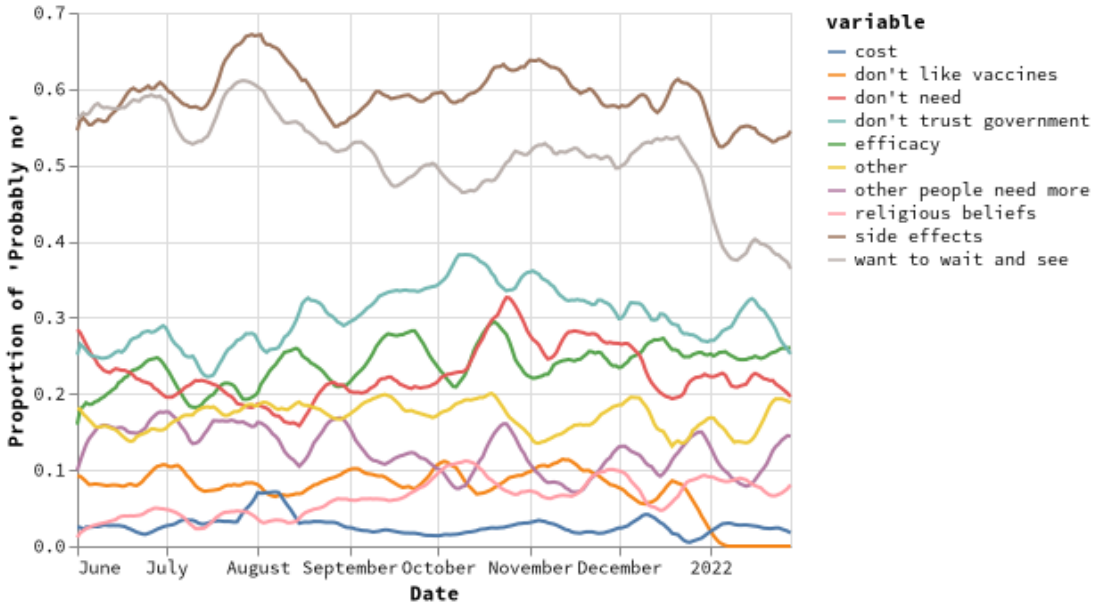
Vaccine Acceptance Components over Time



Vaccine Acceptance adjusted to include scheduled appointments

- Steady rise in acceptance over the past couple months
- Unvaccinated Acceptance shows ~20% of those who are unvaccinated are definitely or probably willing to be vaccinated
- Scheduled appointments for vaccination have increased through August but seem to be leveling off

Reasons among those that are Probably not going to Vaccinate

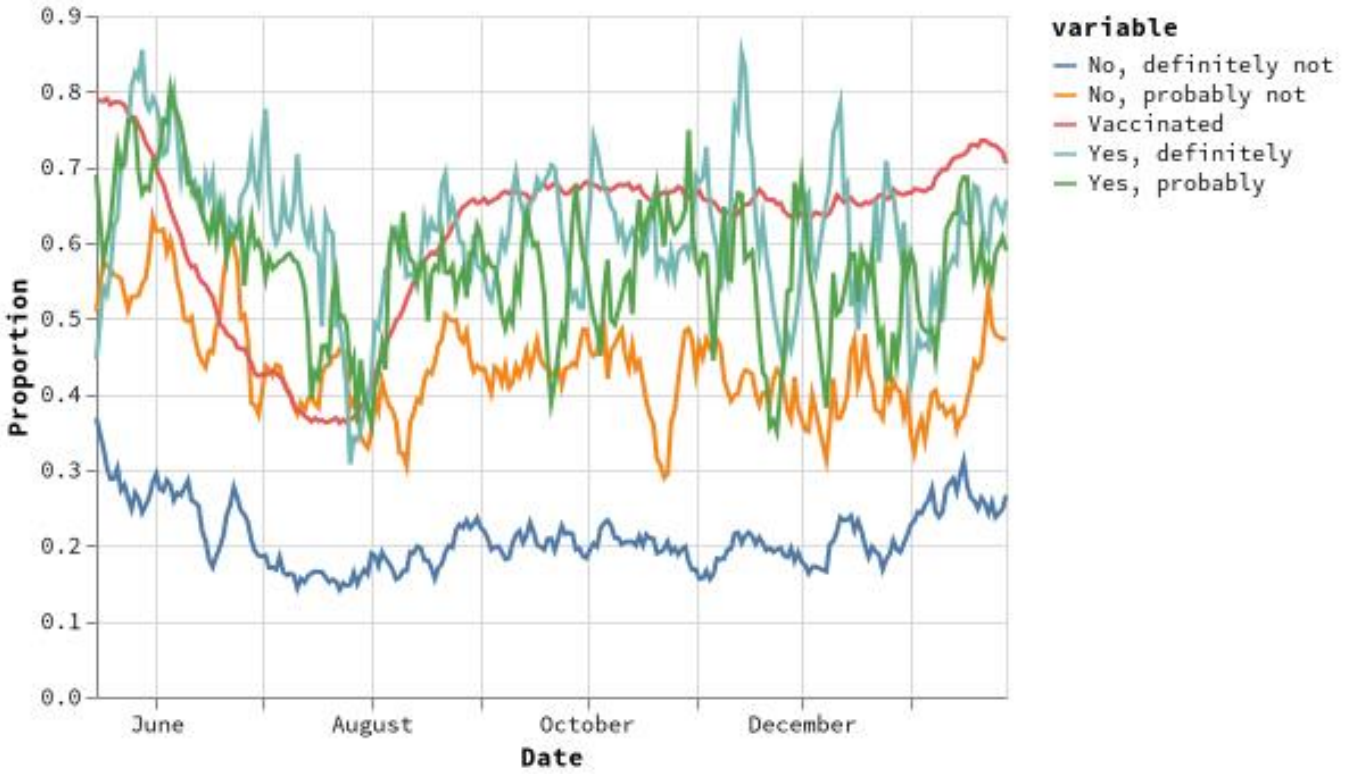


Data Source: https://covidcast.cmu.edu

Mask Usage dips back down slightly

Self-reported mask usage has dipped back to low 70%s after briefly rising to 75%

- US and VA experienced similar increases over the course of last month
- Mask wearing remains lower among unvaccinated, especially among least willing to be vaccinated



Data Source: https://covidcast.cmu.edu

SARS-CoV2 Variants of Concern

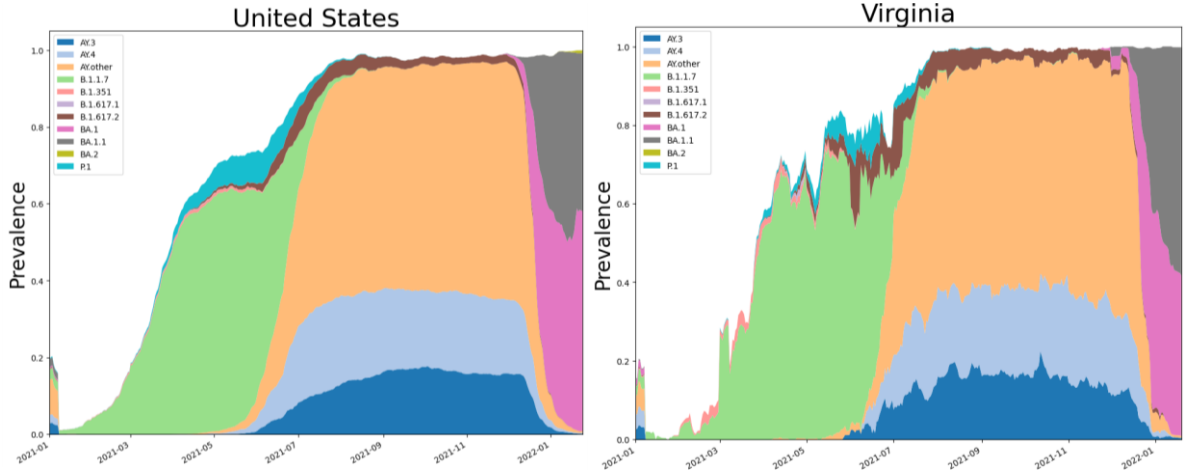
Emerging new variants will alter the future trajectories of pandemic and have implications for future control

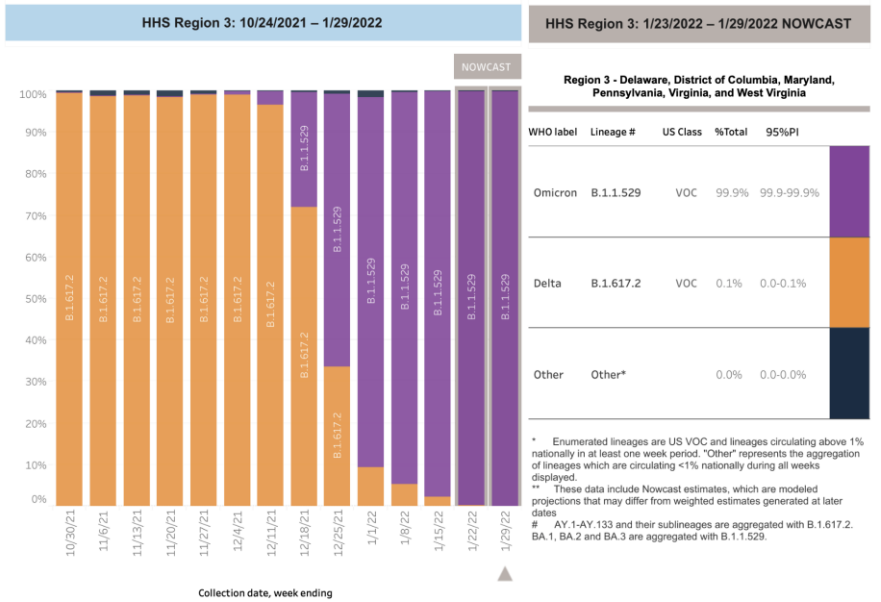
- Emerging variants can:
  - Increase transmissibility
  - Increase severity (more hospitalizations and/or deaths)
  - Limit immunity provided by prior infection and vaccinations
- Genomic surveillance remains very limited
  - Challenges ability to estimate impact in US to date and estimation of arrival and potential impact in future

WHO label	Pango lineage*	GISAID clade	Nextstrain clade	Additional amino acid changes monitored*	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	+S:484K +S:452R	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351	GH/501Y.V2	20H (V2)	+S:L18F	South Africa, May-2020	18-Dec-2020
Gamma	P.1	GR/501Y.V3	20J (V3)	+S:681H	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	+S:417N +S:484K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron*	B.1.1.529	GRA	21K, 21L	+R346K	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

World Health Organization [WHO]

GISAID outbreak.info

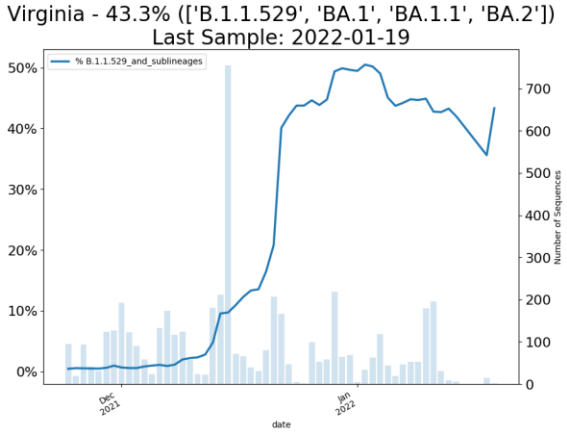


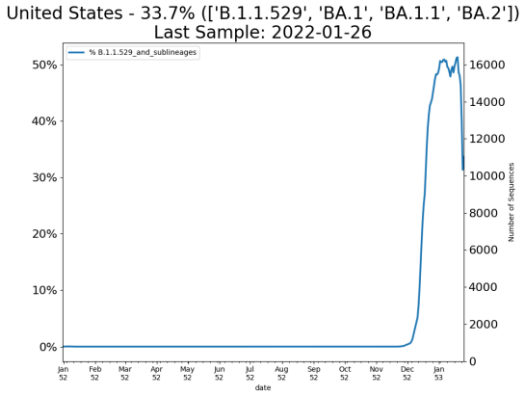


CDC [CDC Variant Tracking]

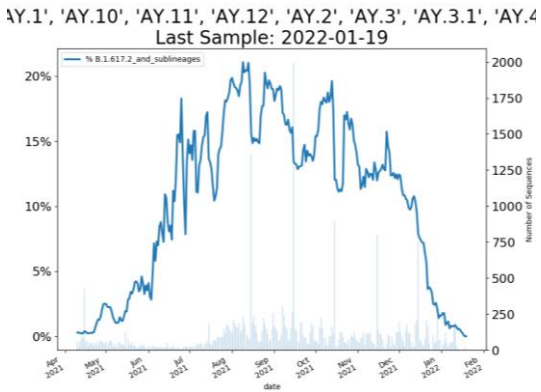
SARS-CoV2 Variants of Concern

Omicron ο - Lineage B.1.1.529



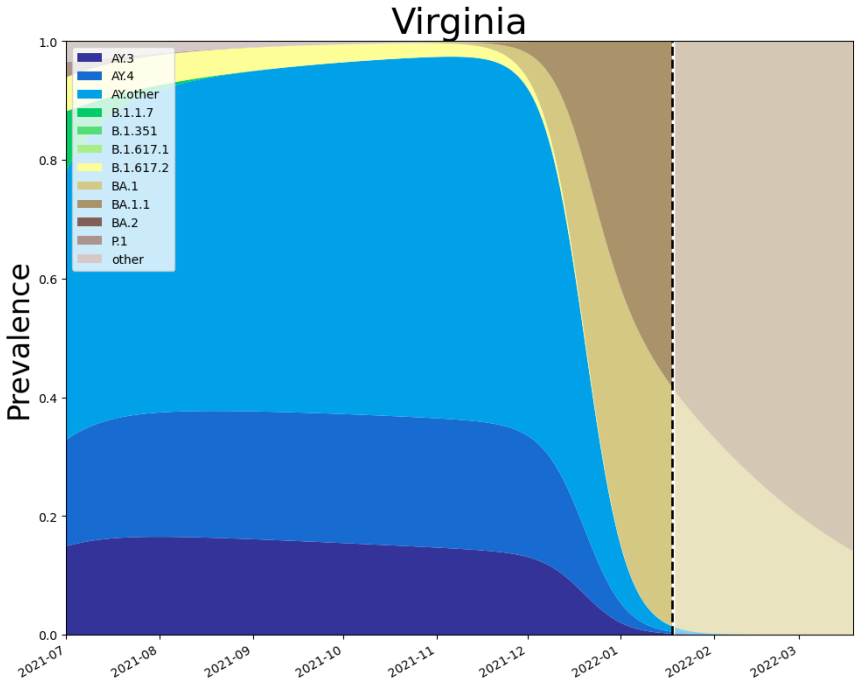


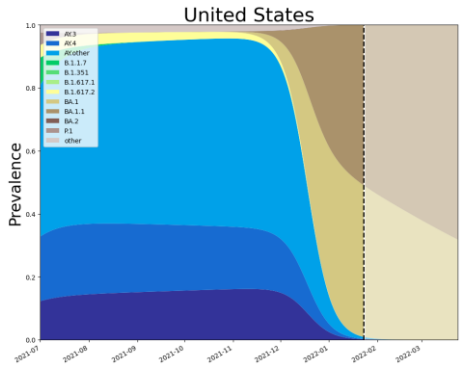
Delta δ - Lineage B.1.617.2



GISAID outbreak.info

VoC Polynomial Fit Projections



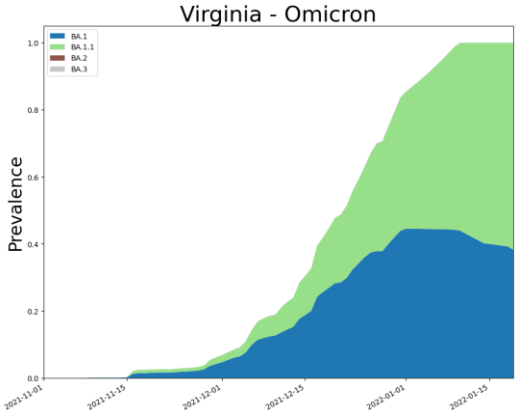


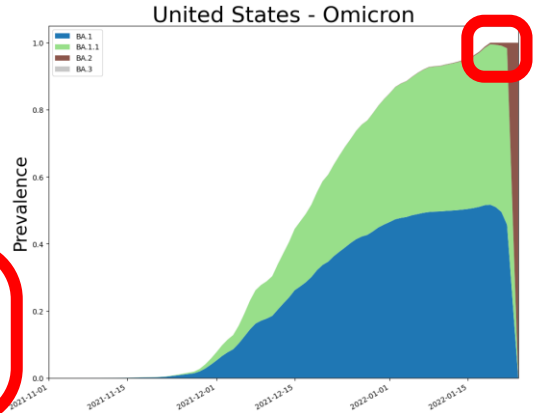
SARS-CoV2 BA.2 subvariant Tracking

BA.2 subvariant growing rapidly in some European countries

- Both Delta and the Omicron BA.2 subvariant don't have the SGTF signal with PCR tests, so the reduction caused by Omicron BA.1 SGTF can be an imperfect signal for increased BA.2
- Subvariant BA.2 in at least 20 states, not VA so far, but increasingly present in US and North America

Whole Genomes in public repositories

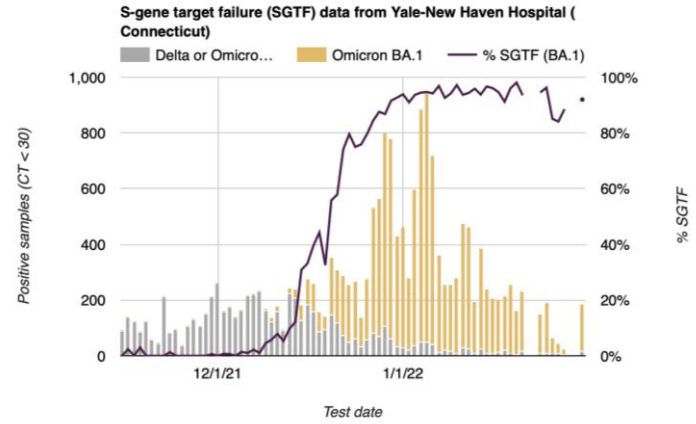




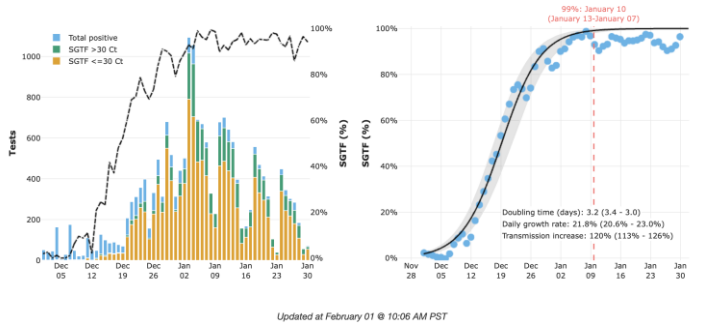
GISAID outbreak.info

SGTF proxy in US

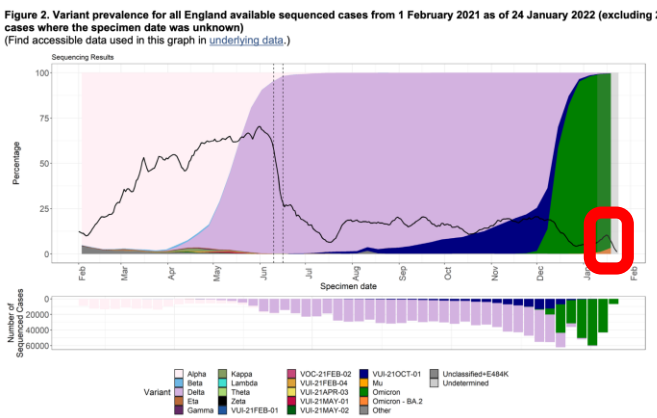
Yale- New Haven



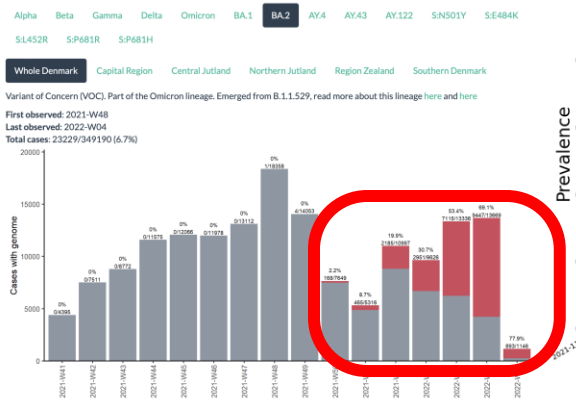
San Diego



United Kingdom



Denmark



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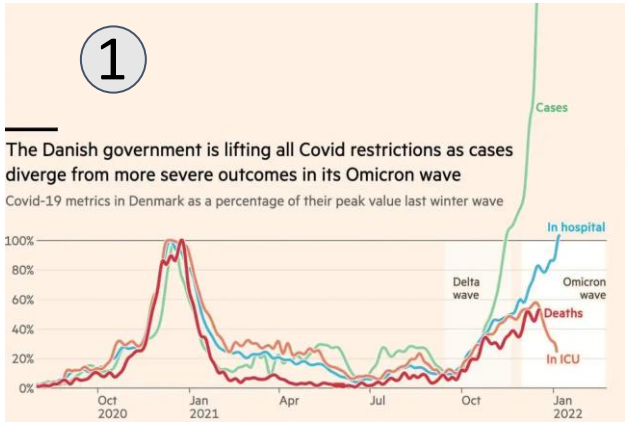
Omicron

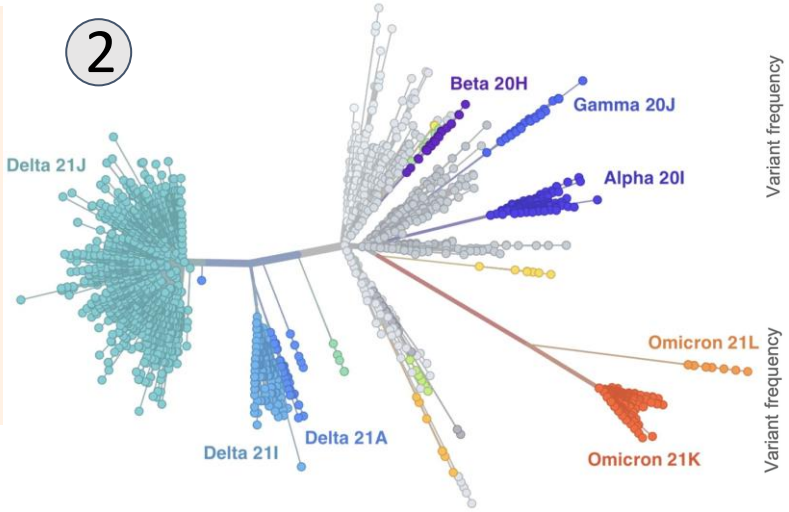
1. Omicron immune escape leads to significant case and hospitalization count in Denmark.
2. Omicron sub-lineage BA.2 rapidly increasing in prevalence in multiple countries around the world.
3. Initial surveillance indicates potentially higher intrinsic transmissibility of BA.2
4. A study of breakthrough infections suggest that Omicron-induced immunity may not be sufficient to prevent infection from another, more pathogenic variant, should it emerge in the future.

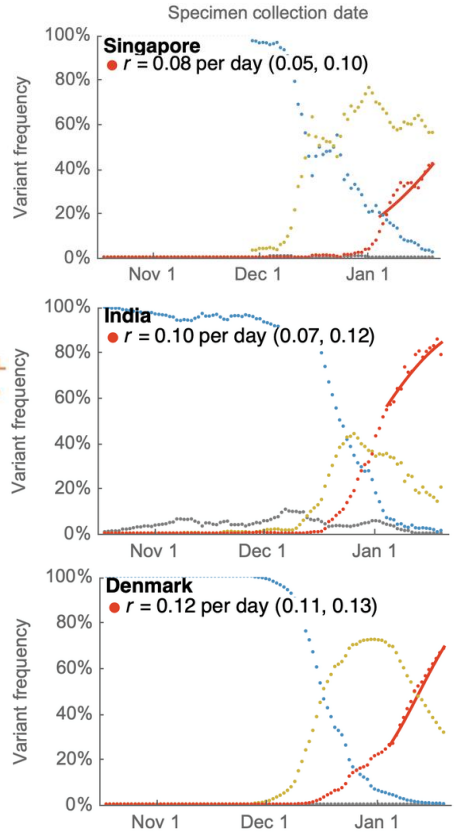
1



Denmark will be a country to watch as they have chosen to lift Covid restrictions. Here surveillance reveals both decoupling of severe outcomes from case count and potentially a significant challenge to health care resources compared to previous peaks.
https://www.ft.com/content/037a3ac9-830b-4592-9ff3-feed2008bdb7l

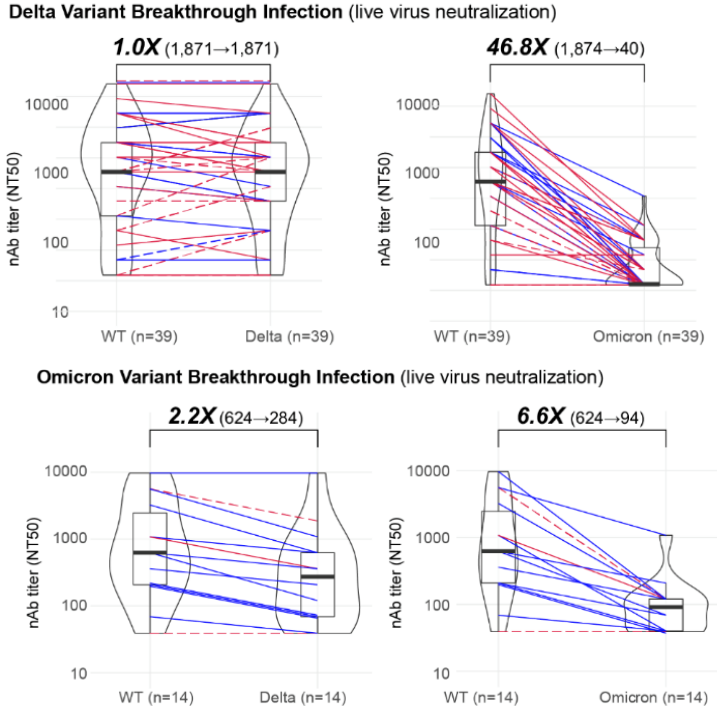
2





Growth advantage for BA.2 (21L) observed in multiple countries. Sequences of BA.2 differ by ~40 AA from BA.1 (21K) which is as different as Alpha, Beta, Gamma are from one another.
https://twitter.com/trvrb/status/1487105396879679488

4



This California based study also highlights the continued importance of vaccine boosters in enhancing immunity, as breakthrough infection alone may not be reliable in eliciting protective titers against re-infection or future infection from different variants (majority of individuals in this study not boosted).
https://www.medrxiv.org/content/10.1101/2022.01.25.22269794v1

Variant	Household contacts becoming cases / all household contacts	Secondary attack rate amongst household contacts (95% CI)
VUI-22JAN-01 (BA.2)	64 / 476	13.4% (10.7%-16.8%)
Omicron excluding VUI-22JAN-01	10,444 / 101,773	10.3% (10.1%-10.4%)

3

Preliminary estimates from UK Health Security Agency put the SAR for BA.2 higher than previous Omicron BA.1. Combined with roughly equivalent Vaccine Effectiveness implicates a higher inherent transmissibility over BA.1 (initial Omicron).
https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1050999/Technical-Briefing-35-28January2022.pdf

https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1050721/Vaccine-surveillance-report-week-4.pdf

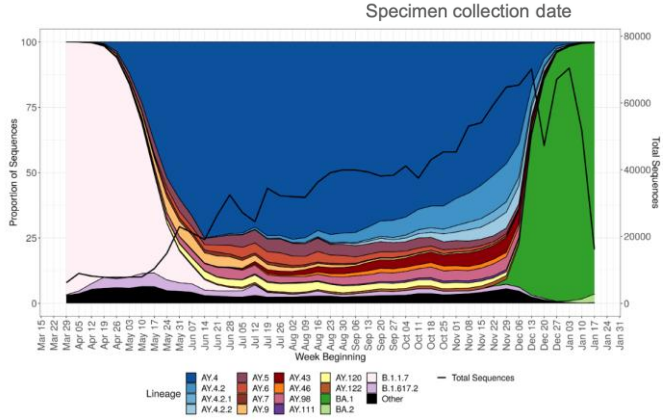


Table 3. Vaccine effectiveness against symptomatic disease (all vaccine brands combined) for BA.1 and BA.2. OR = odds ratio, VE = vaccine effectiveness.

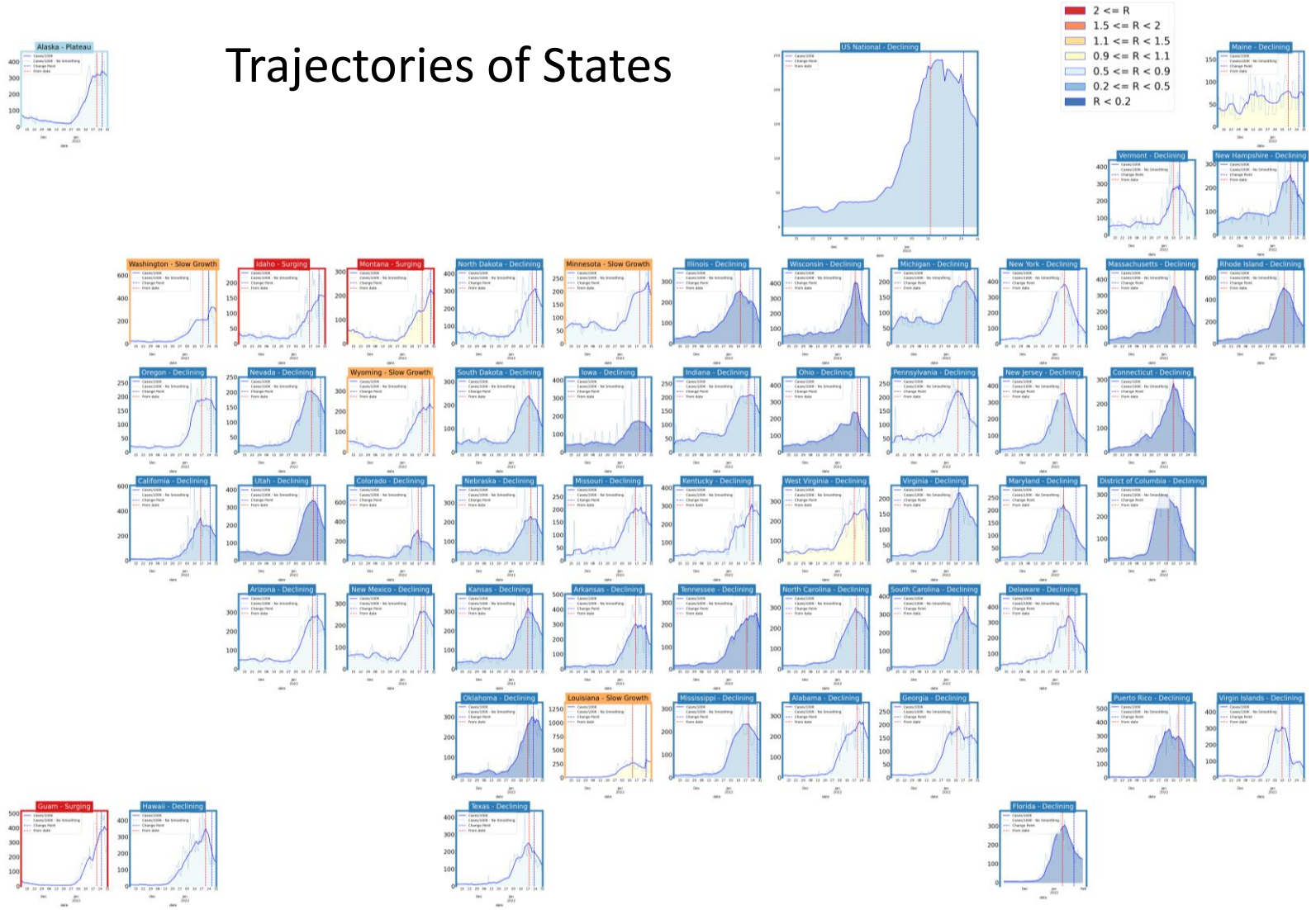
Dose	Interval after dose	BA.1 (VE (95% CI))	BA.2 (VE (95% CI))
2	25+ weeks	9% (7-10)	13% (-26-40)
3	2+ weeks	63% (63-64)	70% (58-79)

United States Case Rates

- Most of nation has shifted to a declining trajectory
- Growth remains but mainly along the northern border

Status	# States
Declining	46 (30)
Plateau	1 (1)
Slow Growth	4 (9)
In Surge	3 (14)

Trajectories of States



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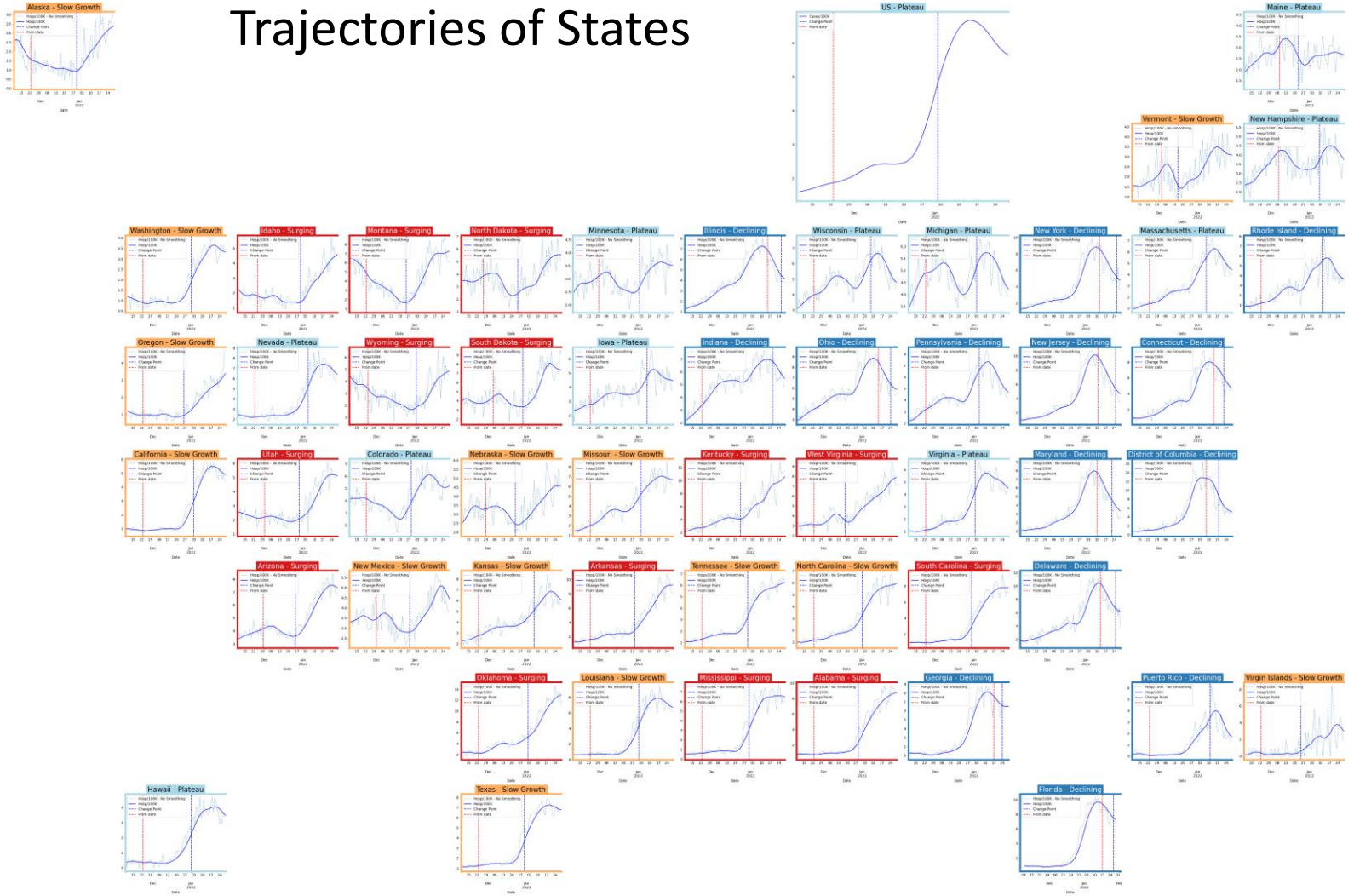
United States Hospitalizations

- Hospital admissions are lagging case rates, but are mixed across the states
- Many states in growth trajectories show signs of slowing

Status	# States
Declining	14
Plateau	11
Slow Growth	14
In Surge	14

Trajectories of States



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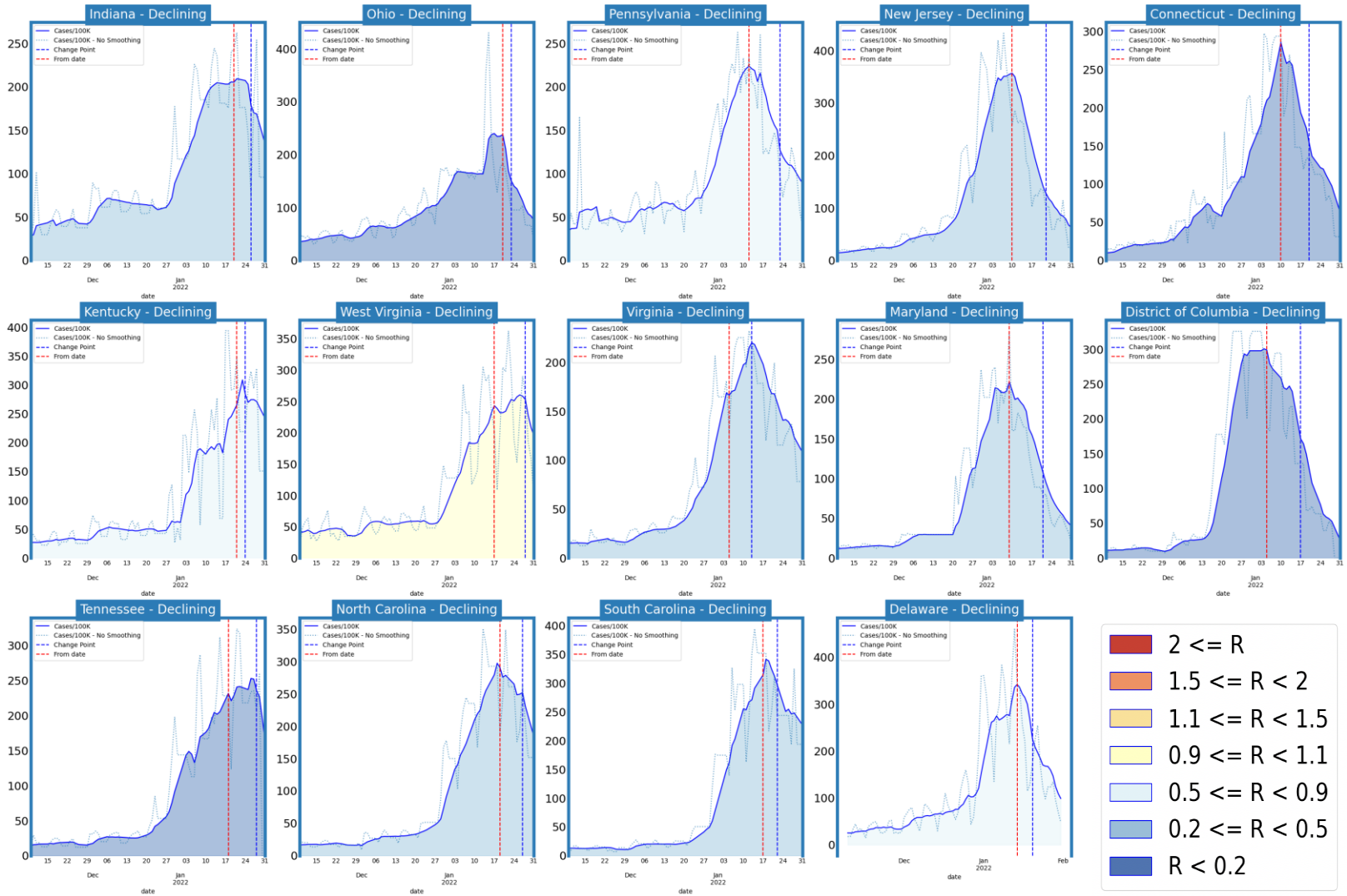
Virginia and Her Neighbors

- Growth has slowed significantly for many states in the neighborhood
- All states show signs of slowing
- Rates remain high, though substantially lower than in previous weeks for most states
- Neighbors to west and south remain near or above the 100/100K daily incident case rates, to the north and east rates have fallen to ~50/100K



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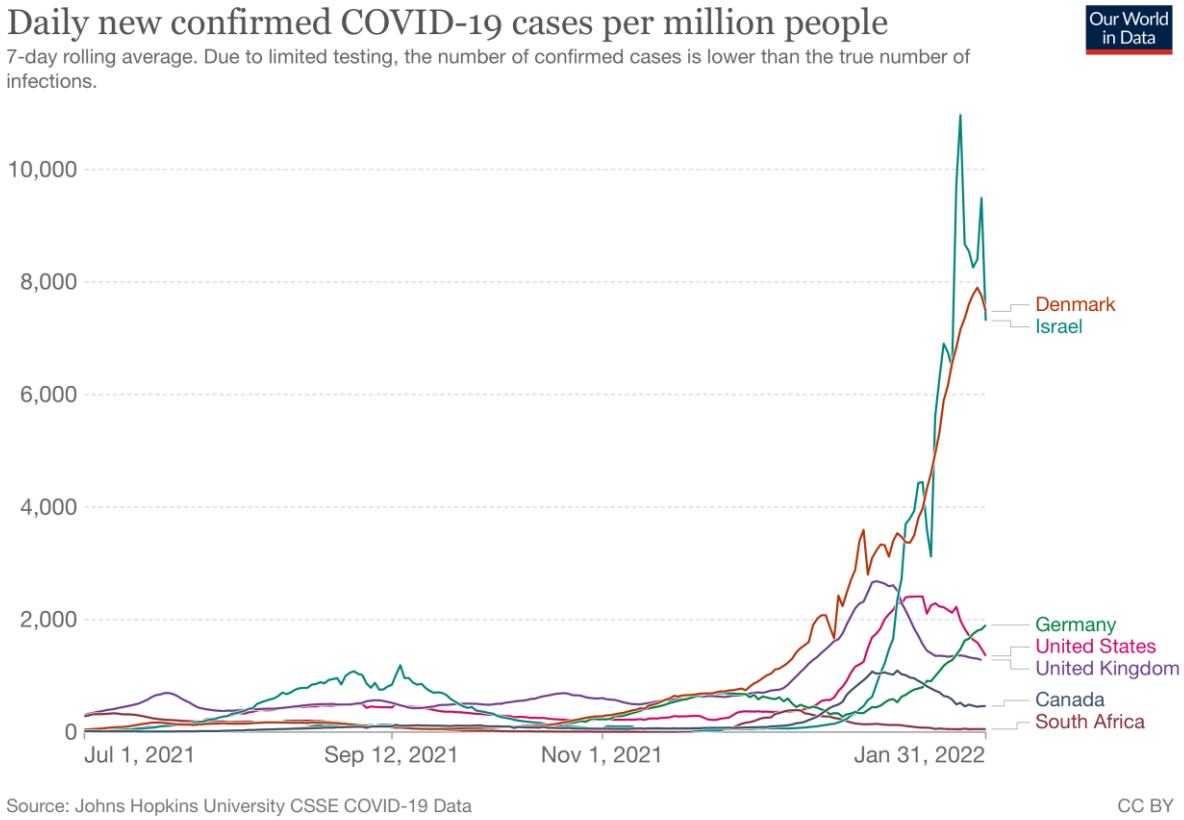
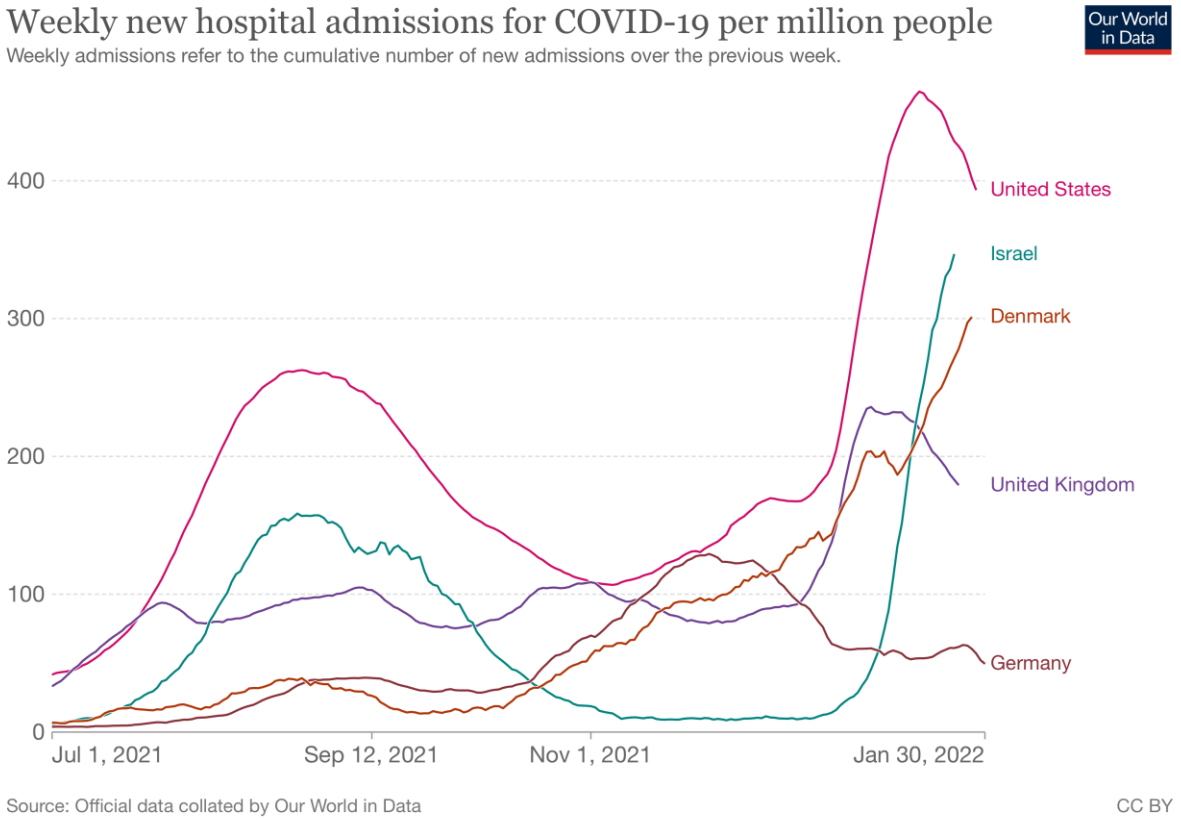
Other Countries

- UK and Canada see case rates flattening out of steep declines
- Extremely high case rates in Denmark and Israel start to slow
- US continues to have highest per capita hospitalization rate in world

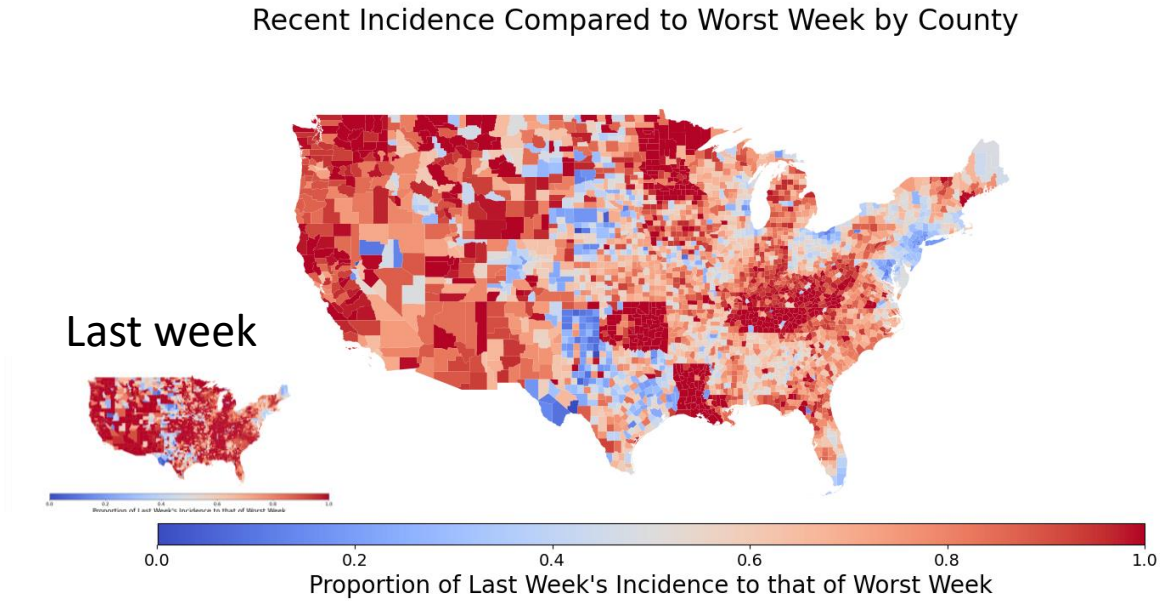


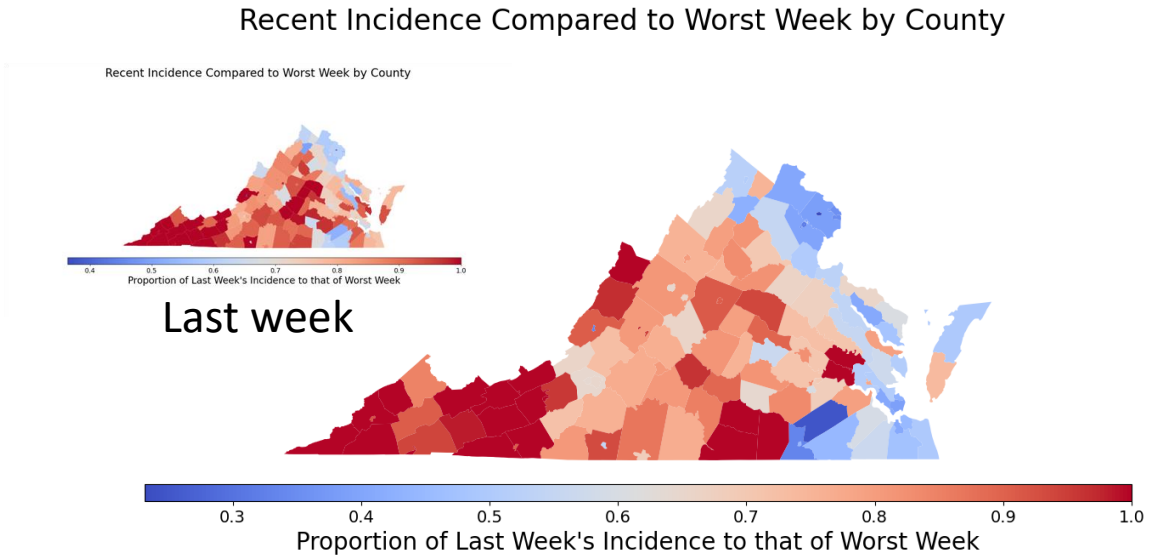


[Our World in Data]

County-level comparison to previous highest peak

- Most counties in VA have had the highest case rate of the pandemic in the last week
- Nationally the number of counties at their highest rate has expanded considerably





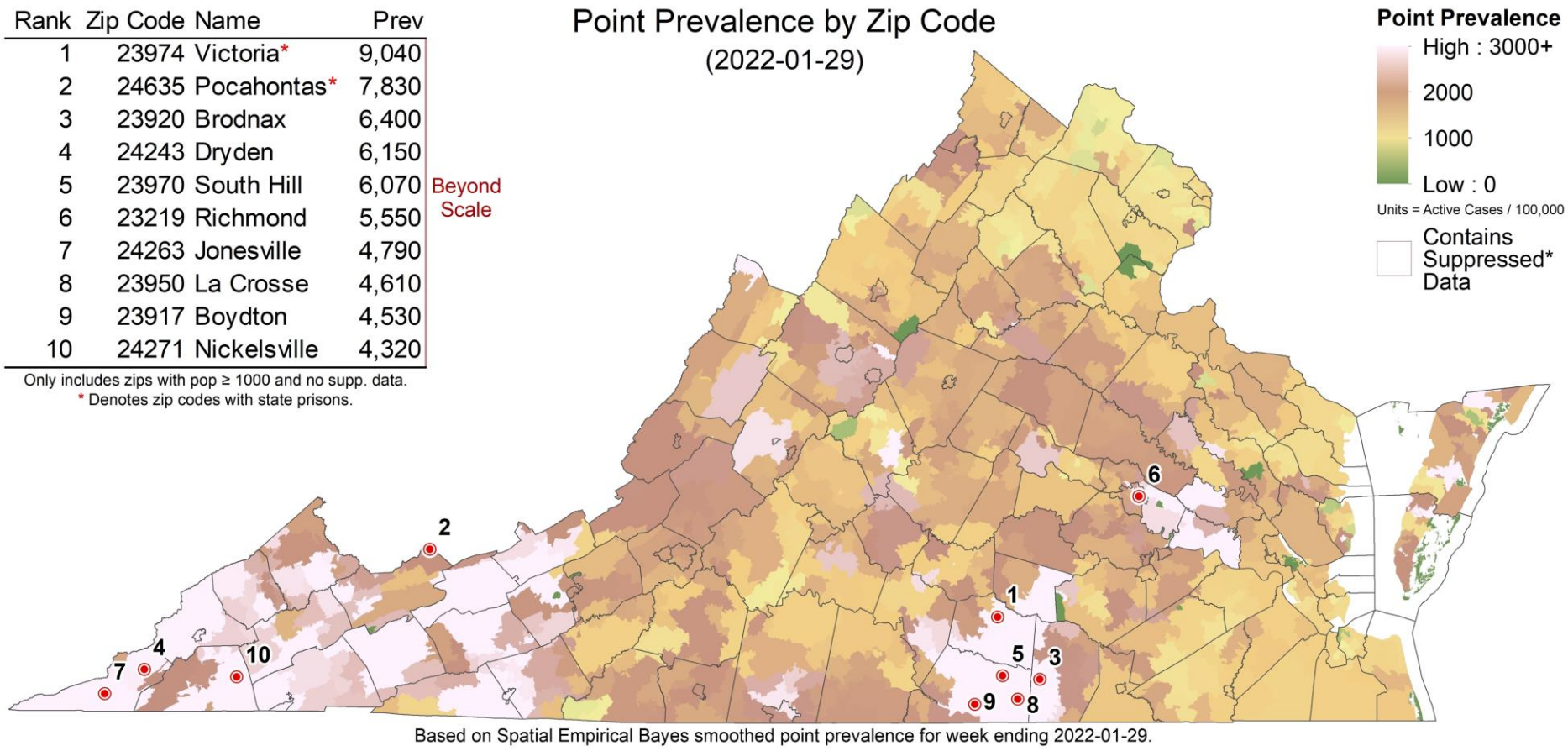
Zip code level weekly Case Rate (per 100K)

Case Rates in the last week by zip code

- Color scaled adjusted to accommodate the very high prevalence levels this week
- Clusters of high prevalence in South
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code	Name	Prev	
1	23974	Victoria*	9,040	
2	24635	Pocahontas*	7,830	
3	23920	Brodnax	6,400	
4	24243	Dryden	6,150	
5	23970	South Hill	6,070	Beyond Scale
6	23219	Richmond	5,550	
7	24263	Jonesville	4,790	
8	23950	La Crosse	4,610	
9	23917	Boydton	4,530	
10	24271	Nickelsville	4,320	

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



Based on Spatial Empirical Bayes smoothed point prevalence for week ending 2022-01-29.

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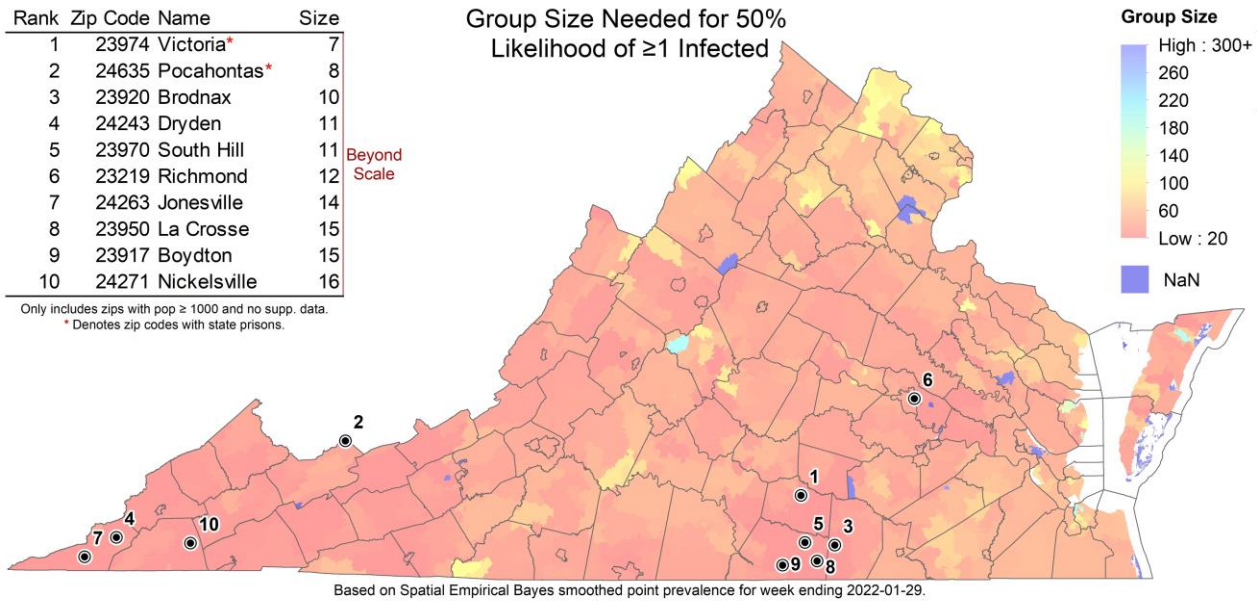
Risk of Exposure by Group Size and HCW prevalence

Case Prevalence in the last week by zip code used to calculate risk of encountering someone infected in a gathering of randomly selected people (group size 25)

- **Group Size**: Assumes 2 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 (eg in a group of 7 in Victoria, there is a 50% chance someone will be infected)
- **HCW ratio**: Case rate among health care workers (HCW) in the last week using patient facing health care workers as the denominator / general population's case prevalence

Rank	Zip Code	Name	Size
1	23974	Victoria*	7
2	24635	Pocahontas*	8
3	23920	Brodnax	10
4	24243	Dryden	11
5	23970	South Hill	11
6	23219	Richmond	12
7	24263	Jonesville	14
8	23950	La Crosse	15
9	23917	Boydton	15
10	24271	Nickelsville	16

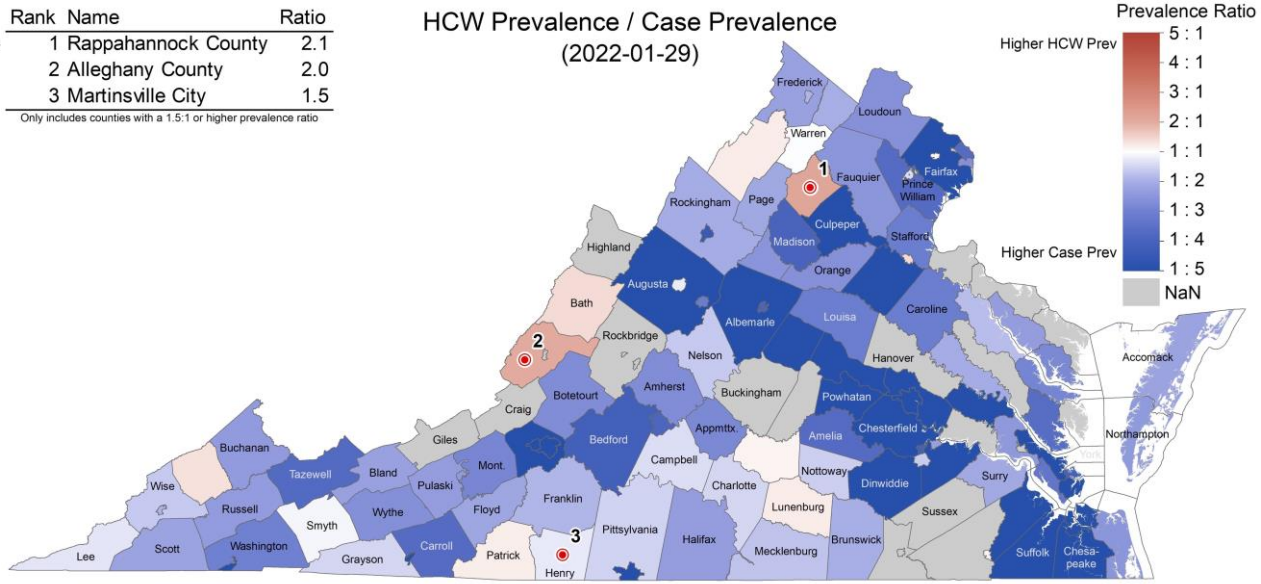
Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.



Based on Spatial Empirical Bayes smoothed point prevalence for week ending 2022-01-29.

Rank	Name	Ratio
1	Rappahannock County	2.1
2	Alleghany County	2.0
3	Martinsville City	1.5

Only includes counties with a 1.5:1 or higher prevalence ratio



Current Hot-Spots

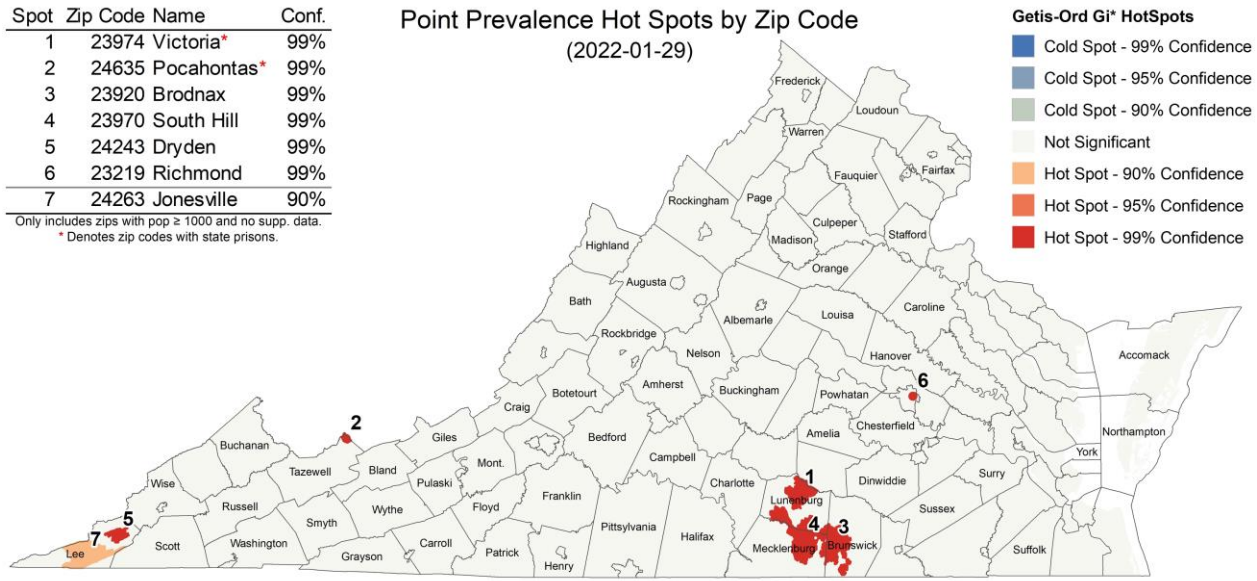
Case rates that are significantly different from neighboring areas or model projections

- **Spatial**: Getis-Ord Gi* based hot spots compare clusters of zip codes with weekly case prevalence higher than nearby zip codes to identify larger areas with statistically significant deviations
- **Temporal**: The weekly case rate (per 100K) projected last week compared to observed by county, which highlights temporal fluctuations that differ from the model's projections

Spatial Hotspots

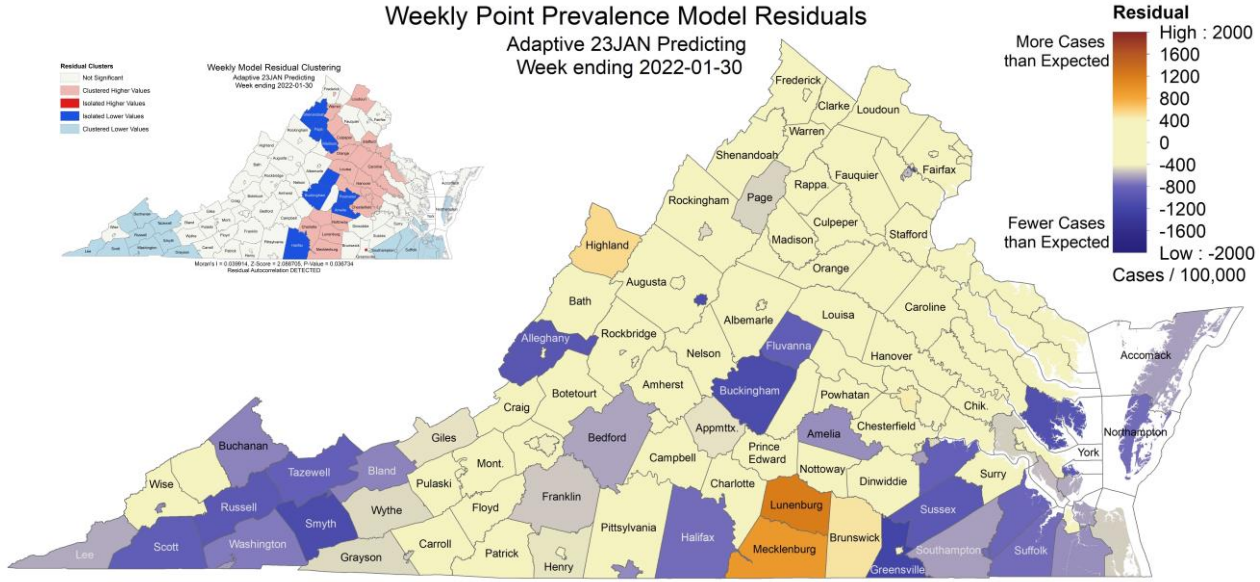
Spot	Zip Code	Name	Conf.
1	23974	Victoria*	99%
2	24635	Pocahontas*	99%
3	23920	Brodnax	99%
4	23970	South Hill	99%
5	24243	Dryden	99%
6	23219	Richmond	99%
7	24263	Jonesville	90%

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



Based on Global Empirical Bayes smoothed point prevalence for week ending 2022-01-29.

Clustered Temporal Hotspots

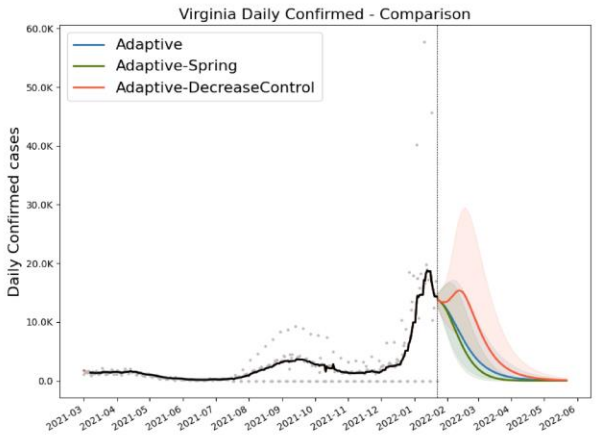


Moran's I = 0.039914, Z-Score = 2.088705, P-Value = 0.036734
Residual Autocorrelation DETECTED

Scenario Trajectory Tracking

Which scenario from last projection did each county track closest?

- Adaptive-Scenario from 2 weeks ago tracked the growth from Omicron well, however, has likely significantly underestimated total infections and lack of multi-strain support
- The other Omicron scenarios were very similar two weeks ago and the western area of the state tracked its growth well

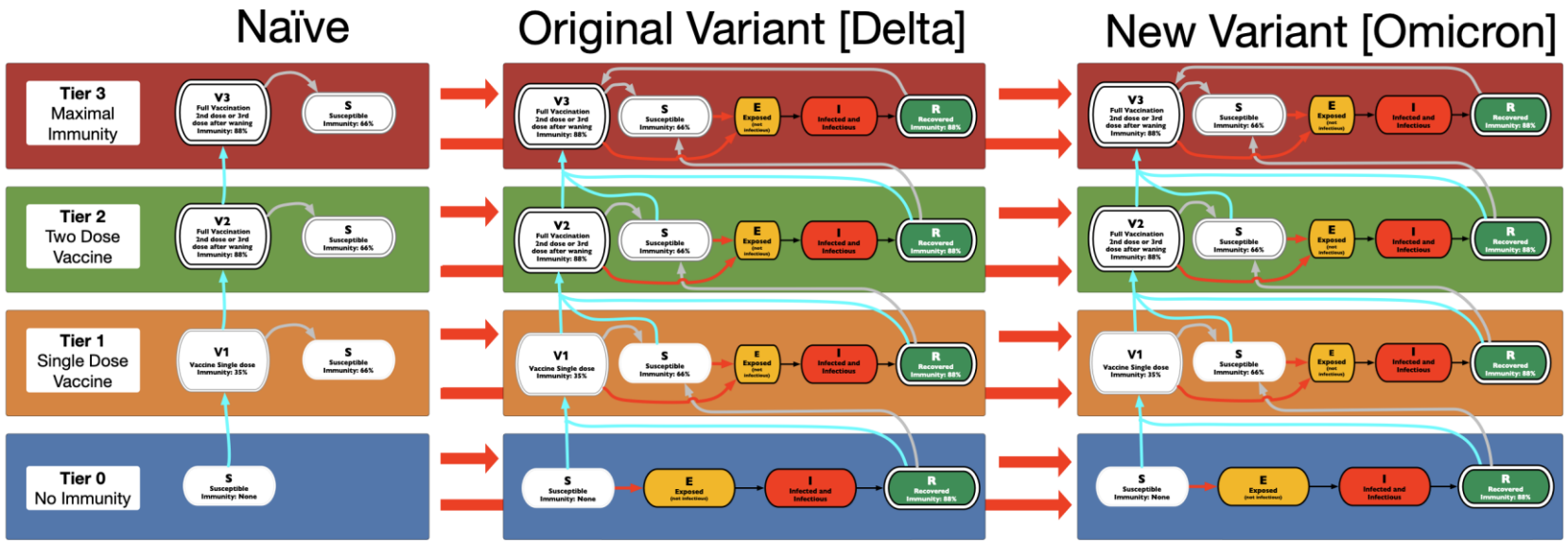


Model Update – Adaptive Fitting

Model Structure Extended for Multiple Strains

Omicron escapes immunity from vaccinated and those infected with Delta

- Multiple strain support allows representation of differential protection based on immunological history
- Severity of Outcomes varies by strain and level of immunity, thus allowing model to better capture hospitalizations and deaths from Omicron
- Adaptive fitting approach continues to use simulation to generate the full distribution of immune states across the population



Adaptive Fitting Approach

Each county fit precisely, with recent trends used for future projection

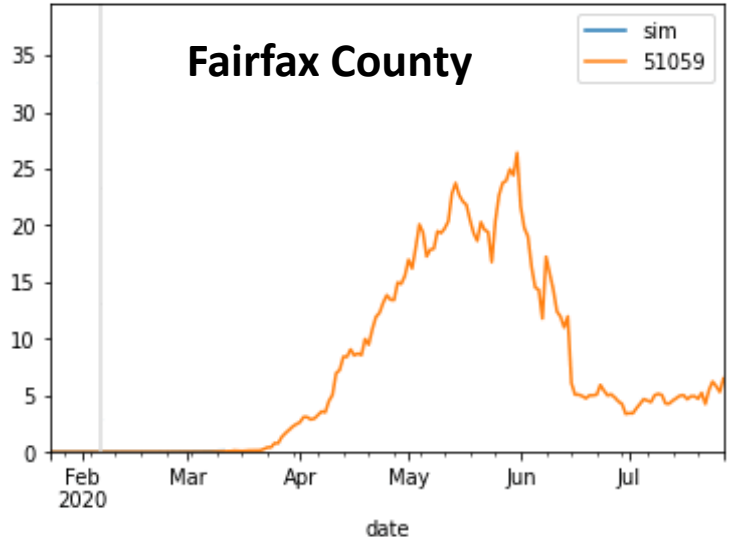
- Allows history to be precisely captured, and used to guide bounds on projections

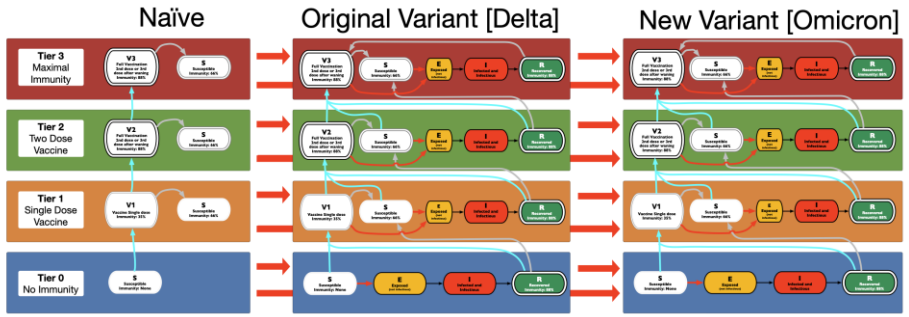
Model: An alternative use of the same meta-population model, PatchSim with multiple tiers of immunity

- Allows for future "what-if" Scenarios to be layered on top of calibrated model
- Allows for waning of immunity and for partial immunity against different outcomes (eg lower protection for infection than death)

External Seeding: Steady low-level importation

- Widespread pandemic eliminates sensitivity to initial conditions, we use steady 1 case per 10M population per day external seeding





Using Ensemble Model to Guide Projections

Ensemble methodology that combines the Adaptive with machine learning and statistical models such as:

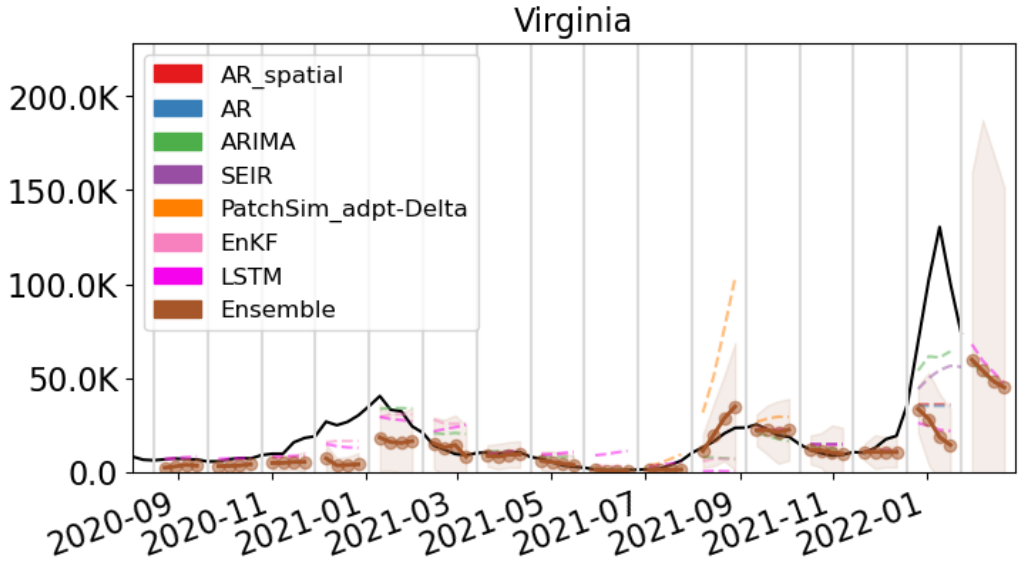
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

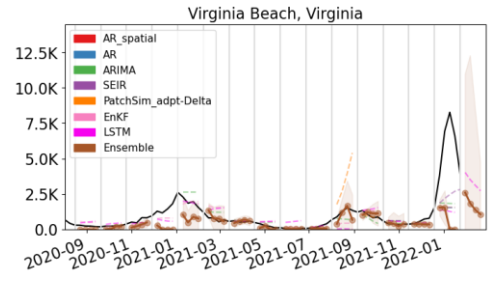
<u>Weekly forecasts</u> done at county level.

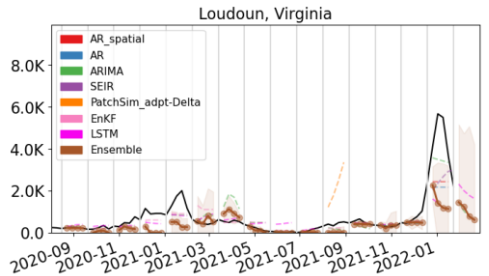
Models chosen because of their track record in disease forecasting and to increase diversity and robustness.

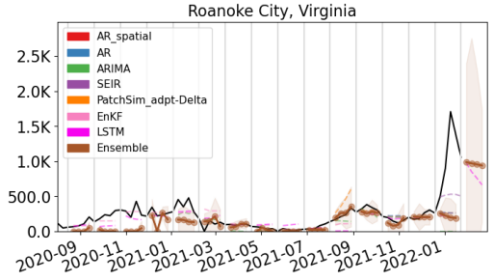
Ensemble forecast provides additional ‘surveillance’ for making scenario-based projections.

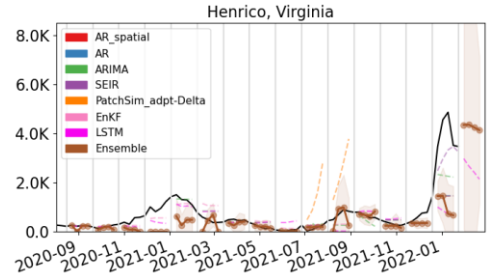
Also submitted to CDC Forecast Hub.











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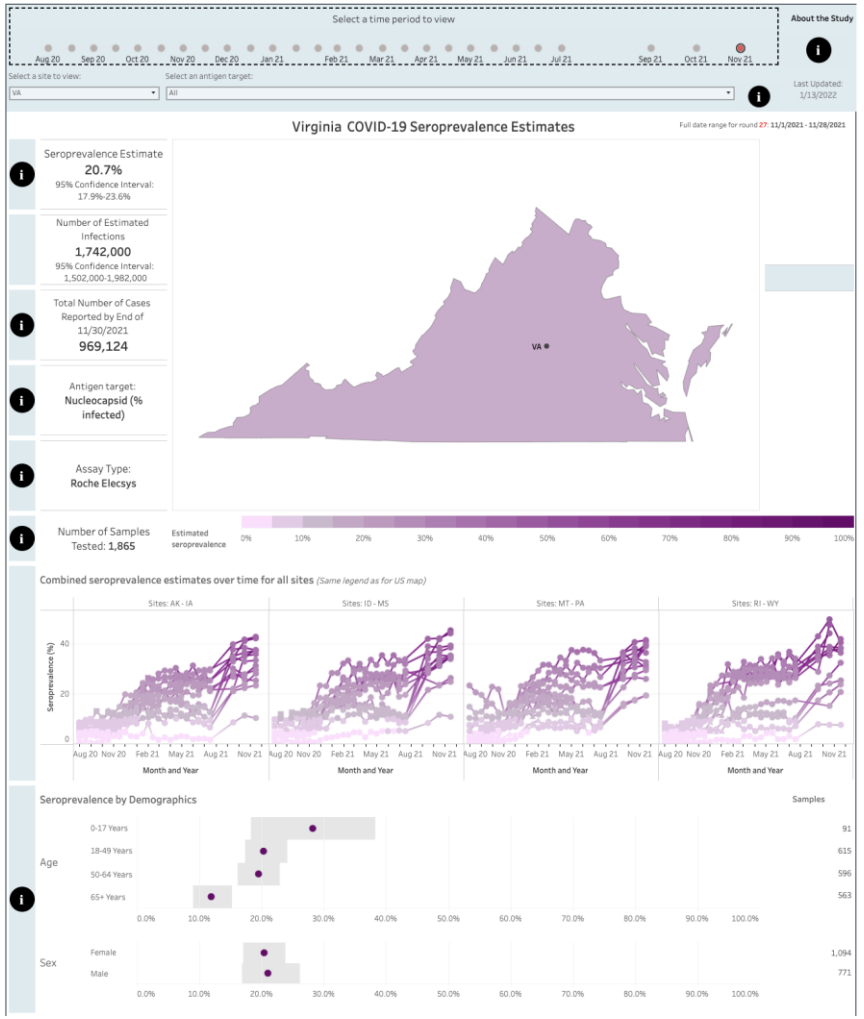
Seroprevalence updates to model design

Several seroprevalence studies provide better picture of how many actual infections have occurred

- CDC Nationwide Commercial Laboratory Seroprevalence Survey

These findings are equivalent to an ascertainment ratio of ~2x in the future, with bounds of (1.3x to 3x)

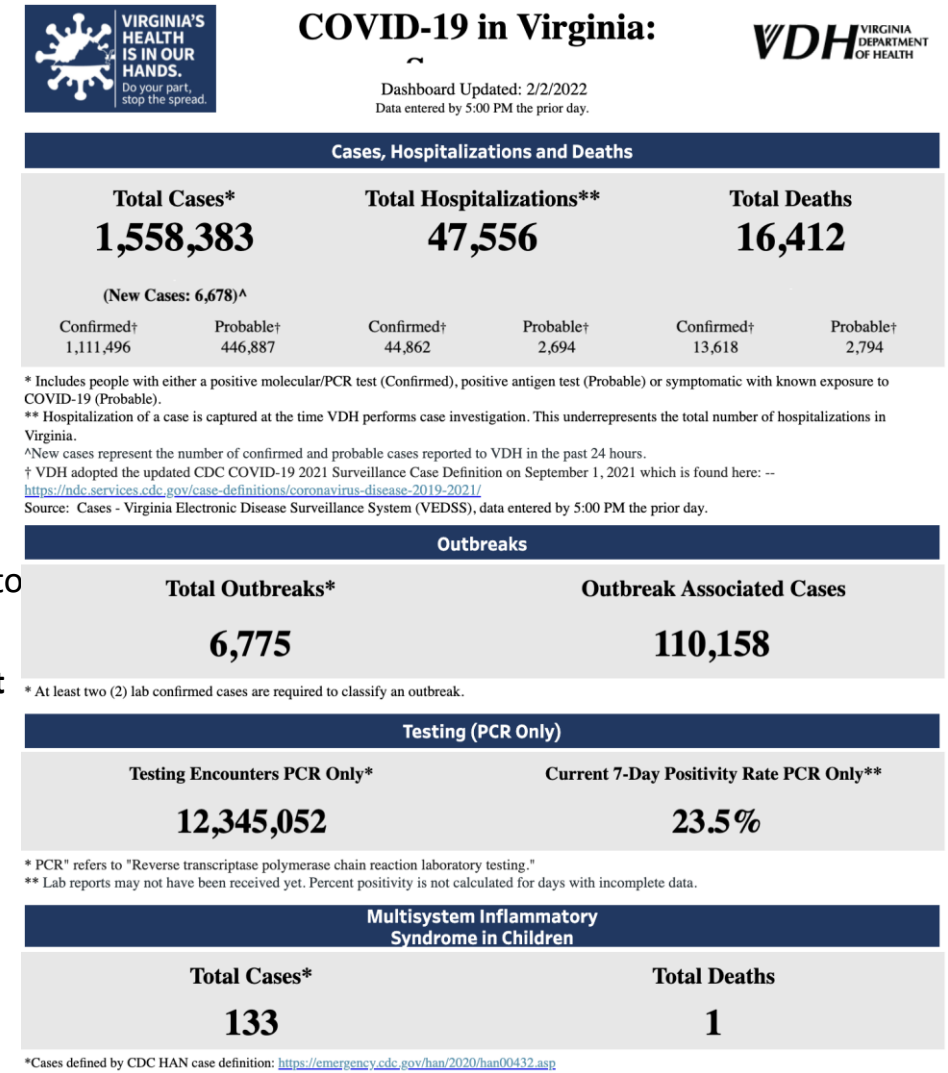
- Thus for 2x there are 2 total infections in the population for every confirmed case recently
- **Case ascertainment is half of that for those with prior immunity**
- Uncertainty design has been shifted to these bounds (previously higher ascertainments as was consistent earlier in the pandemic were being used)



https://covid.cdc.gov/covid-data-tracker/#national-lab

Calibration Approach

- **Data:**
  - County level case counts by date of onset (from VDH)
  - Confirmed cases for model fitting
- **Calibration:** fit model to observed data and ensemble's forecast
  - Tune transmissibility across ranges of:
    - Duration of incubation (5-9 days), infectiousness (3-7 days)
    - Undocumented case rate (1x to 7x) guided by seroprevalence studies
    - Detection delay: exposure to confirmation (4-12 days)
  - Approach captures uncertainty, but allows model to precisely track the full trajectory of the outbreak
- **Project:** future cases and outcomes generated using the collection of fit models run into the future
  - **Mean trend from last 7 days of observed cases and first week of ensemble's forecast used**
  - Outliers removed based on variances in the previous 3 weeks
  - 2 week interpolation to smooth transitions in rapidly changing trajectories
- **Outcomes**: Data driven by shift and ratio that has least error in last month of observations
  - Hospitalizations: 3 days from confirmation, 6.8% of cases hospitalized
  - Deaths: 11 days from confirmation, 1.45% of cases die



VIRGINIA'S HEALTH IS IN OUR HANDS. Do your part, stop the spread.

COVID-19 in Virginia:

VDH VIRGINIA DEPARTMENT OF HEALTH

Dashboard Updated: 2/2/2022
Data entered by 5:00 PM the prior day.

Cases, Hospitalizations and Deaths

Total Cases*	Total Hospitalizations**	Total Deaths
1,558,383	47,556	16,412
(New Cases: 6,678)^		

Confirmed†	Probable†	Confirmed†	Probable†	Confirmed†	Probable†
1,111,496	446,887	44,862	2,694	13,618	2,794

* Includes people with either a positive molecular/PCR test (Confirmed), positive antigen test (Probable) or symptomatic with known exposure to COVID-19 (Probable).
** Hospitalization of a case is captured at the time VDH performs case investigation. This underrepresents the total number of hospitalizations in Virginia.
^New cases represent the number of confirmed and probable cases reported to VDH in the past 24 hours.
† VDH adopted the updated CDC COVID-19 2021 Surveillance Case Definition on September 1, 2021 which is found here: -- https://ndc.services.cdc.gov/case-definitions/coronavirus-disease-2019-2021/
Source: Cases - Virginia Electronic Disease Surveillance System (VEDSS), data entered by 5:00 PM the prior day.

Outbreaks

Total Outbreaks*	Outbreak Associated Cases
6,775	110,158

* At least two (2) lab confirmed cases are required to classify an outbreak.

Testing (PCR Only)

Testing Encounters PCR Only*	Current 7-Day Positivity Rate PCR Only**
12,345,052	23.5%

* PCR" refers to "Reverse transcriptase polymerase chain reaction laboratory testing."
** Lab reports may not have been received yet. Percent positivity is not calculated for days with incomplete data.

Multisystem Inflammatory Syndrome in Children

Total Cases*	Total Deaths
133	1

*Cases defined by CDC HAN case definition: https://emergency.cdc.gov/han/2020/han00432.asp

Accessed 10:00am February 2, 2022
https://www.vdh.virginia.gov/coronavirus/

Scenarios – Transmission Conditions

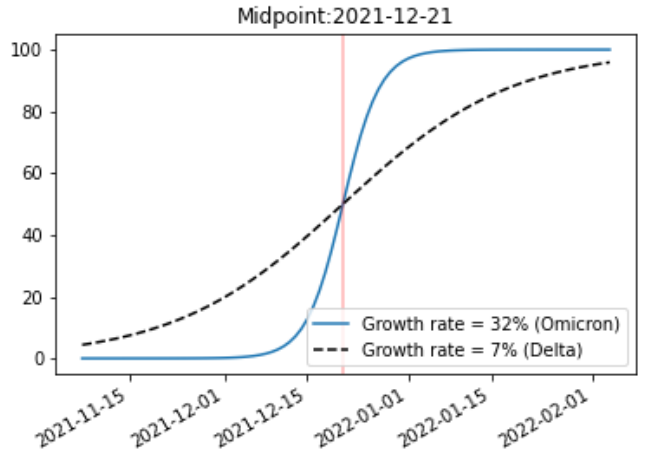
- Variety of factors continue to drive transmission rates
  - Seasonal impact of weather patterns, travel and gatherings, fatigue and premature relaxation of infection control practices
- **Waning Immunity**: Mean of 6 months to a year protection (rate of 0.0027) similar to Pfizer study
- **Projection Scenarios**:
  - **Adaptive:** Control remains as is currently experienced into the future with assumption that Omicron remains as the majority strain, and that infection with Omicron provides protection against Omicron infection in the future
  - **Adaptive-Spring:** Same as Adaptive, except transmission rates are driven down by behaviors and seasonal effects by 60% over the next 2 months (as observed last Fall-Winter wave
  - **Adaptive-DecreasedControl:** Same as Adaptive, except transmission rates are driven up by 60% in the coming 2 weeks
  - **Adaptive-VariantBA2:** Same as Adaptive, but with gradual emergence of BA2 subvariant with a 2x transmission advantage over existing Omicron subvariants

Scenarios – Omicron Description

Omicron shown ability to evade immunity and may be more transmissible

- **Transmissibility**: New evidence suggests that Omicron has **similar transmissibility** to Delta
- **Immune Evasion**: Strong evidence demonstrates that Omicron can cause infection in those with some immunity (natural and vaccine induced). Consensus estimate of **80% immune evasion** allows Omicron to infect 80% of individuals that would have otherwise been protected against Delta. Assume that recovery from Omicron provides protection to infection with Omicron similar pre-Omicron variants
- **Prevalence**: Proportion of cases caused by Omicron variant estimated from growth rates observed in other countries with similar levels of immunity (growth of 32%, doubling in ~3 days)
- **Severity:** Several reports suggest Omicron may not cause as severe disease as Delta, we use a 50% reduction in severity for hospitalizations and deaths
- Studies: South Africa, UK, Canada

Estimated Prevalence curve for US



Predominance occurs before Jan 1, 2022

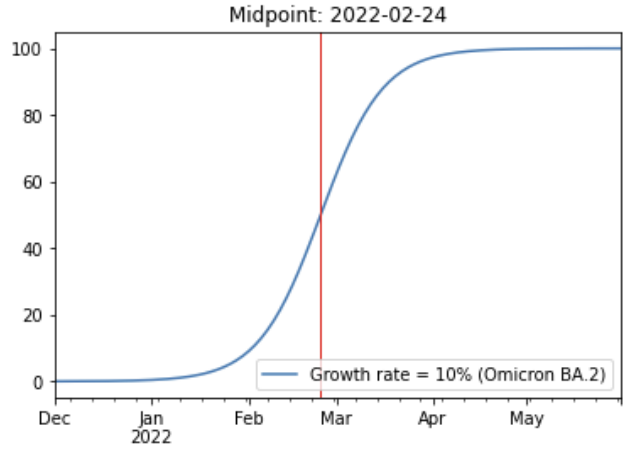
Previous conservative estimates proved to be so, as last projections underpredicted growth.
These consensus estimates may over predict as human behavior and testing may be outpaced by rapid growth.

Scenarios – Omicron BA.2 Description

BA.2 shows signs of increased transmissibility

- **Transmissibility**: Analysis of household contacts in Denmark and the UK suggests a 40% to 3x increase in transmission. We assume a 2x boost for this scenario
- **Prevalence**: Detection in US has been widespread but limited, given growth in Denmark and some foothold assume 50% by end of February
- **Severity:** Assumed to be same as for other Omicron subvariants

Estimated BA2 prevalence projection



This projected prevalence is based on the increase experienced in Denmark the growth rate in VA may be markedly different

Table 3: Relative effect of Omicron VOC BA.2 vs. BA.1

	Susceptibility			Transmissibility		
	Unvaccinated	Fully vaccinated	Booster vaccinated	Unvaccinated	Fully vaccinated	Booster vaccinated
Omicron BA.2 households	2.19 (1.58-3.04)	2.45 (1.77-3.40)	2.99 (2.11-4.24)	2.62 (1.96-3.52)	0.60 (0.42-0.85)	0.62 (0.42-0.91)
Omicron BA.1 households	ref (.)	ref (.)	ref (.)	ref (.)	ref (.)	ref (.)
Number of observations	17,945	17,945	17,945	17,945	17,945	17,945
Number of households	8,541	8,541	8,541	8,541	8,541	8,541

Notes: This table shows odds ratio estimates for the effect of living in a household infected with BA.2 relative to BA.1. Column 1 and 4 shows the relative transmission of BA.2, conditional on being unvac- cinated. Column 2 and 5 shows the relative transmission of BA.2, conditional on being fully vaccinated. Column 3 and 6 shows the relative transmission of BA.2, conditional on being booster vaccinated. Note, all estimates are from the same model, but with a different reference category across column 1-6. The estimates are adjusted for age and sex of the primary case, age and sex of the potential secondary case, size of the household, and primary case sample date. The estimates are furthermore adjusted for vacci- nation status of the potential secondary case and primary case interacted with the household subvariant. 95% confidence intervals are shown in parentheses. Standard errors are clustered on the household level. The odds ratio estimates for the full model are presented in Appendix Table 12, column I

Danish Household Study - MedArxiv

Variant	Household contacts becoming cases / all household contacts	Secondary attack rate amongst household contacts (95% CI)
VUI-22JAN-01 (BA.2)	64 / 476	13.4% (10.7%-16.8%)
Omicron excluding VUI-22JAN-01	10,444 / 101,773	10.3% (10.1%-10.4%)

UK Household Study
PHE Report

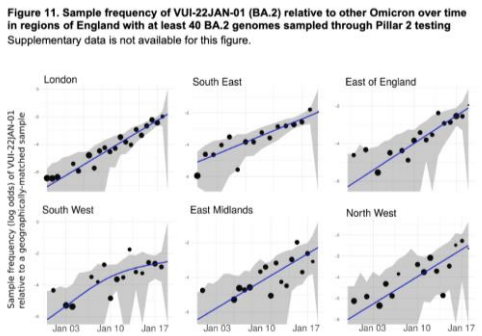


Figure 11. Sample frequency of VUI-22JAN-01 (BA.2) relative to other Omicron over time in regions of England with at least 40 BA.2 genomes sampled through Pillar 2 testing
Supplementary data is not available for this figure.

To provide context surrounding the high growth rate of BA.2 lineage, a comparison was made to cocirculating BA.1 clades in England. Clades were selected which were sampled between 1 December 2021 and 19 January 2022 and which have a cumulative number of samples within 25% of the number of BA.2 genomes sampled in England. Growth rates for each clade were computed by simple logistic regression on time. Figure 12 shows that the BA.2 lineage has the largest growth rate in comparison to similar BA.1 clades.

Projection Scenarios – Combined Conditions

Name	Txm Controls	Vax	Description
Adaptive	C	SQ	Likely trajectory based on conditions remaining similar to the current experience, includes immune escape due to Omicron
Adaptive-Spring	Spring	SQ	Assumes rapid decrease observed last Fall-Winter wave plays out till spring, resulting an overall decrease in transmission drivers of 60%
Adaptive-DecreaseControl	Decrease	SQ	Transmission rates in the next couple weeks are increased 60% and remain at that level demonstrate that increases in case rates remain possible despite the historically high rates, remaining vigilant has benefits
Adaptive-OmicronBA2	C	SQ	Transmission rates for BA2 infections are doubled. BA2 prevalence rises over the course of next 8 weeks from not detected to ~95%

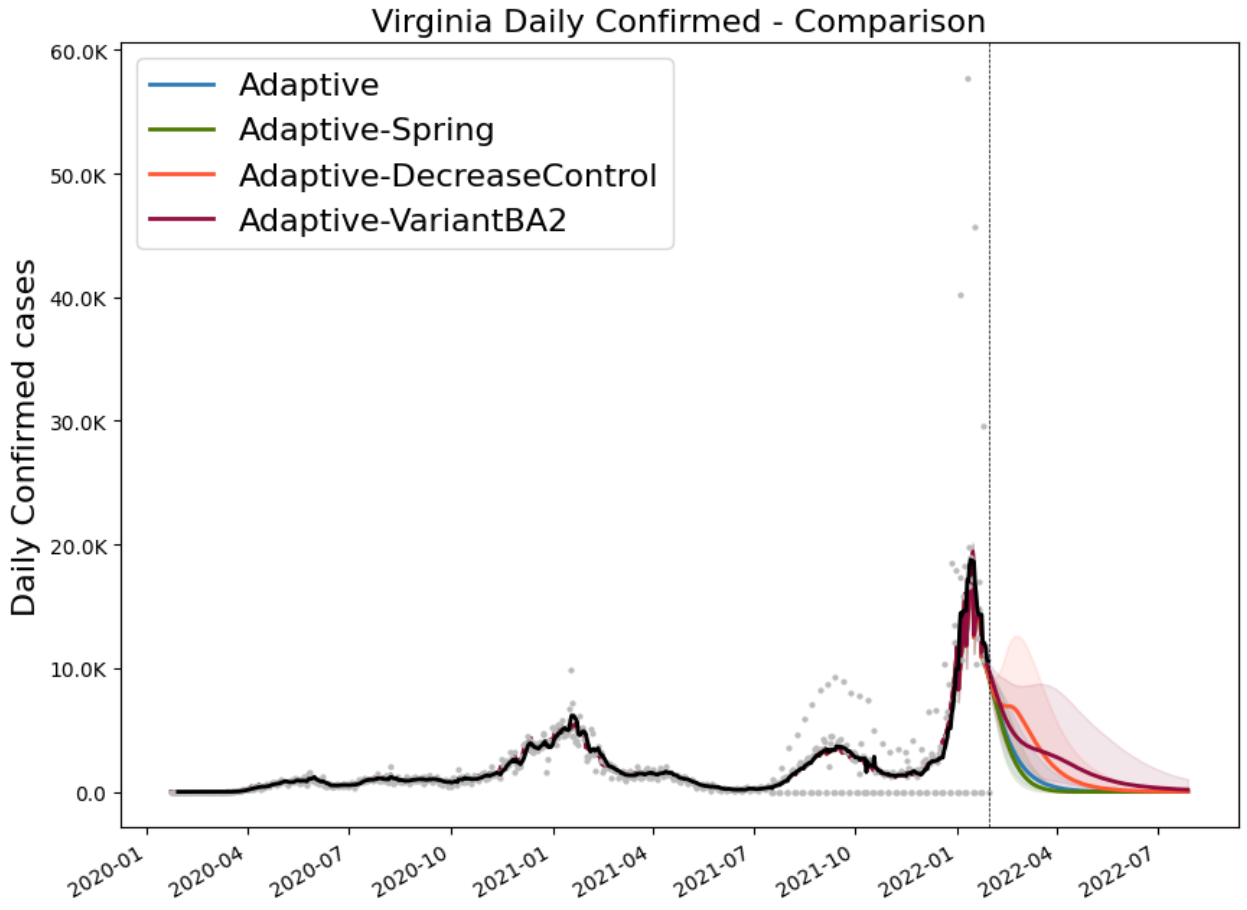
Transmission Controls:
C = Current levels persist into the future
Decrease = Transmission rates are boosted by 60% over next couple weeks and remain at that level
Spring = Transmission rates from mid-Jan 2021 through mid-March 2021 are coarsely replayed, representing a 60% reduction in transmission rate drivers, with Omicron remaining dominant

Vaccinations:
SQ = Status quo acceptance leads to low rates of vaccination through the summer
VO = Vaccination acceptance optimistically expands with increased rates through the summer

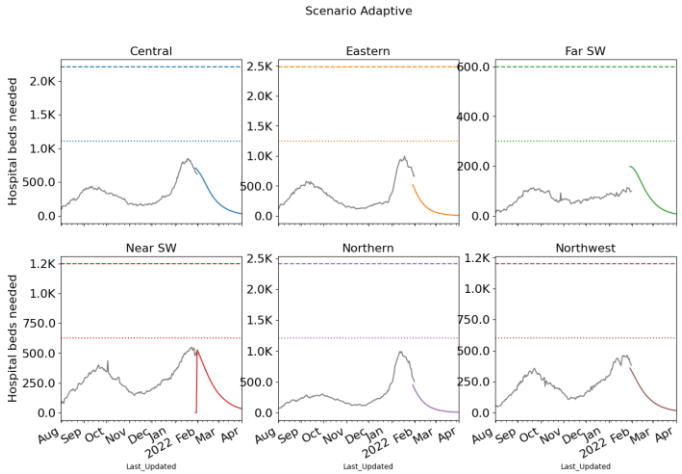
Model Results

Outcome Projections

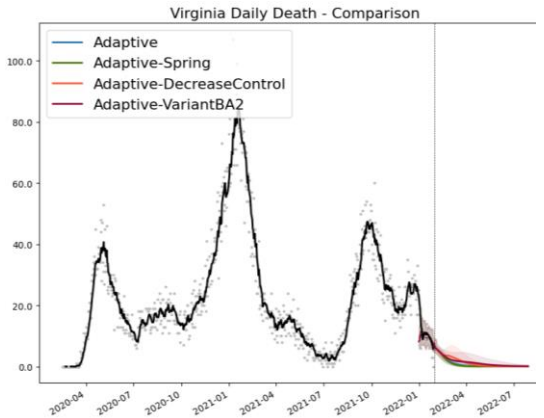
Confirmed cases



Estimated Hospital Occupancy

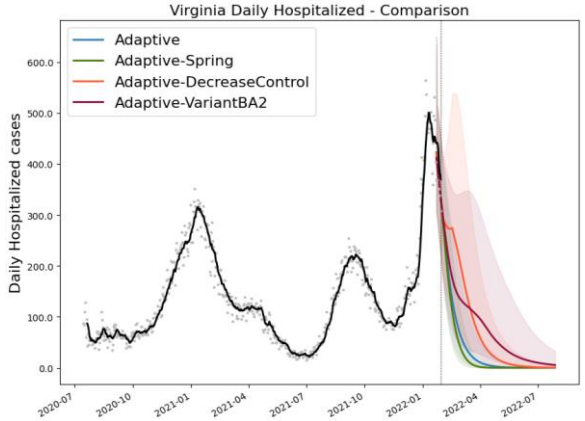


Daily Deaths



Death ground truth from VDH "Event Date" data, most recent dates are not complete

Daily Hospitalized



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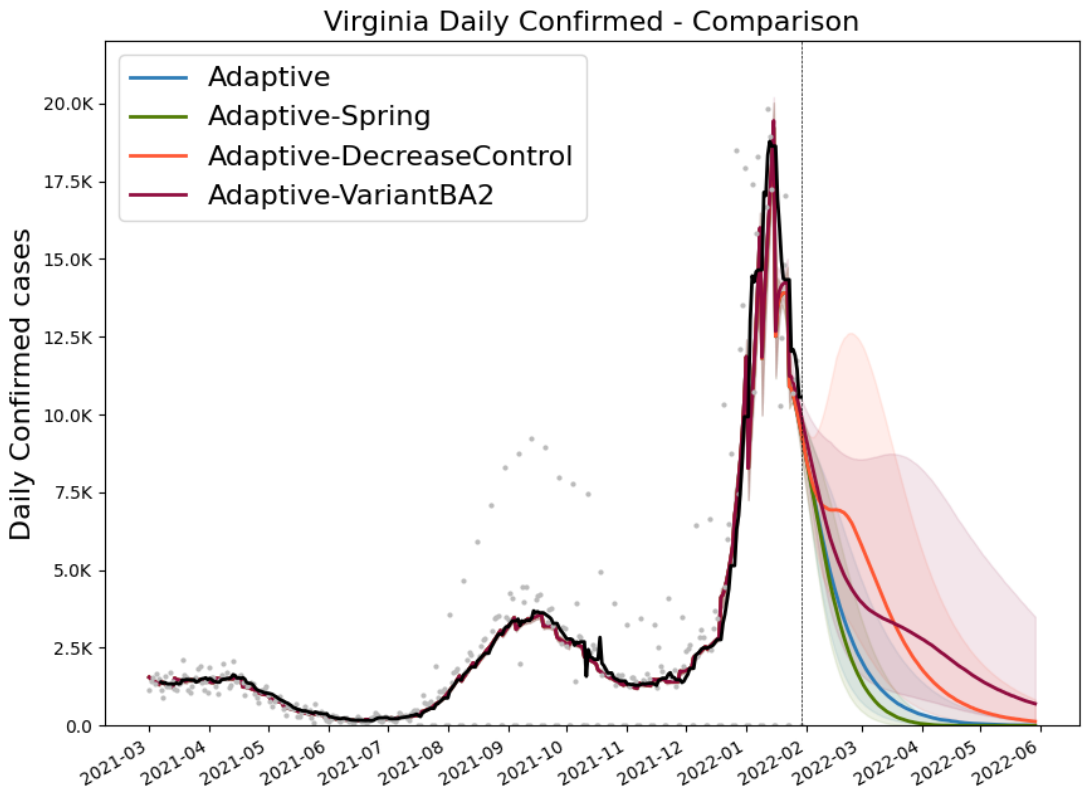
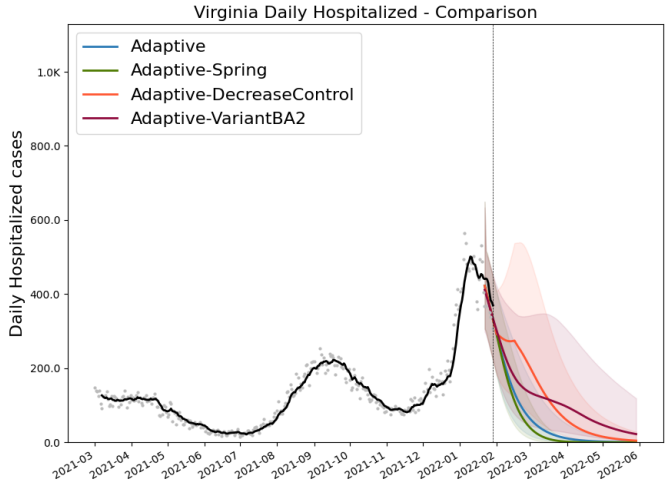
Outcome Projections – Closer Look

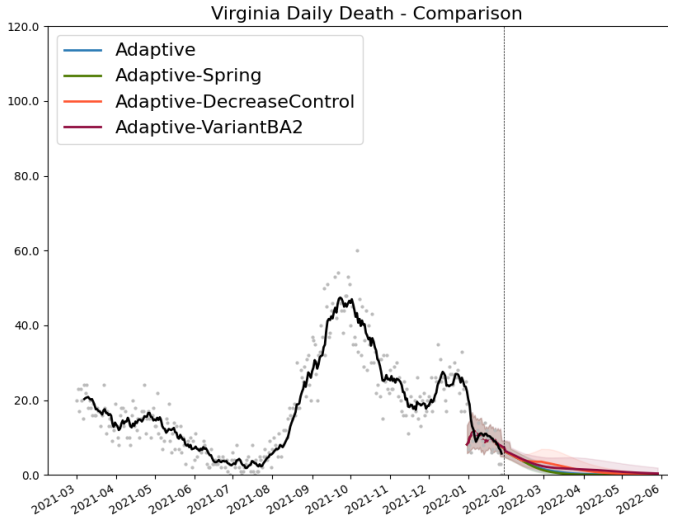
Confirmed cases



Daily Hospitalized



Daily Deaths



Death ground truth from VDH "Event Date" data, most recent dates are not complete

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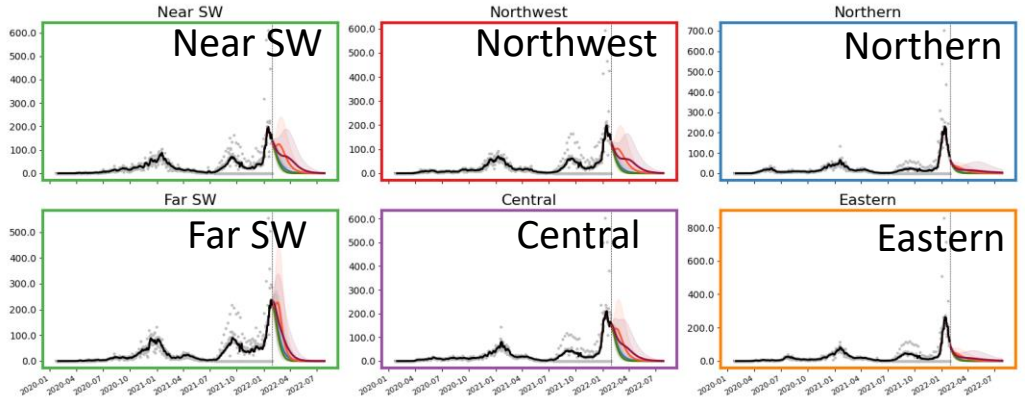
Detailed Projections: All Scenarios

Projections by Region

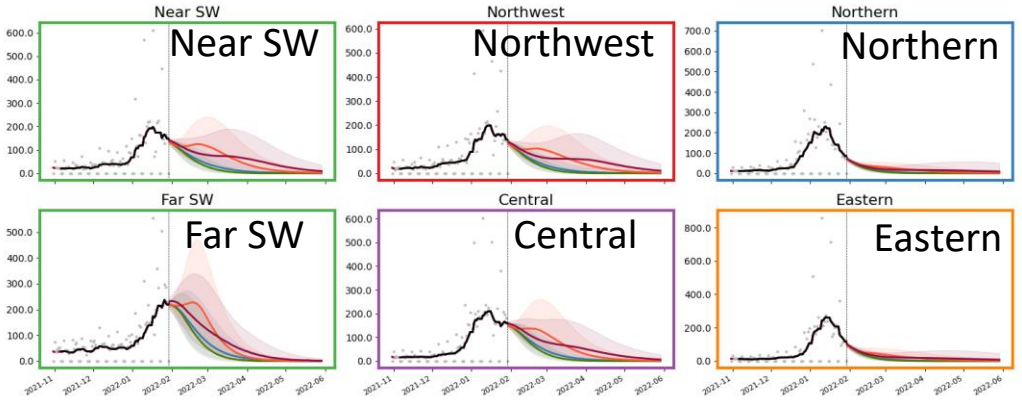


Projections by District

Daily confirmed cases) by rate (per 100K) District (grey with 7-day average in black) with simulation colored by scenario

Detailed Projections: All Scenarios - Closer Look

Projections by Region



Projections by District

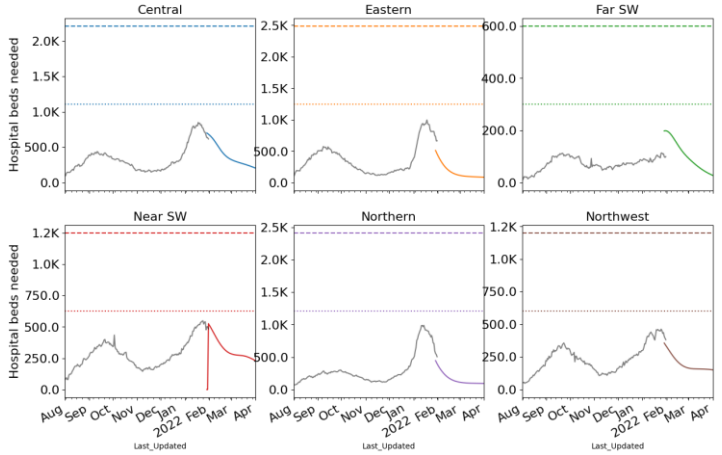
Daily confirmed cases by rate (per 100K) District (grey with 7-day average in black) with simulation colored by scenario

Hospital Demand and Bed Capacity by Region

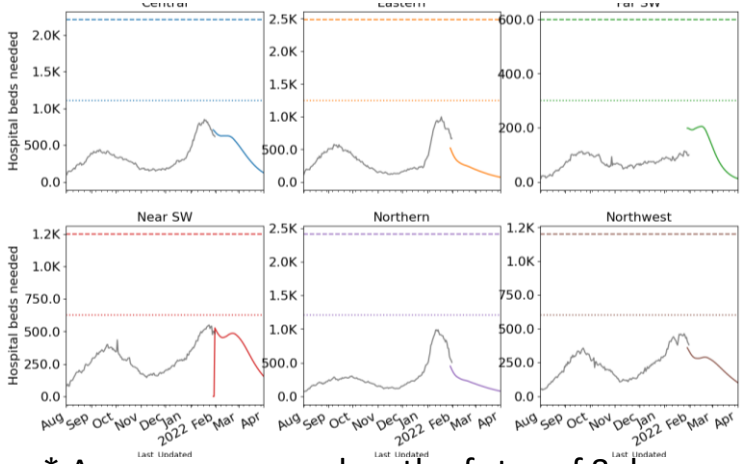
Capacities* by Region

COVID-19 capacity ranges from 80% (dots) to 120% (dash) of total beds

Adaptive



Adaptive – Decrease Control



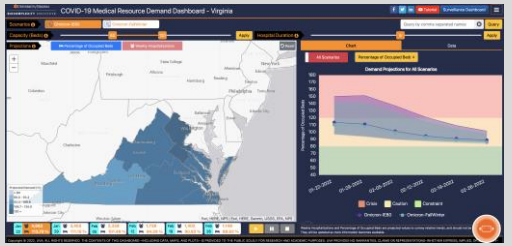
* Assumes average length of stay of 8 days

Length of Stay more variable with Omicron, occupancy projections may vary as a result, ad-hoc estimation performed per region

Current occupancies are pressuring initial capacities in some regions

Projections show continued declines and with expanded capacities, and adjusted length of stay, no capacities exceeded

Interactive Dashboard with regional projections



https://nssac.bii.virginia.edu/covid-19/vmrddash/

Population Immunity

Omicron evades traditional immunity, from the fitted model we estimate tiers of immunity based on variety of immune events experienced by the population

Naïve: No immunity from vaccine or natural infection

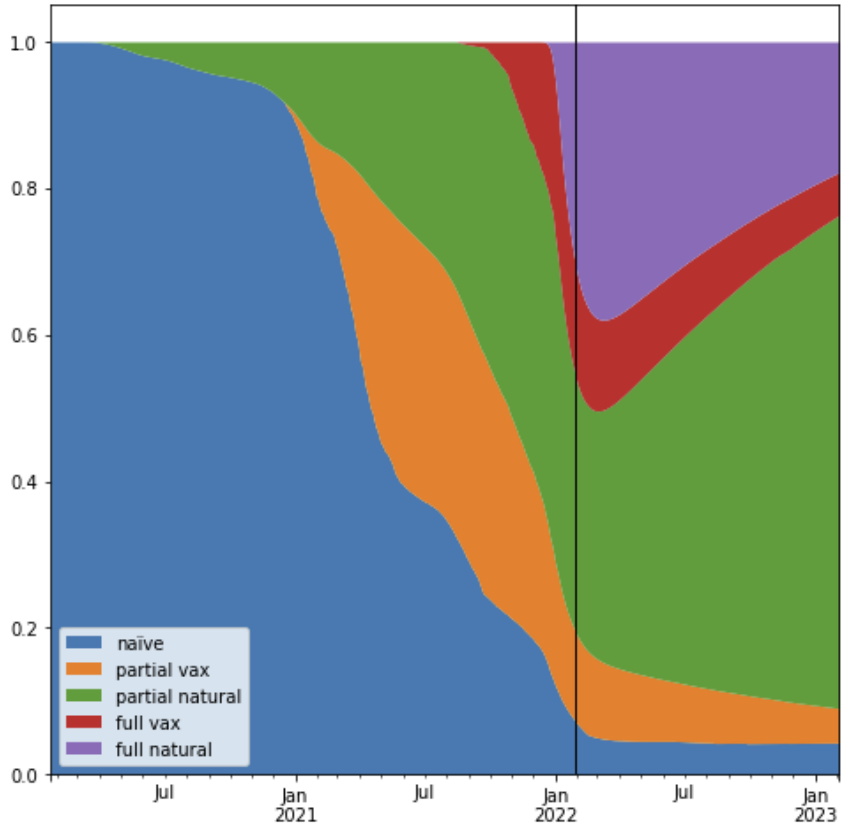
Partial from Vax Only: Weakened immunity from waned vaccinations with no natural infection from Omicron

Partial + Natural: Weakened immunity from waned vaccination or natural infection (including Omicron)

Full from Vax Only: Full immunity from vaccination (3 doses) with no natural infection from Omicron

Full + Natural: Full immunity from recent natural immunity from infection with Omicron for all vaccine tiers

Immunity Levels in Virginia



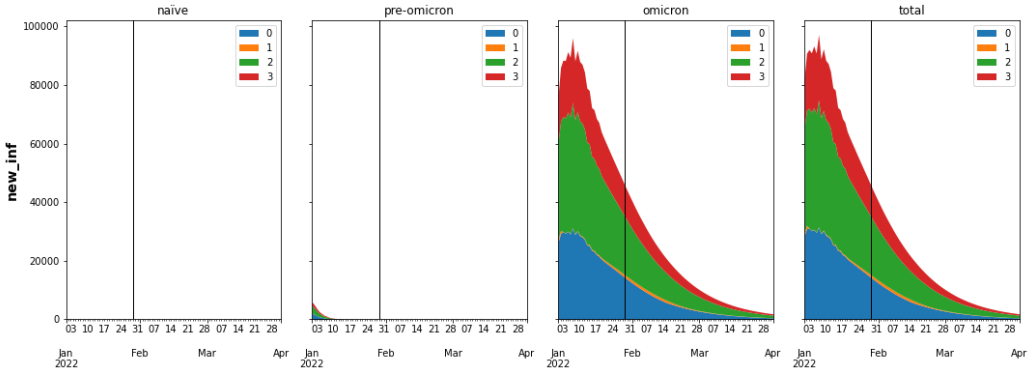
Immunity type	% of pop
Naïve	7.2%
Partial from Vax Only	12.2%
Partial + Natural	34.9%
Full from Vax Only	15.2%
Full + Natural	30.3%

Population Tiers and Strains

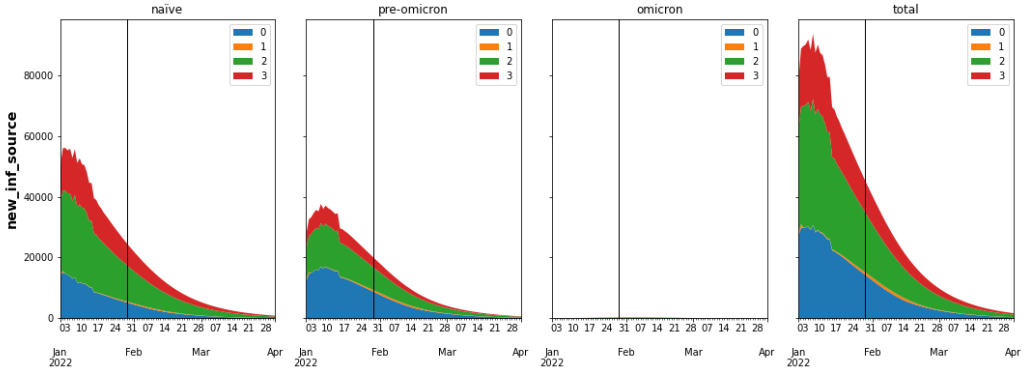
Multi-strain multi-tiered model tracks disease state and immunity of population across variants and 3 levels of vaccination

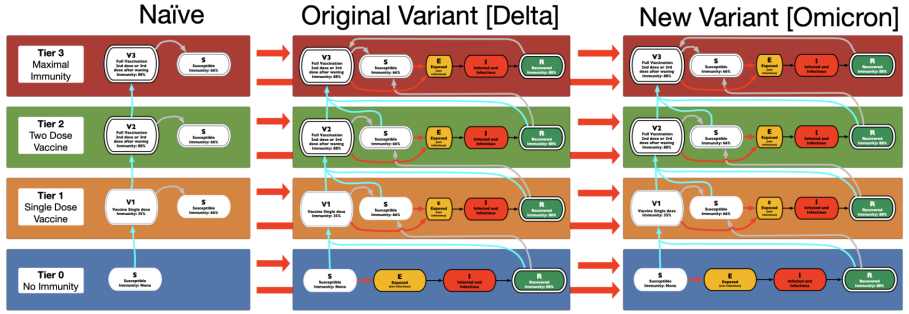
- Detailed look allows view of model's fitted estimate of fractions of the population in any of these immune and infection classes

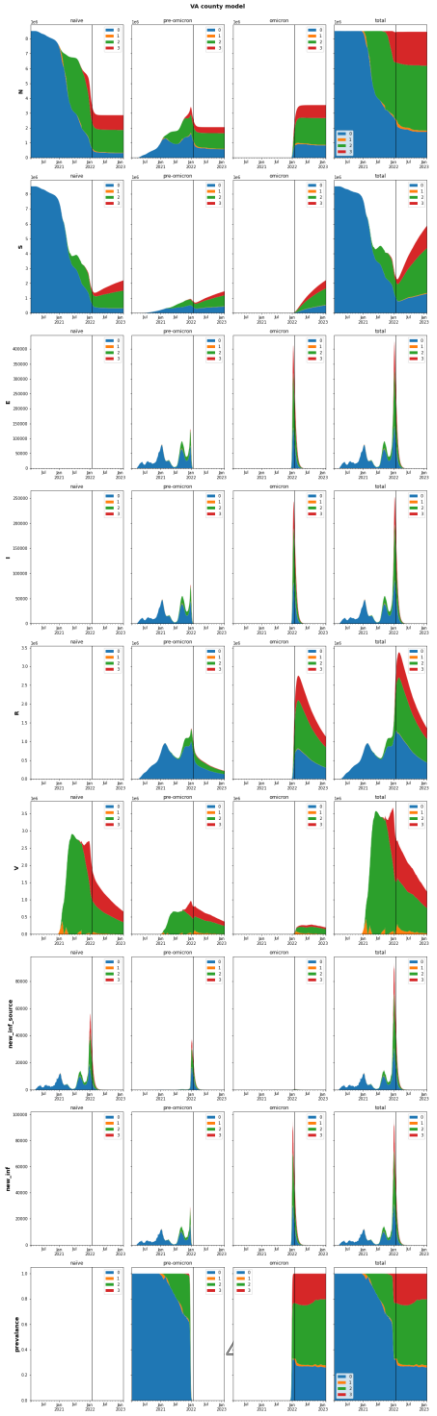
New Infections – Closer Look



Source of Infections – Closer Look







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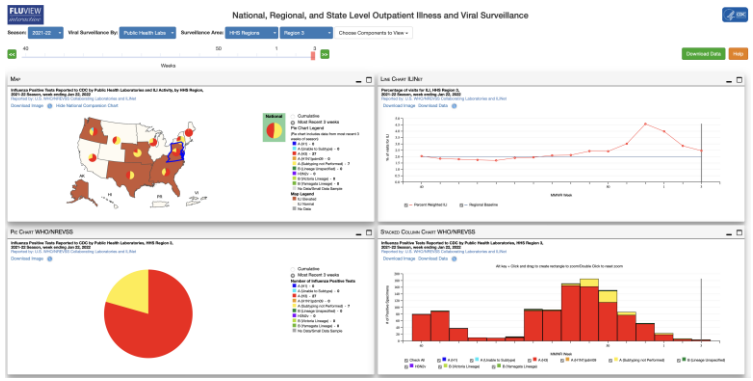
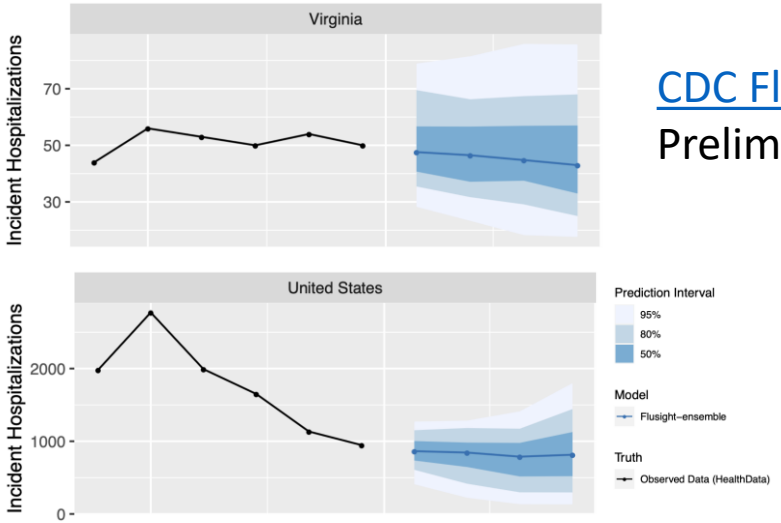
Current Influenza Hospitalization Forecast

Statistical models for submitting to CDC FluSight forecasting challenge

- Similar to COVID-19 case forecasts, uses a variety of statistical and ML approaches to forecast weekly hospital admissions for the next 4 weeks for all states in the US

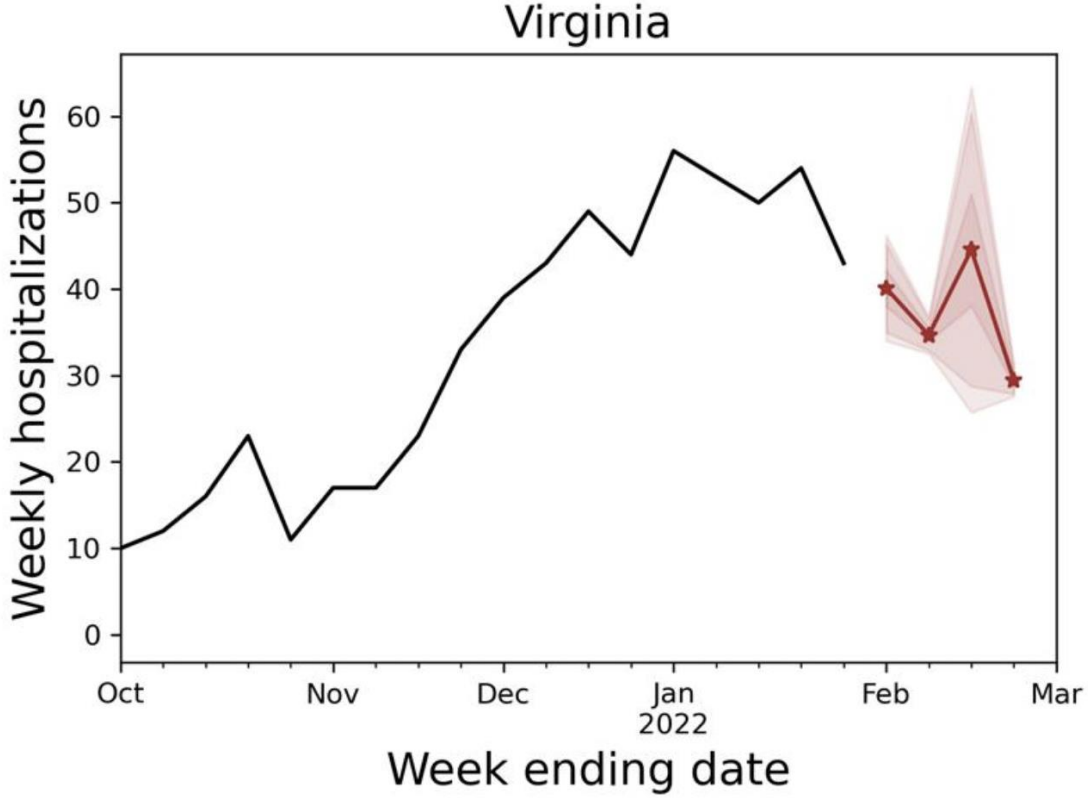


Influenza A activity dropping in our region
Labs show high levels of H3 this season (Influenza A H3N2 is more severe)



[CDC FluSight](#)
Prelim models

Hospital Admissions for Influenza and Forecast for next 4 weeks (UVA ensemble)



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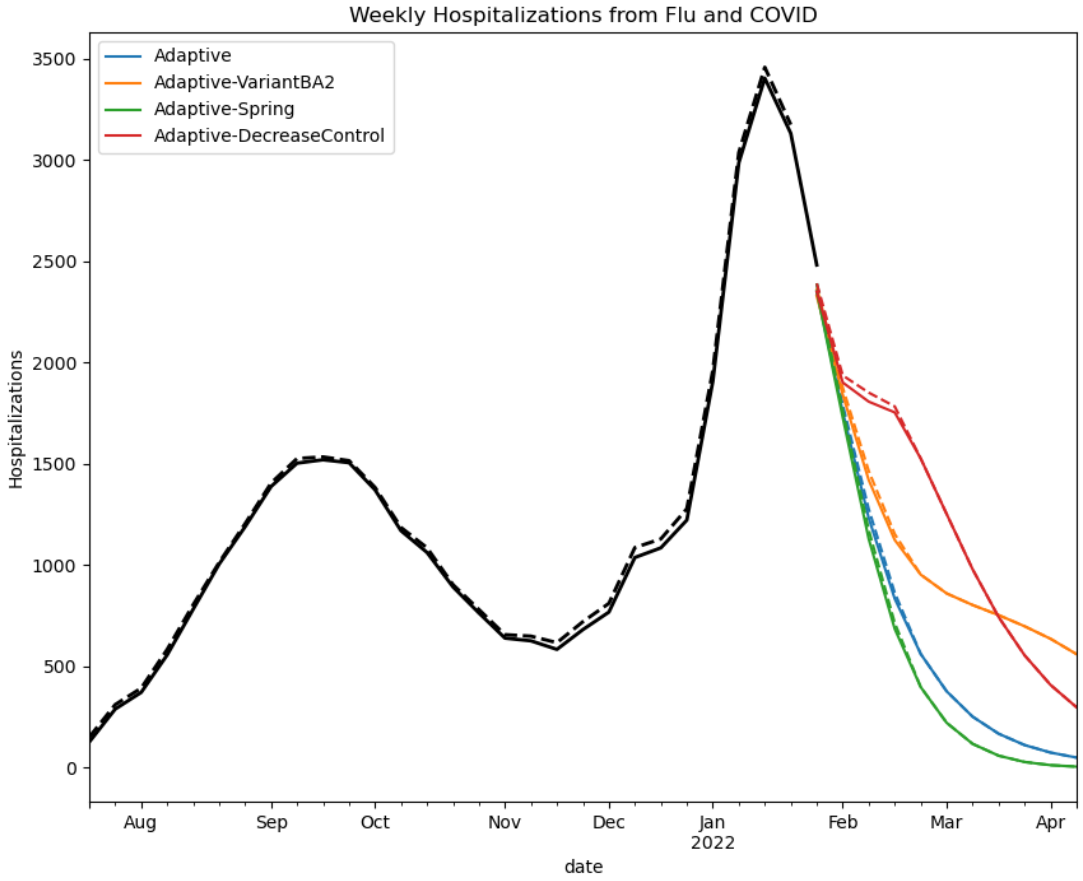
Hospital Admissions from Influenza and COVID-19

Combining Projected COVID-19 admissions with Forecasted Influenza admissions

- Influenza activity is declining as were hospital admissions
- COVID-19 hospitalizations are still at very high levels, but declining
- Scale of COVID hospitalizations remains significantly larger than Influenza

COVID Hospitalizations from Adaptive + Flu Hospitalizations from UVA forecast



Key Takeaways

Projecting future cases precisely is impossible and unnecessary.
Even without perfect projections, we can confidently draw conclusions:

- **Case rates and hospitalizations seem to be leveling off and projections suggest we are nearing the peak**
- VA 7-day mean daily case rate is sharply down to 99/100K from 141/100K
  - US is also considerably down to 132/100K (from 194/100K)
- Projections anticipate continued declines:
  - Potential emerging BA2 subvariant of Omicron could slow and create a “small plateau” in coming weeks
  - Rapidity decline and final level of decline depends on degree of protection to Omicron garnered by previous Omicron infection
- Recent model updates:
  - Further refined model to be multi-variant model structure further refined to better capture different tiers of immunity and the immune evasion of the Omicron variant

The situation continues to change. Models continue to be updated regularly.

Additional Analyses

Weekly Cases and Hospitalizations

Weekly confirmed cases

Week Ending	Adaptive	Adaptive -Spring	Adaptive-Decrease Control	Adaptive-VariantBA2
1/30/22	70283	70280	70280	73504
2/6/22	54940	54676	56218	59897
2/13/22	40272	38454	49438	47114
2/20/22	28258	24698	48357	37248
2/27/22	19397	14924	45332	30827
3/6/22	13070	8554	38458	26910
3/13/22	8747	4652	30881	24680
3/20/22	5826	2430	23791	23144
3/27/22	3908	1175	17900	21579
4/3/22	2604	488	13276	19768
4/10/22	1720	158	9772	17730
4/17/22	1166	36	7149	15427
4/24/22	728	8	5214	13152
5/1/22	448	0	3793	11054

Weekly Hospitalizations

Week Ending	Adaptive	Adaptive-Spring	Adaptive-Decrease Control	Adaptive-VariantBA2
1/30/22	2499	2499	2499	2492
2/6/22	1868	1838	2022	1971
2/13/22	1310	1201	1921	1520
2/20/22	887	729	1865	1203
2/27/22	598	424	1623	1020
3/6/22	401	236	1331	921
3/13/22	268	126	1041	860
3/20/22	179	64	791	806
3/27/22	119	31	590	747
4/3/22	80	14	435	681
4/10/22	54	6	317	600
4/17/22	36	2	231	510
4/24/22	24	1	168	426
5/1/22	17	0	122	355

Overview of relevant on-going studies

Other projects coordinated with CDC and VDH:

- **Scenario Modeling Hub:** Consortium of academic teams coordinated via MIDAS / CDC to that provides regular national projections based on timely scenarios
- **Genomic Surveillance:** Analyses of genomic sequencing data, VA surveillance data, and collaboration with VA DCLS to identify sample sizes needed to detect and track outbreaks driven by introduction of new variants etc.
- **Mobility Data driven Mobile Vaccine Clinic Site Selection:** Collaboration with VDH state and local, Stanford, and SafeGraph to leverage anonymized cell data to help identify

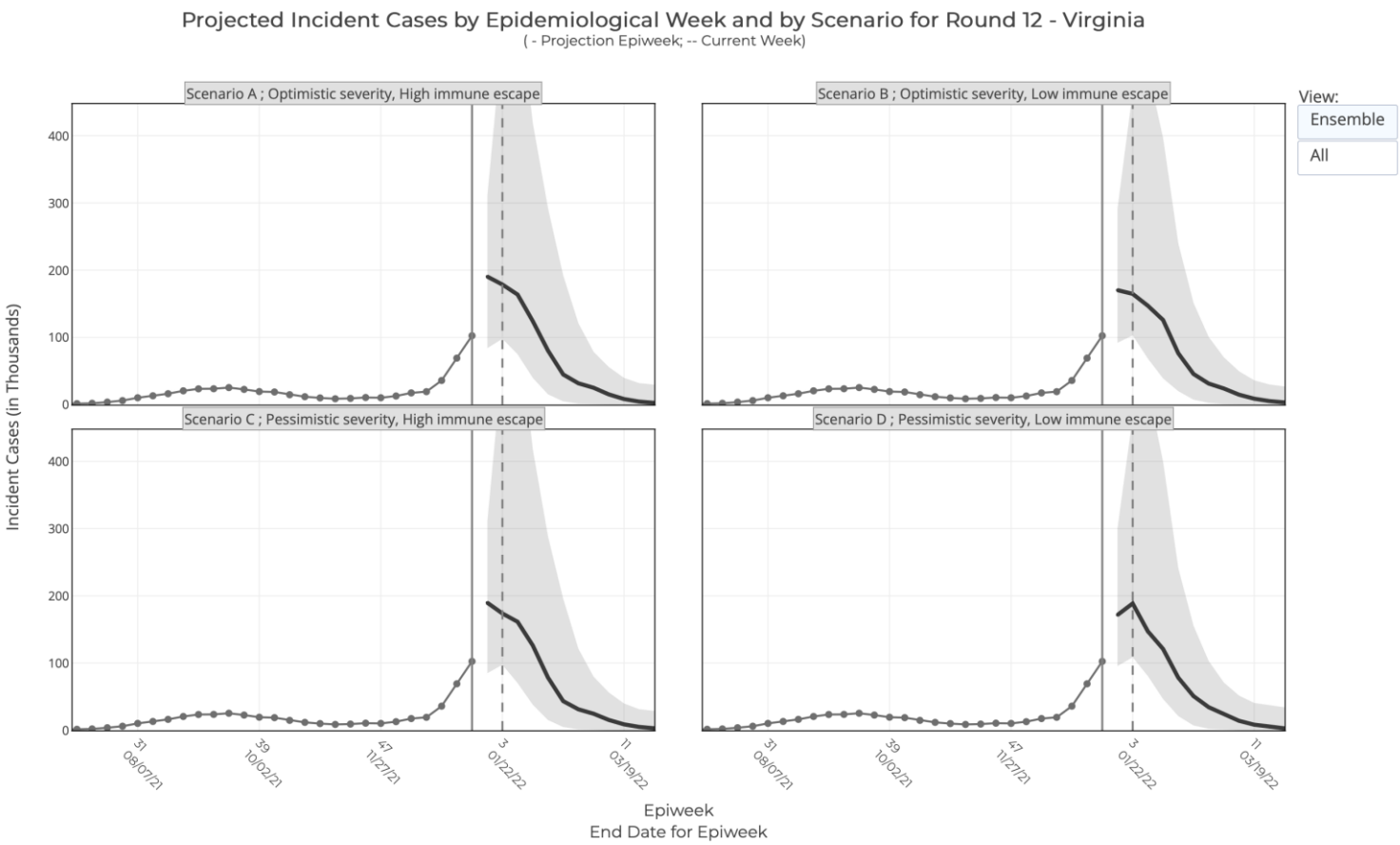
COVID-19 Scenario Modeling Hub

Collaboration of multiple academic teams to provide national and state-by-state level projections for 4 aligned scenarios that vary vaccine rates (high – low) and impact of the Delta variant (high and low)

- Round 12 recently released to assist in federal response to Omicron wave
- Only national consortium tracking Omicron wave well
- Rounds 4-11 now available

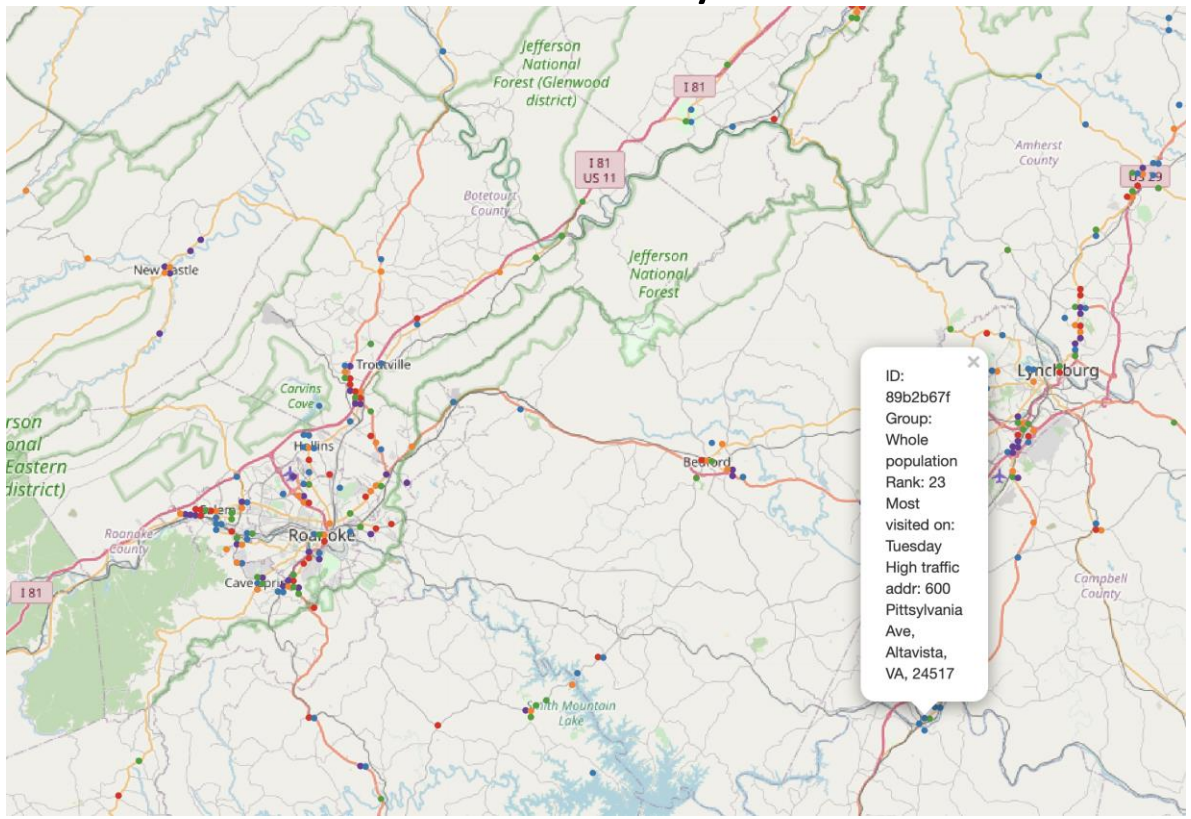
Round 4 Results were published May 5th, 2021 in MMWR

https://covid19scenariomodelinghub.org/viz.html



Data Recommended Mobile Vax Clinic Sites

Detailed and Timely Locations



Data Delivered and Disseminated to Locals

Provides a list of areas most visited by a given demographic group based on SafeGraph mobility data that links visits to specific sites and the home Census Block Group of the anonymized visitors

Demographic Groups: Black, Lantinx, Young Adults (20-40), Unvaccinated, and Whole Population

Data Included: Rank, Weight, most visited Day of Week, Highly Visited Address, and Lat-Long of area

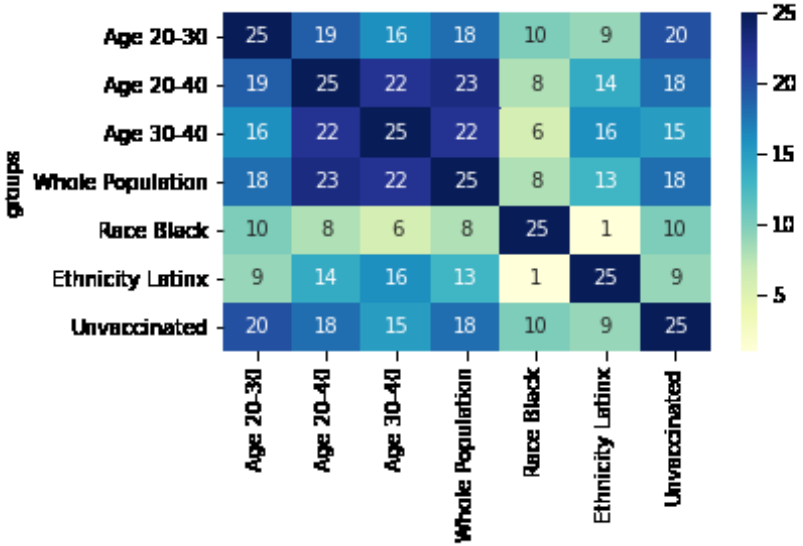
Goal: Provide frequently visited locations based on populations and vaccination levels one desires to reach

Example: List of location in the Southside frequented by 20-40 year olds

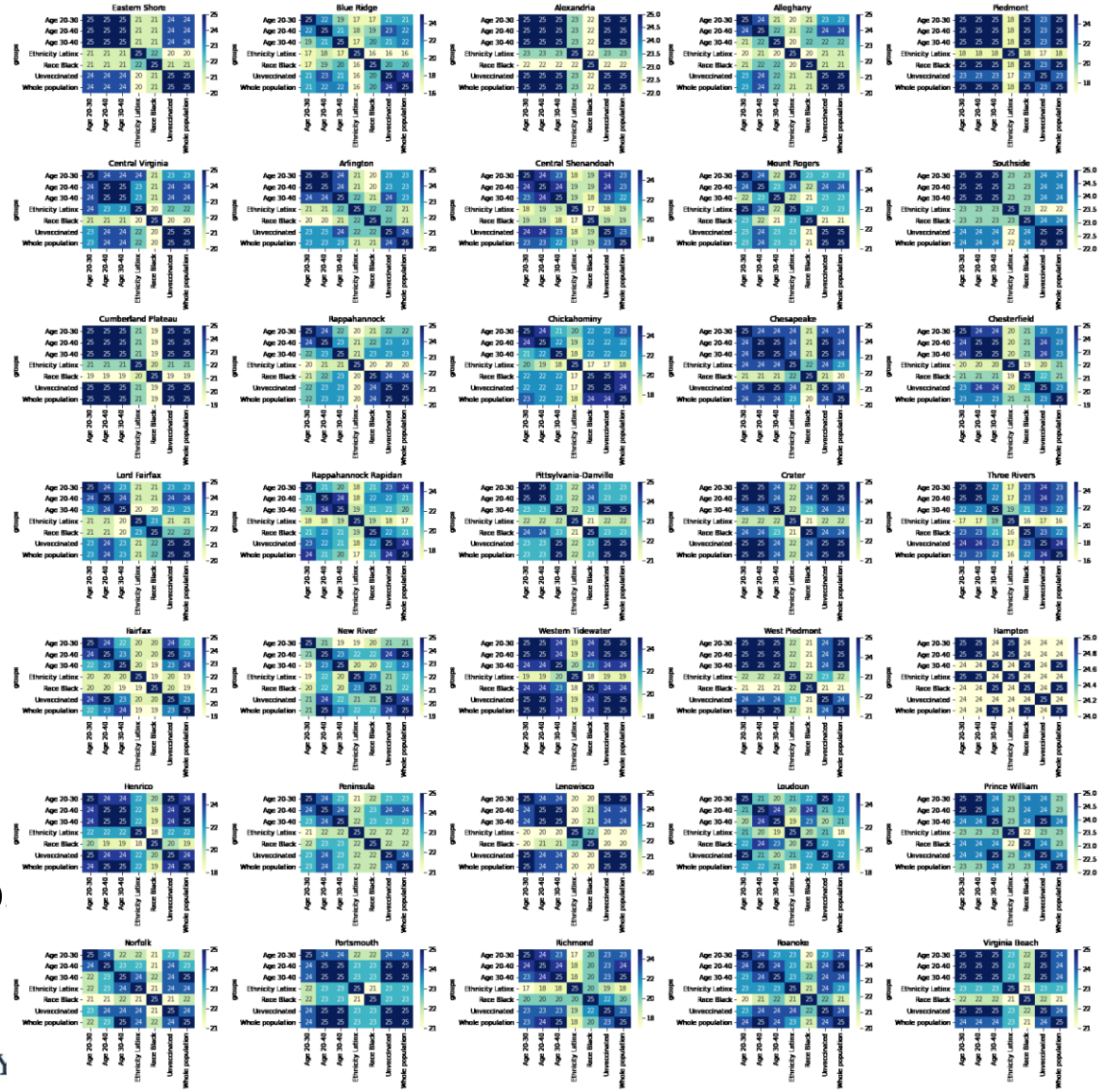
Data Recommended Mobile Vax Clinic Sites

Overlap of locations between groups

State Level



Within VDH Health Districts



Different groups visit different areas

- Least overlap between Black and Latinx
- Overlap in ages highest, but drops with large gap
- Districts have different overlap patterns

References

Venkatramanan, S., et al. "Optimizing spatial allocation of seasonal influenza vaccine under temporal constraints." *PLoS Computational Biology* 15.9 (2019): e1007111.

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NSSAC. PatchSim: Code for simulating the metapopulation SEIR model. https://github.com/NSSAC/PatchSim

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Biocomplexity Institute. COVID-19 Surveillance Dashboard. https://nssac.bii.virginia.edu/covid-19/dashboard/

Google. COVID-19 community mobility reports. https://www.google.com/covid19/mobility/

Biocomplexity page for data and other resources related to COVID-19: https://covid19.biocomplexity.virginia.edu/

Questions?

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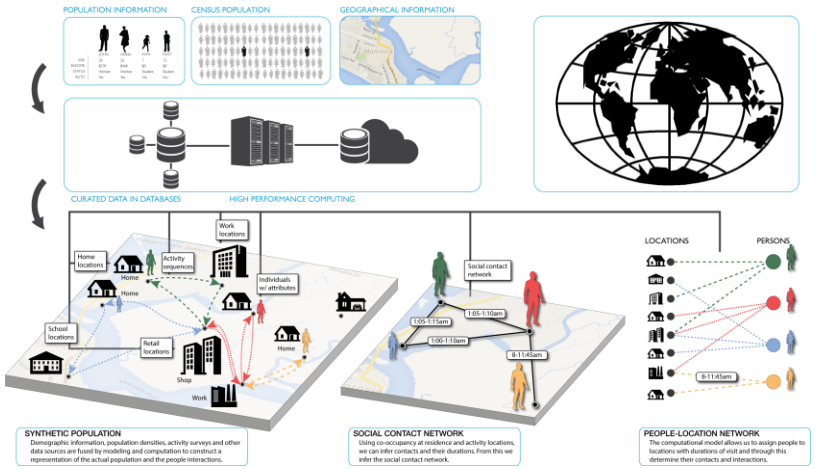
Supplemental Slides

Agent-based Model (ABM)

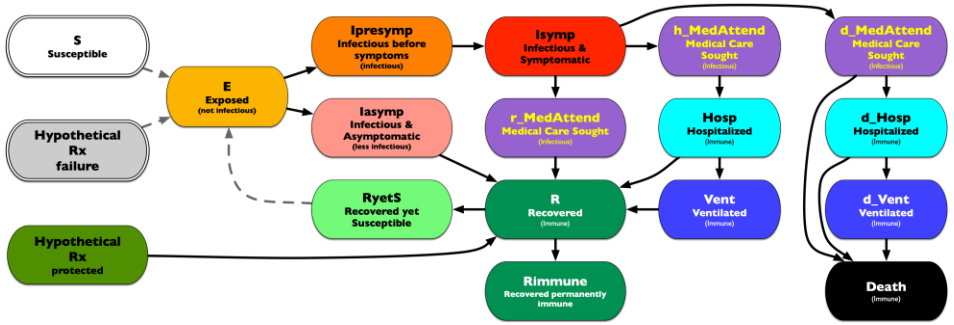
EpiHiper: Distributed network-based stochastic disease transmission simulations

- Assess the impact on transmission under different conditions
- Assess the impacts of contact tracing



Synthetic Population

- Census derived age and household structure
- Time-Use survey driven activities at appropriate locations



Detailed Disease Course of COVID-19

- Literature based probabilities of outcomes with appropriate delays
- Varying levels of infectiousness
- Hypothetical treatments for future developments