Network Systems Science & Advanced Computing

Biocomplexity Institute & Initiative

University of Virginia

Estimation of COVID-19 Impact in Virginia

June 2nd, 2021

(data current to May 29th – June 1st)

Biocomplexity Institute Technical report: TR 2021-066

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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

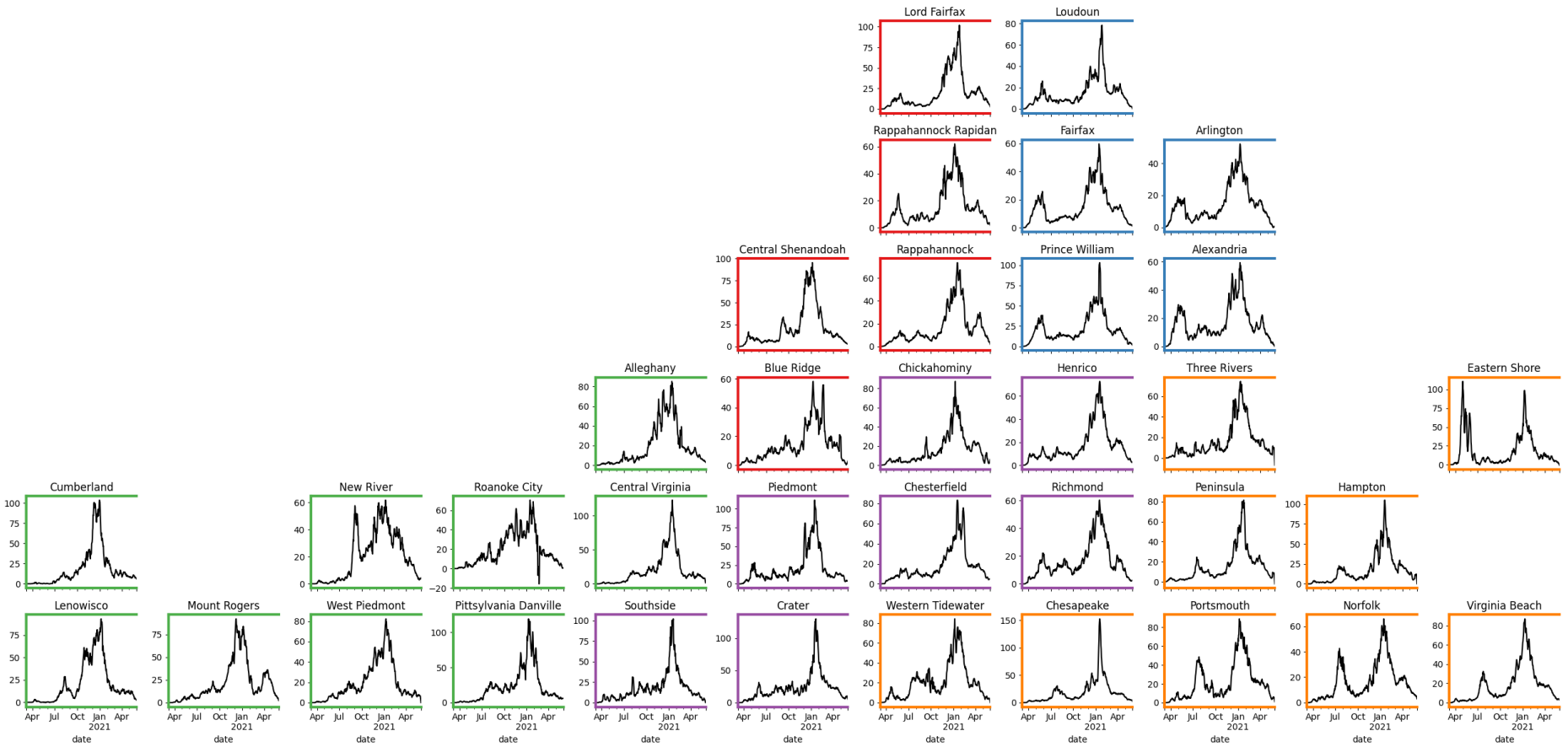
Projecting future cases precisely is impossible and unnecessary.
Even without perfect projections, we can confidently draw conclusions:

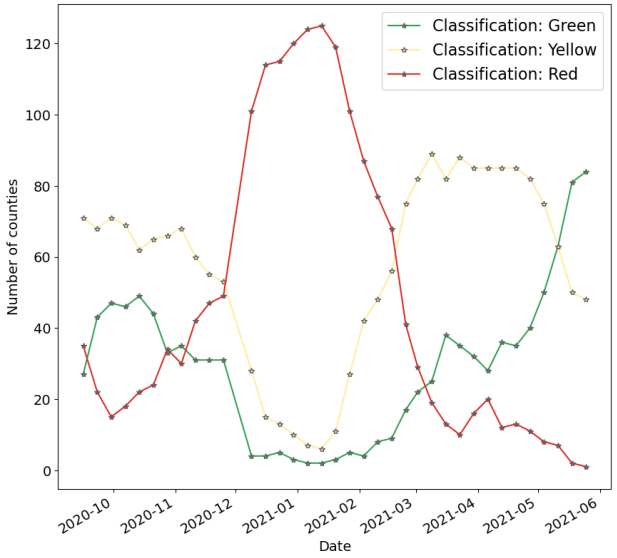
- **Case rates in Virginia continue to decline though some districts have small rebounds in rates**
- VA mean weekly incidence flat at 4/100K, US down to 5/100K from 8/100K
- Vaccination rates continue to decline after rebound from 12-16 year-olds
- Projections show declining rate overall across Commonwealth
- Recent updates:
  - Minor updates to measured acceptance levels and expanded optimistic vaccination scenario
  - Additional Fall resurgence study scenario testing resilience of population
  - Limited waning of natural immunity included in fit and projections, also with seroprevalence update
  - Mobile CVC placement side study undertaken

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

Situation Assessment

Case Rates (per 100k) and Test Positivity





https://data.cms.gov/stories/s/q5r5-gjyu

County level test positivity from RT-PCR tests.

Green: <5.0%

(or with <20 tests in past 14 days)

Yellow: 5.0%-10.0%

(or with <500 tests and <2000 tests/100k and >10% positivity over 14 days

Red: >10.0%

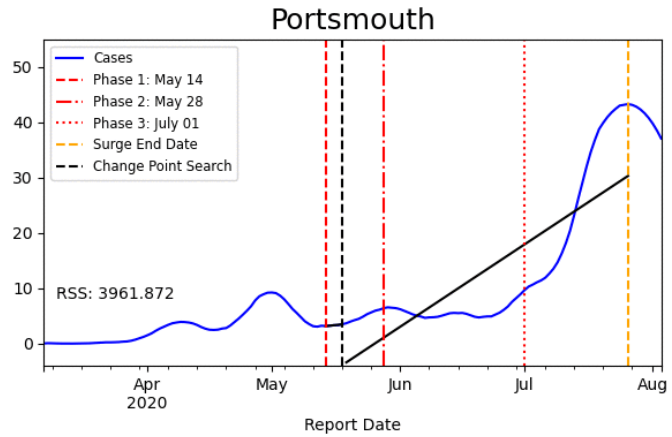
(and not "Green" or "Yellow")

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

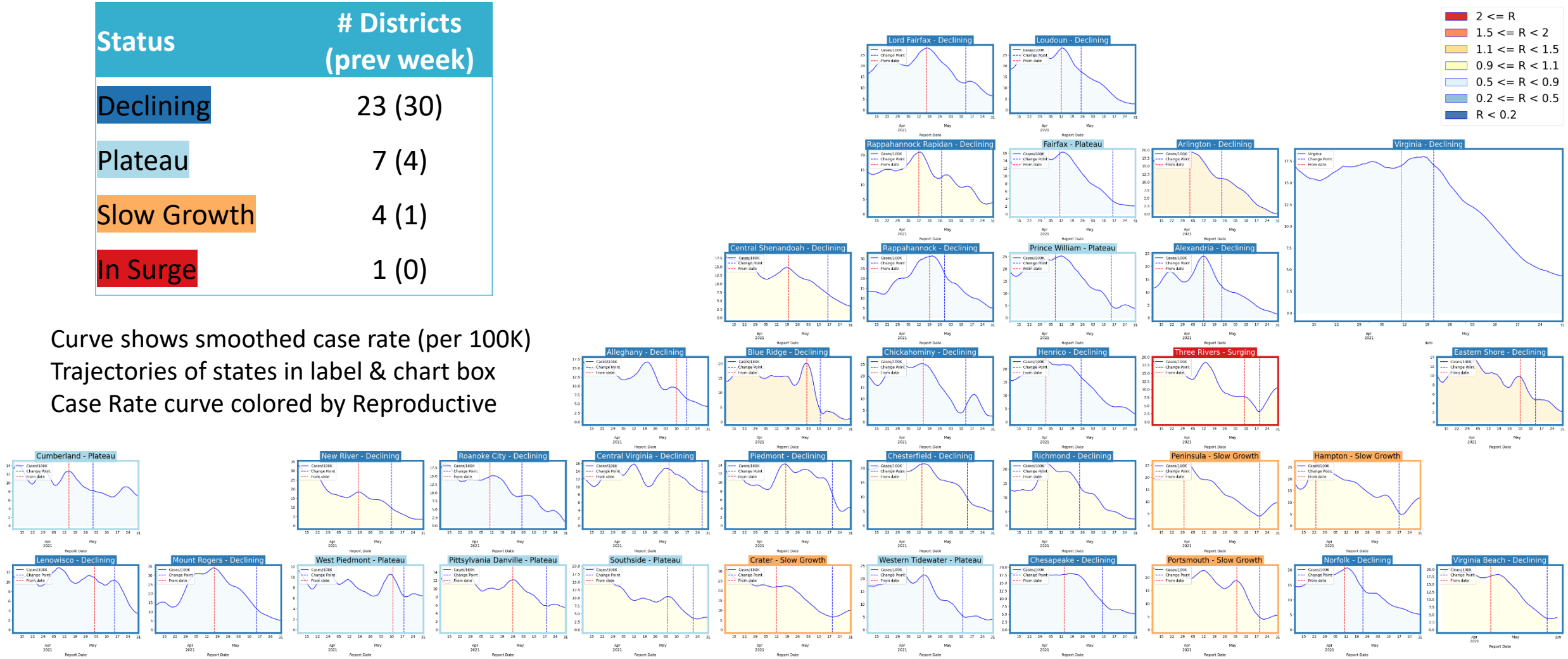


Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	23 (30)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	7 (4)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	4 (1)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	1 (0)

District Trajectories – last 10 weeks

Status	# Districts (prev week)
Declining	23 (30)
Plateau	7 (4)
Slow Growth	4 (1)
In Surge	1 (0)

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



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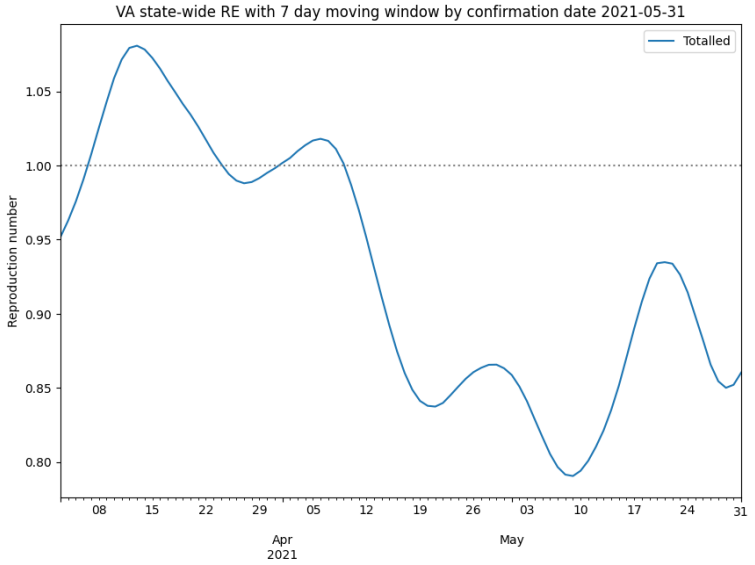
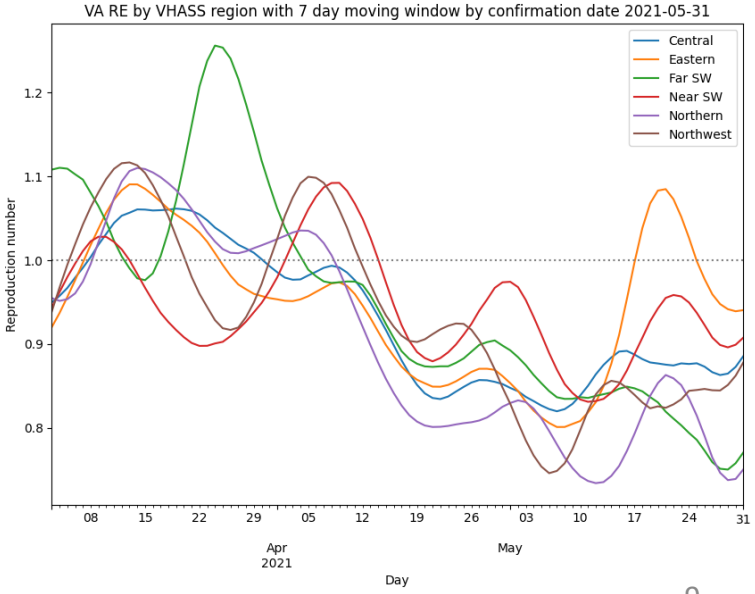
Estimating Daily Reproductive Number

May 31st Estimates

Region	Date Confirmed R_e	Date Confirmed Diff Last Week
State-wide	0.860	0.091
Central	0.886	0.064
Eastern	0.940	0.126
Far SW	0.771	-0.034
Near SW	0.908	0.085
Northern	0.750	0.003
Northwest	0.878	0.190





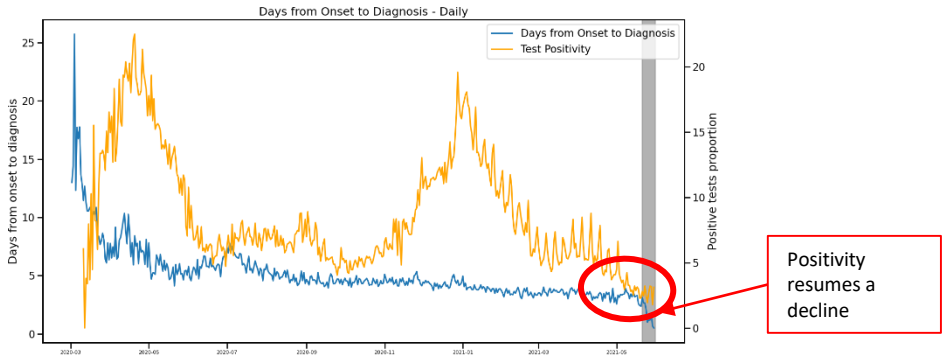
Methodology

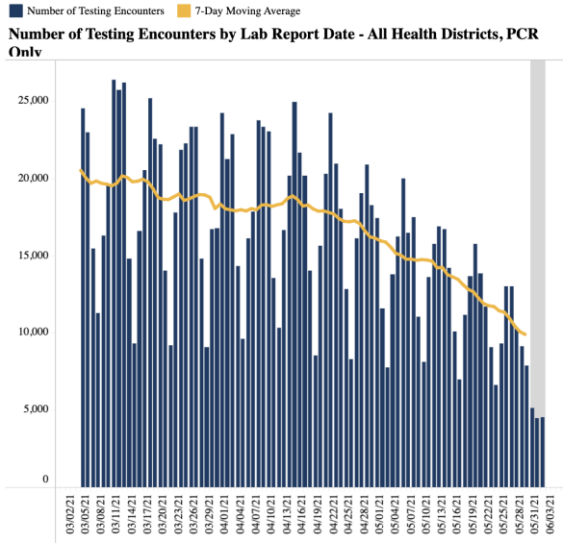
- Wallinga-Teunis method (EpiEstim[1]) for cases by **confirmation date**
- Serial interval: updated to discrete distribution from observations (mean=4.3, Flaxman et al, Nature 2020)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

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

Changes in Case Detection

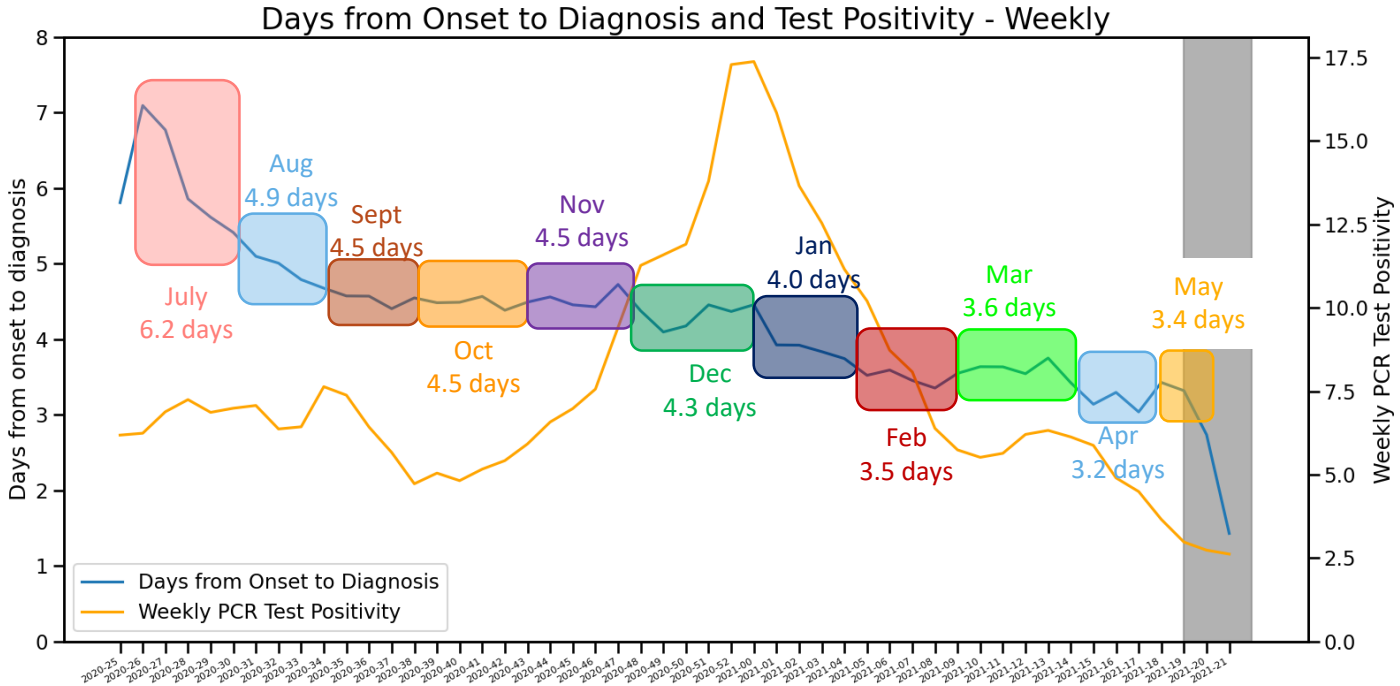
Test positivity vs. Onset to Diagnosis



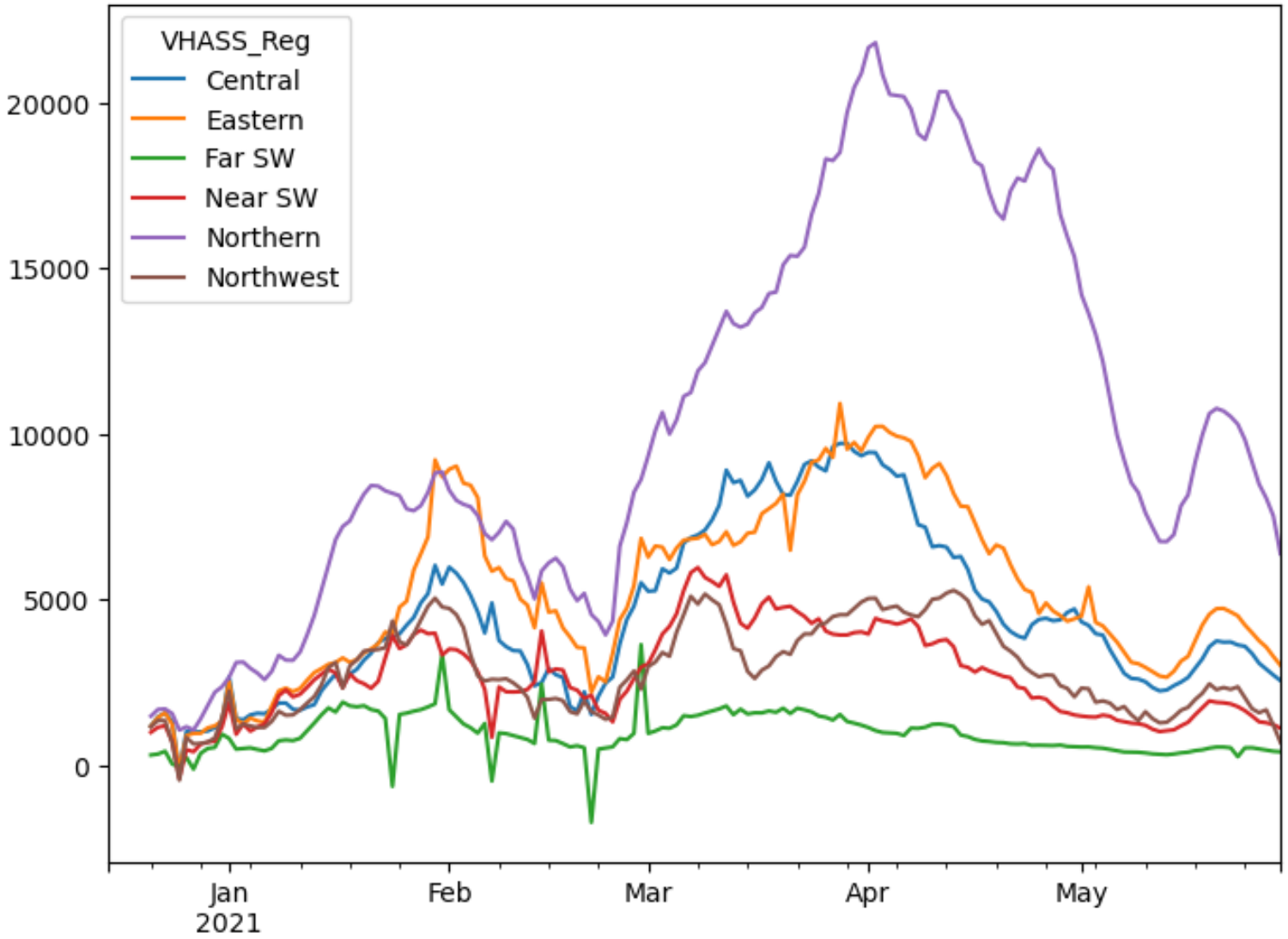


Accessed 9:00am June 2, 2021
https://www.vdh.virginia.gov/coronavirus/

Timeframe (weeks)	Mean days	% difference from overall mean
July (26-30)	6.2	-2%
Aug (31-34)	4.9	-22%
Sept (35-38)	4.5	-28%
Oct (39-43)	4.5	-28%
Nov (44-47)	4.5	-27%
Dec (48-49)	4.3	-31%
Jan (00-04)	4.0	-36%
Feb (05-08)	3.5	-44%
Mar (09-13)	3.6	-42%
Apr (14-17)	3.2	-48%
May (18-19)	3.4	-46%
Overall (13 - 19)	6.3	--

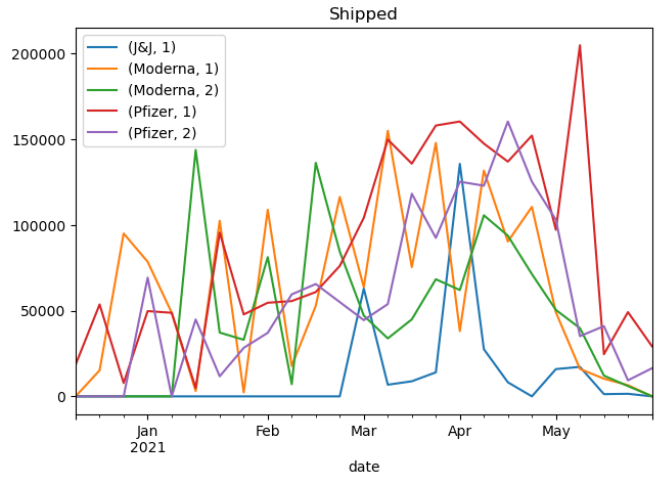


Vaccination Administration Slows



Regional Vaccine courses initiated per day:

- Total counts of first dose of vaccines across regions
- Recent rise due to opening of vaccinations to 12-16 year olds



Shipments have slowed with decreased demand

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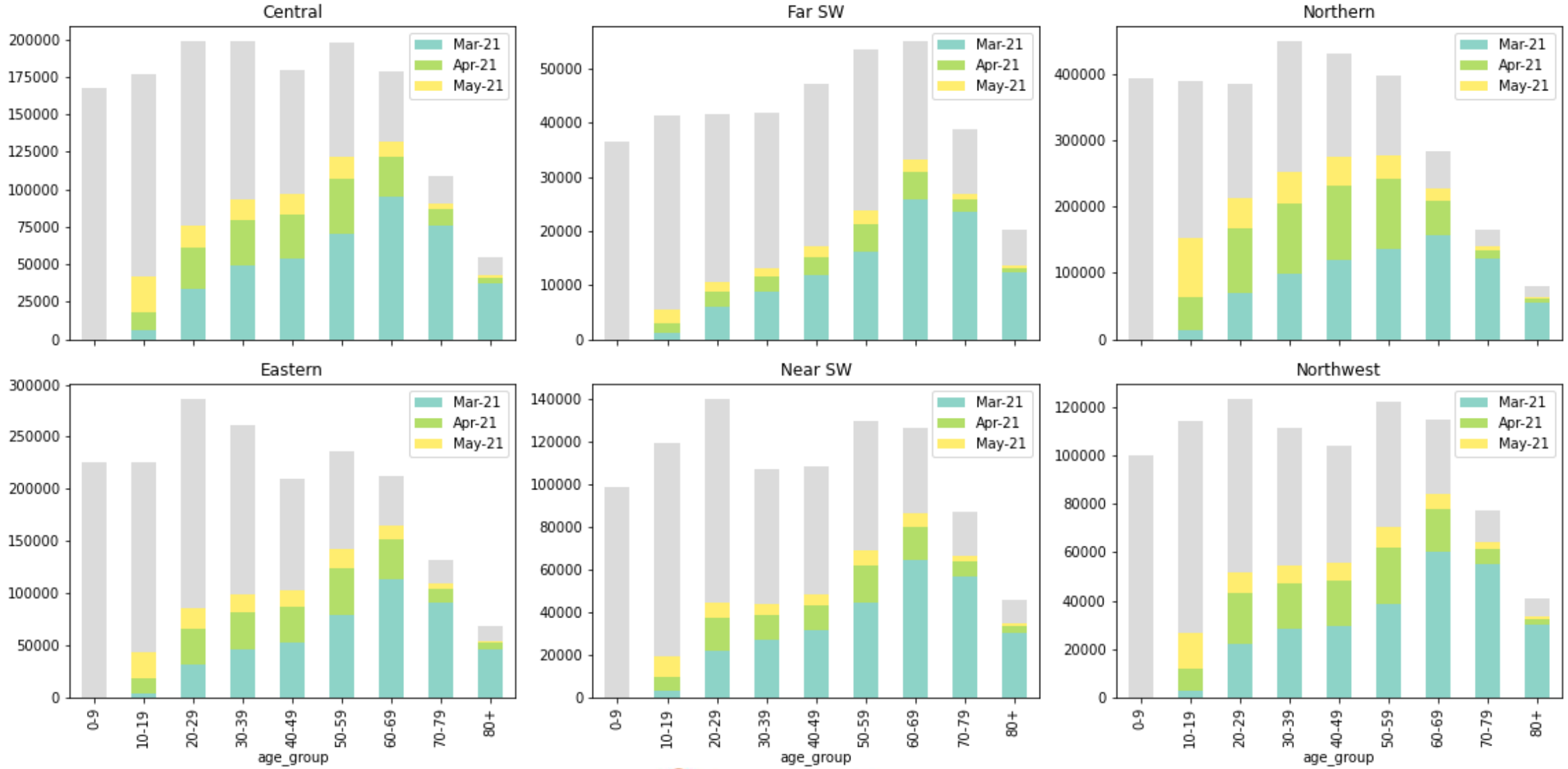
Vaccinations Shift to Younger Populations



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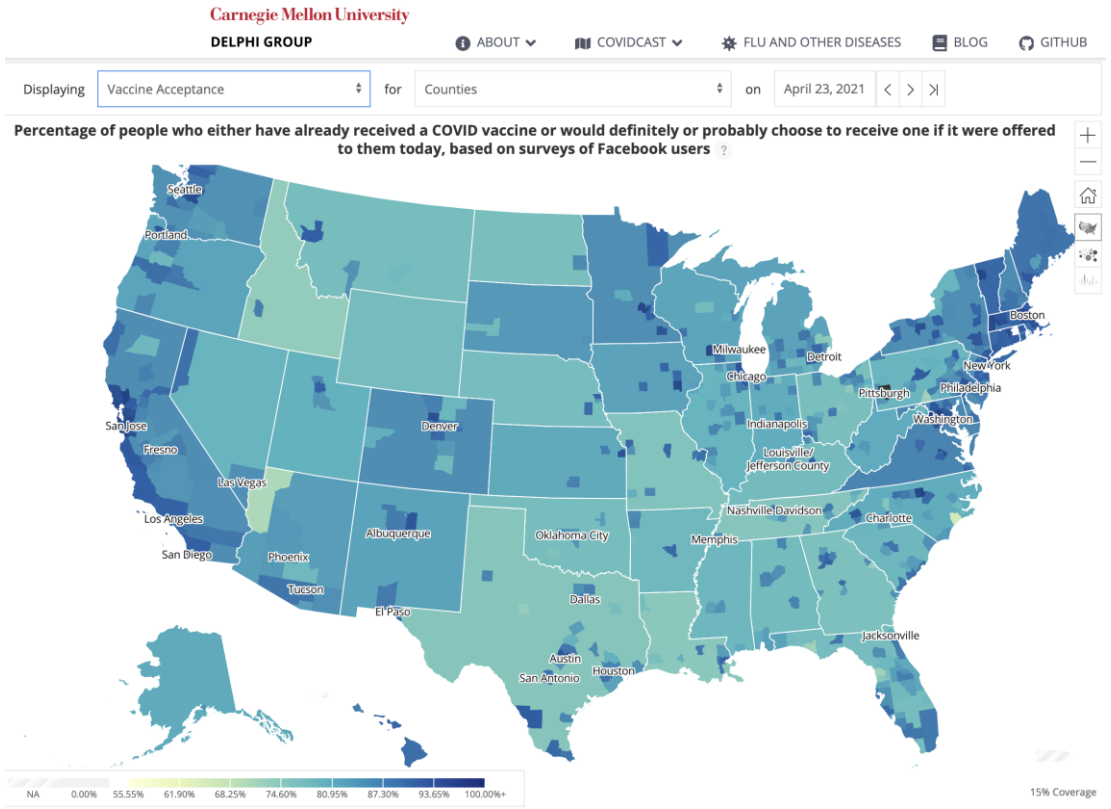
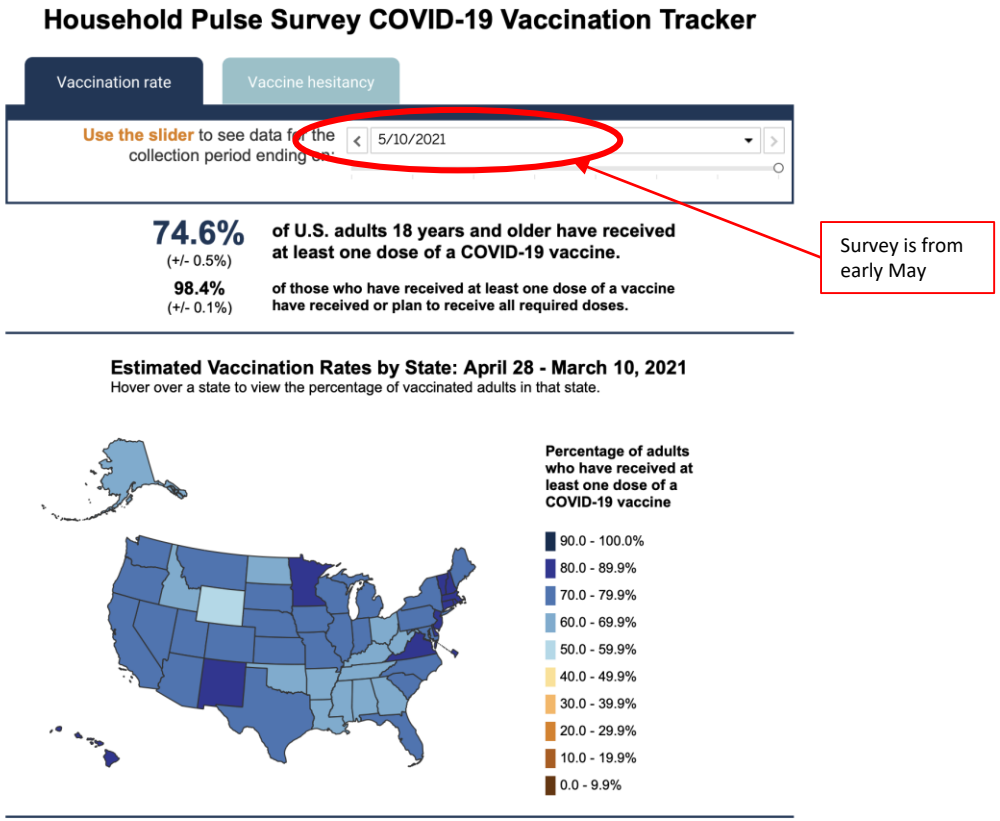
Vaccine Acceptance Data Sources





Survey is from early May

COVIDcast / Facebook Survey

https://covidcast.cmu.edu

Census Household Pulse Surveys (HPS)

https://www.census.gov/library/visualizations/interactive/household-pulse-survey-covid-19-vaccination-tracker.html

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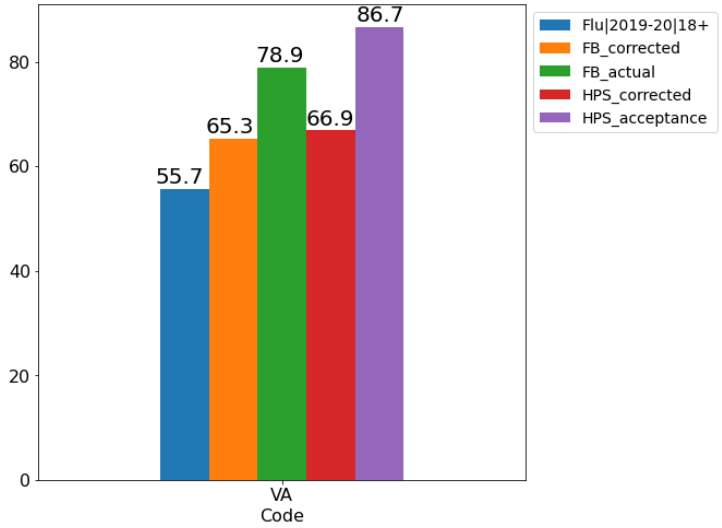
Vaccination Acceptance – Comparison of Sources

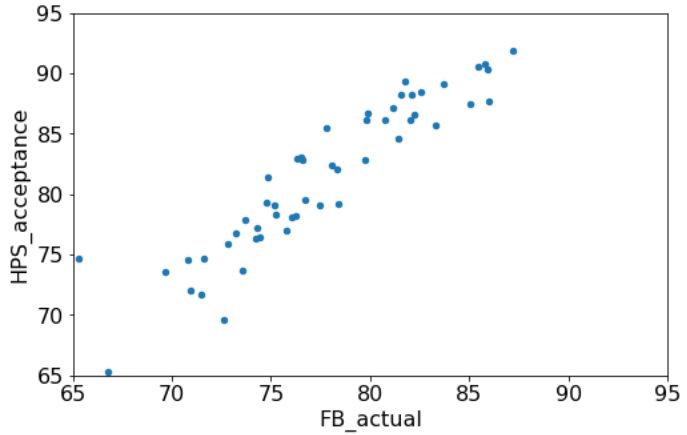
Measured acceptance varies across sources:

- **COVIDcast / Facebook (FB):** Both corrected and actual measurement
- **FluVax:** Acceptance levels in VA for influenza vaccine during 2019-20 flu season
- **Household Pulse (HPS):** Census administered survey, but with some time delay till release (most recent for fortnight ending May 10th, 2021)
- HPS has highest overall, while FluVax is expectedly the lowest
- Corrected HPS and COVIDcast are very similar for VA at the state level, and approach FluVax

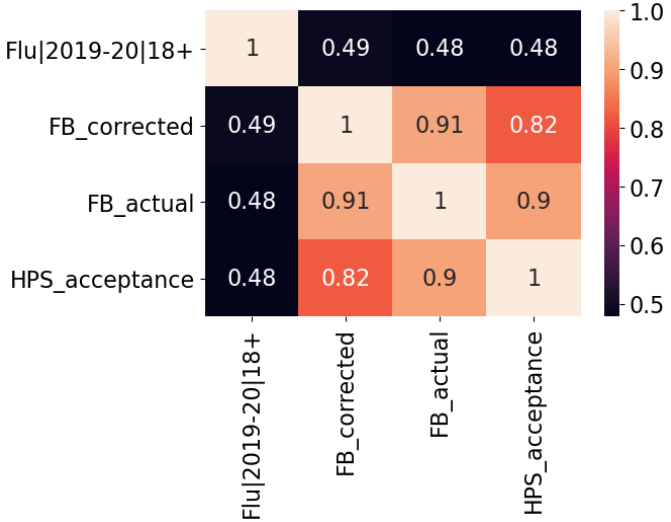
Virginia Vaccine Acceptance levels



State by State correlation COVIDcast and HPS



State level correlation between all four



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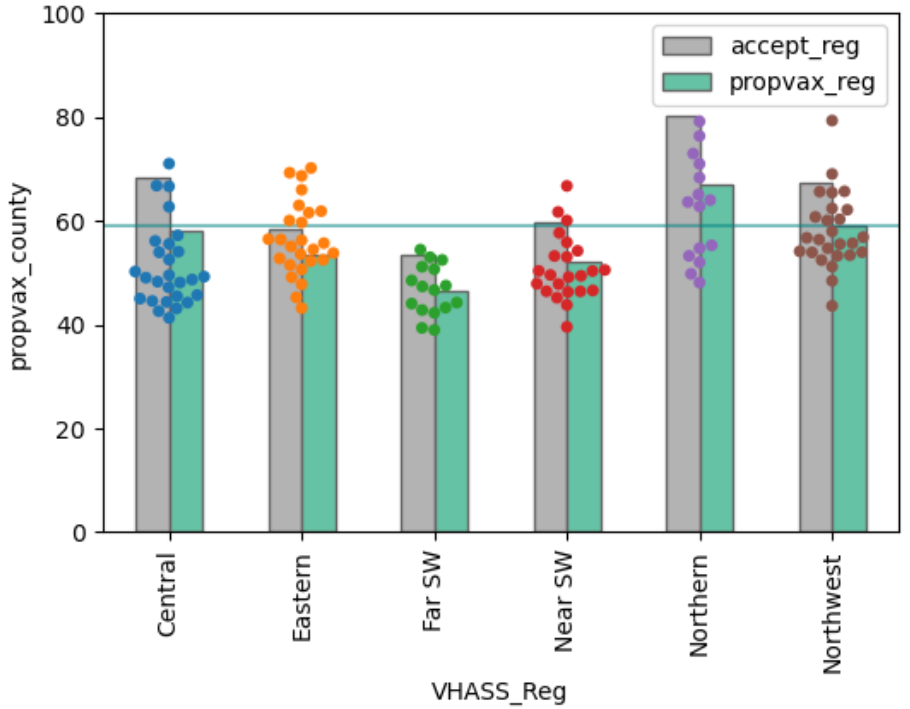
Vaccination Acceptance by Region

Corrections to surveys:

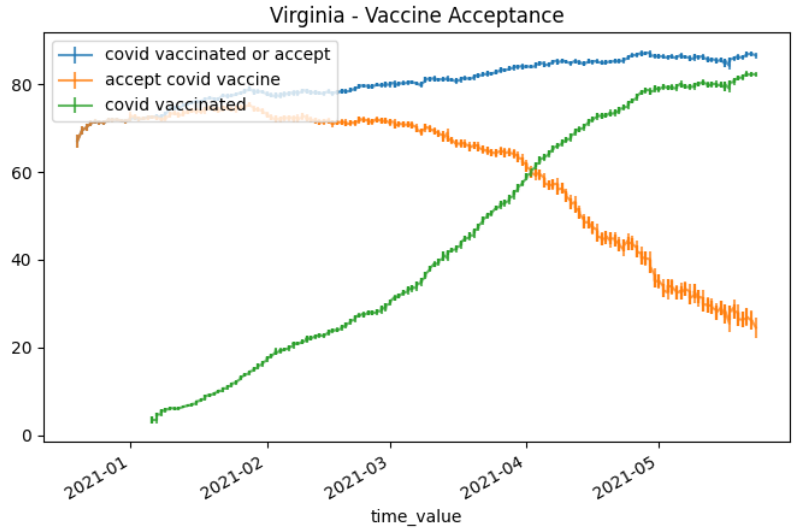
- Facebook administered survey is timely and broad, but biased by who accesses Facebook and answers the survey
- Correction approach:
  - Calculate an over-reporting fraction based on reported vaccinations compared to VDH administration data
  - Cross-validate coarse corrections against HPS survey at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

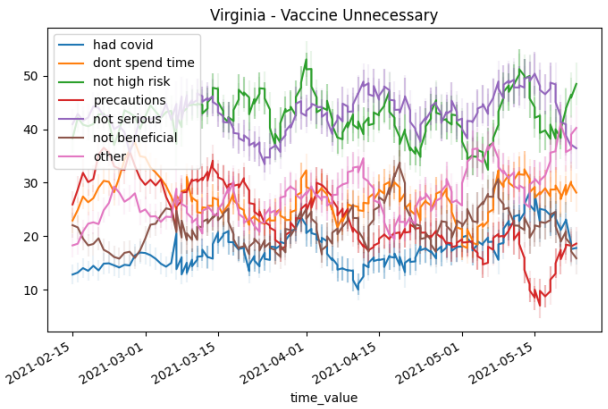
Region	COVIDcast accepting corrected	VDH proportion vaccinated	COVIDcast reported vaccinated
Central	68%	58%	82%
Eastern	58%	52%	84%
Far SW	53%	41%	66%
Near SW	60%	51%	75%
Northern	80%	67%	88%
Northwest	67%	58%	79%



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

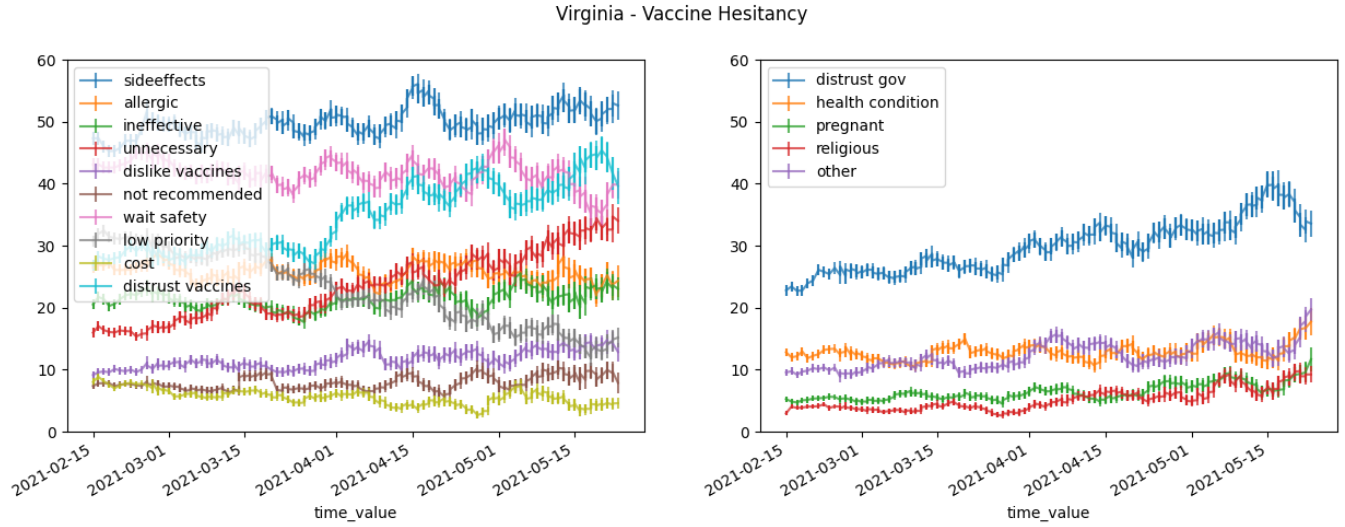
Vaccine Acceptance in Virginia - COVIDcast





Acceptance remains high:

- Proportion of Virginians that have already or would definitely or probably accept vaccination if offered today
- *Survey respondents are reporting high levels of vaccination of ~80% reflecting bias of the mechanism*
- **Top reasons for hesitancy**: side effects, distrust (increasing), unnecessary (increasing)
- **More likely to take if recommended by:** doctors and friends
- **Reasons unnecessary**: Not serious, not high risk, or other



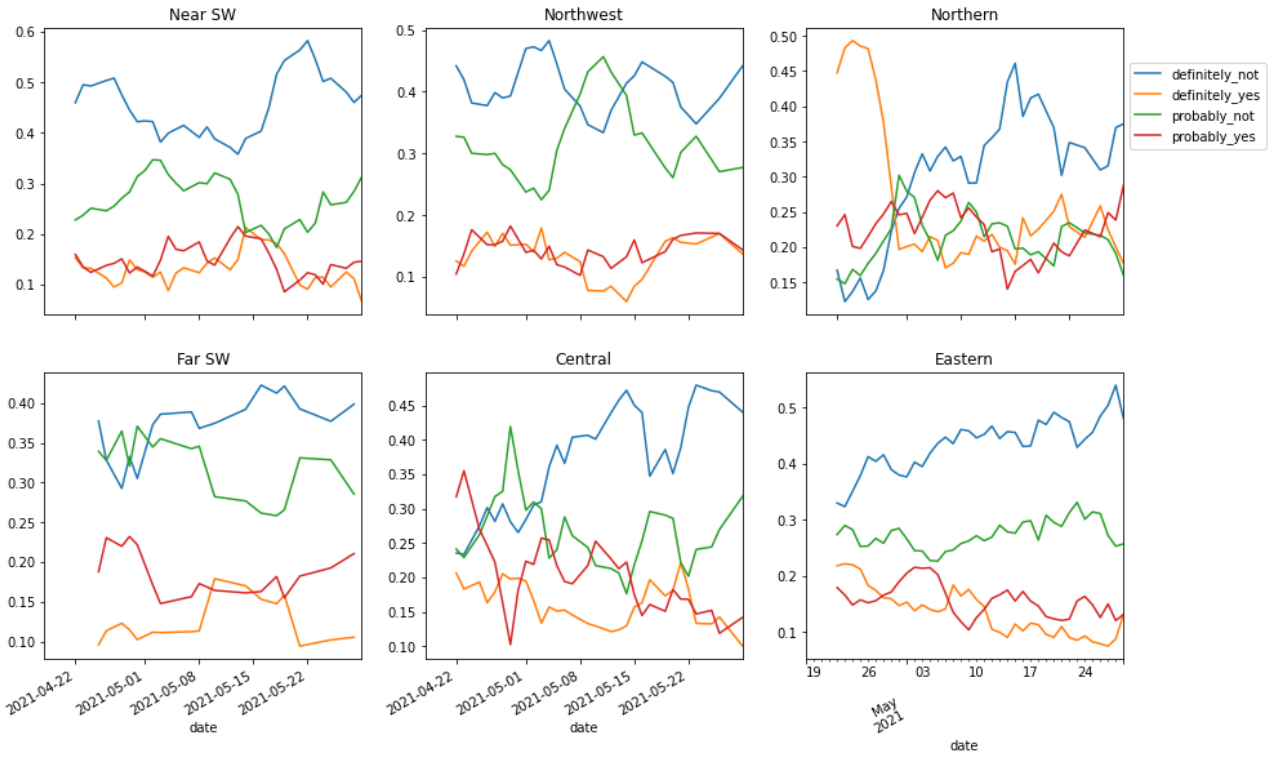
Data Source: https://covidcast.cmu.edu

Vaccine Acceptance by Region- COVIDcast

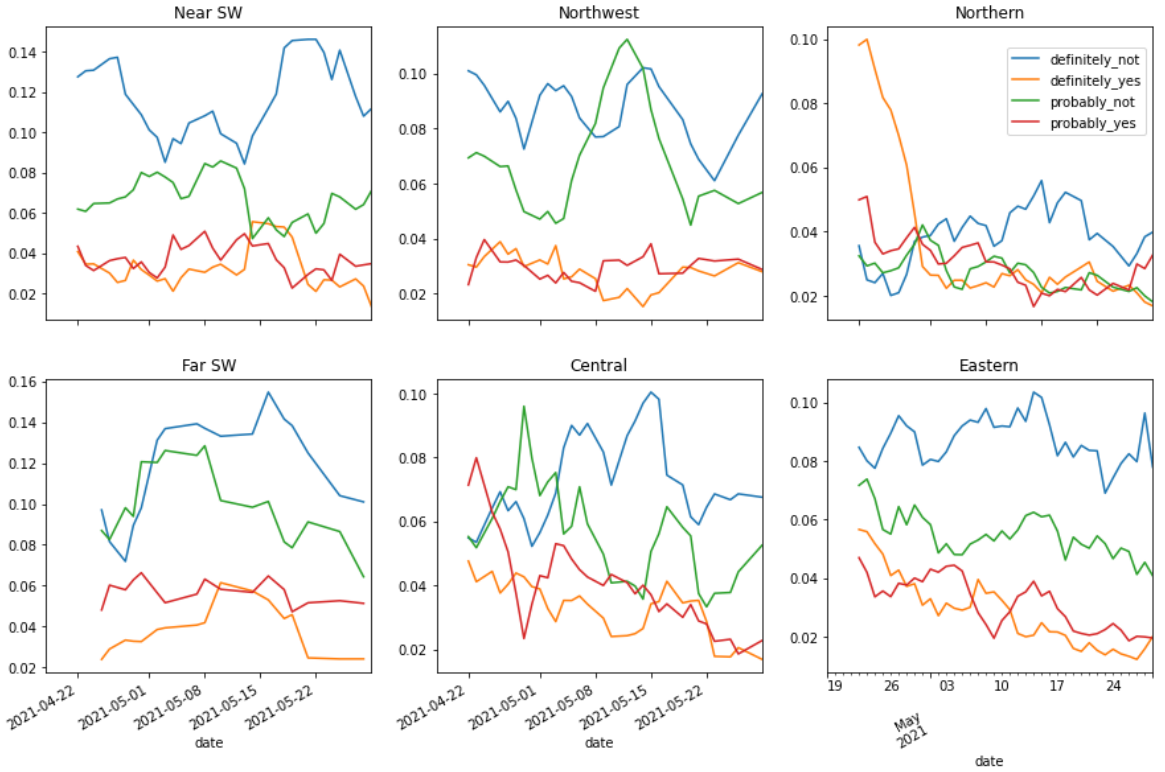
Levels of Acceptance and potential acceptance in flux:

- Nearly all the “Definitely Yes” have been vaccinated, yet there are 5-10% remaining across the regions
- Northwest and Southwest (to lesser degree) see growth in “probably not”, seemingly from “definitely not”

Unvaccinated Only



All Respondents



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

SARS-CoV2 Variants of Concern

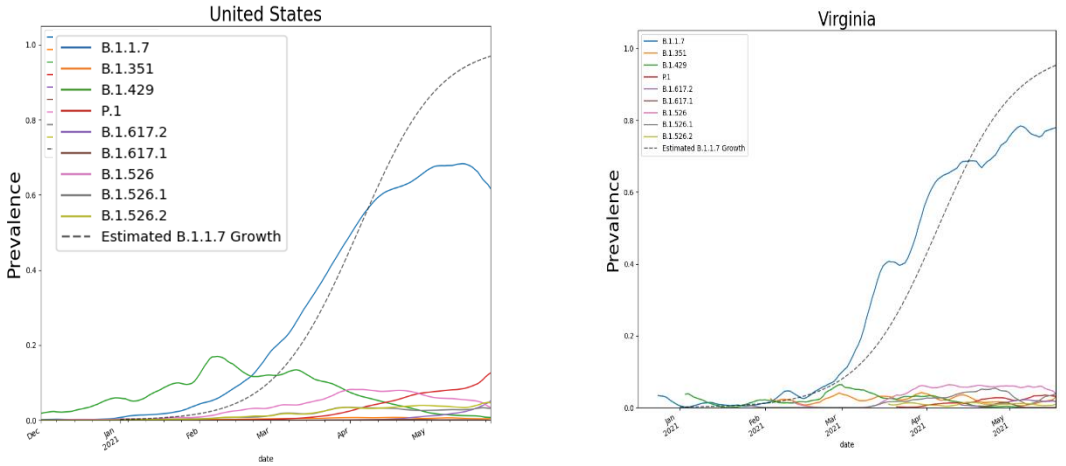
Emerging new variants will alter the future trajectories of pandemic and have implications for future control

- 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

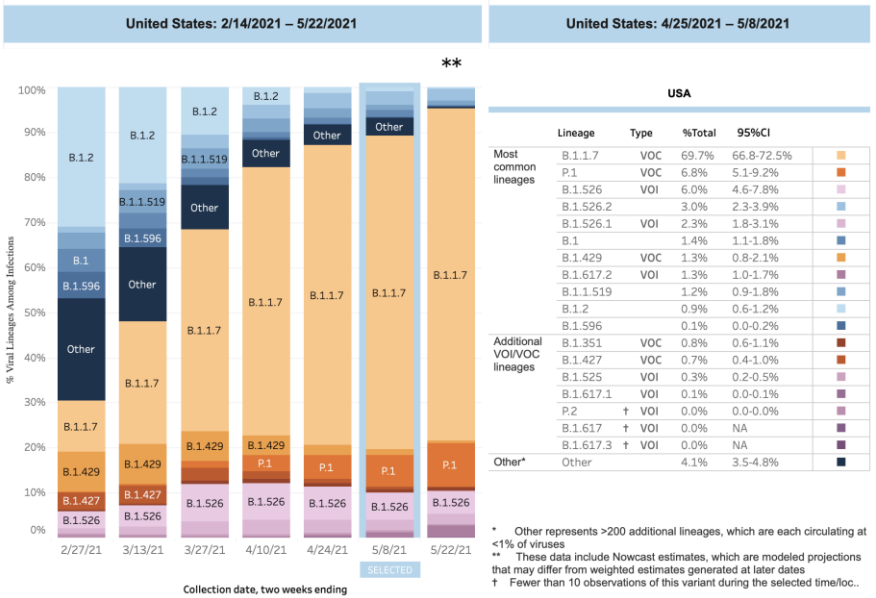
	New WHO Name	Transmissibility	Immune Evasiveness	Vaccine Effectiveness^
Ancestral		—	—	✓
D614G		+	—	✓
B.1.1.7	Alpha	+++	—	✓
B.1.351	Beta	+	++++	✓
P.1	Gamma	++	++	✓
B.1.429	Epsilon	+	+	✓
B.1.526	Iota	+	+	✓
B.1.617.2	Delta	++++*	++#	✓

*Relative transmissibility to B.1.1.7 yet to be fully defined
^Effectiveness from real world evidence vs. severe illness, not all vaccines are effective vs all variants, and importance of 2-doses, especially for B.1.617.2 for which 1 dose of mRNA or AZ is only ~30% effective # May carry more immune escape than P.1, to be determined

World Health Organization [WHO](#) and [Eric Topol](#)



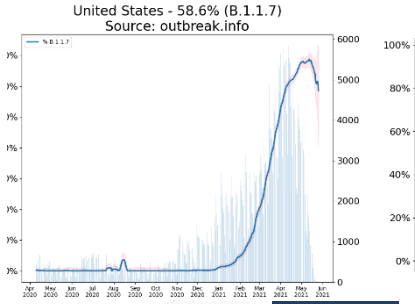
GISAID outbreak.info [Outbreak Info](#)

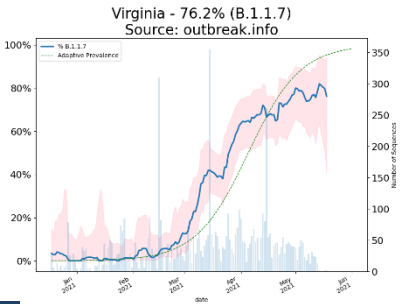


CDC [CDC Variant Tracking](#)

SARS-CoV2 Variants of Concern

Alpha α - Lineage B.1.1.7





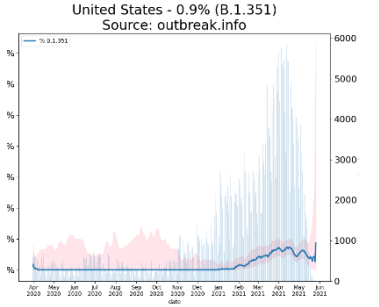
GISAID outbreak.info Outbreak Info

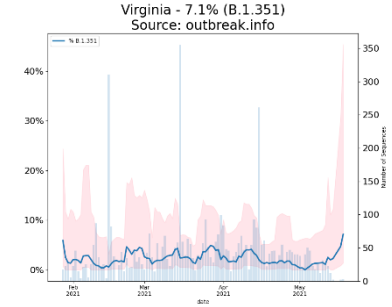
Prevalence: Levels have rapidly risen, as anticipated, and now are plateauing at national level and in many states, seemingly in VA as well

Transmissibility: Estimated increase of 50% compared to previous variants. B.1.1.7's mutations aid its infection efficiency, and thus boosts its overall levels of viremia; study from Public Health England shows contacts of B.1.1.7 cases are more likely (50%) to test positive than contacts of non-B.1.1.7 patients

Severity: Increased viremia also appears to increase the risk of hospitalization (60%) and mortality (60%). Danish study shows B.1.1.7 to have a 64% higher risk of hospitalization, while Public Health Scotland studies showed a range of 40% to 60%; Study in Nature based on UK data estimates B.1.1.7 cases have 60% higher mortality

Beta β - Lineage B.1.351





Prevalence: Levels have remained low, as this variant's transmissibility can't compete with B.1.1.7, however, as more of the population becomes immune it may gain an advantage

Immune Escape: Many studies show that convalescent sera from previously infected individuals does not neutralize B.1.351 virus well which is predictive of protection, however, vaccine induced immunity shows signs of effectiveness

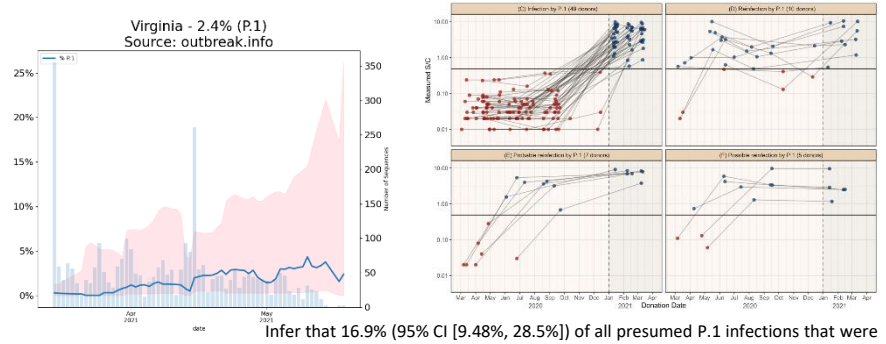
Lineage B.1.429/427 and B.1.526 and subvariants

- Combined account for around 20% of circulating virus, share may be shrinking as B.1.1.7 outcompetes

SARS-CoV2 Variants of Concern

Gamma γ - Lineage P.1

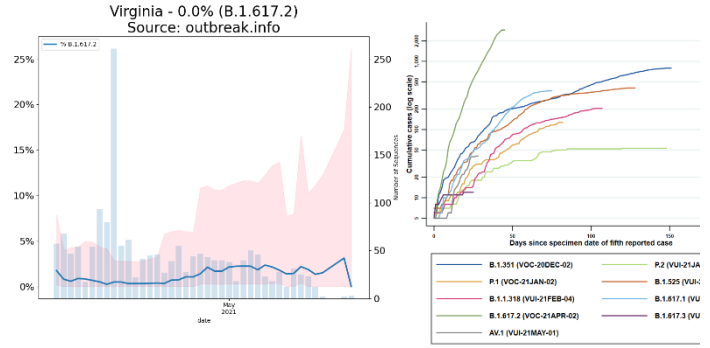
- **Prevalence:** Nationally at 10.7%, lower but increasing in VA at 5.2%
- New study estimates 17-32% of all infections in Manaus in 2021 were reinfections, which helps explain data from Brazil demonstrating P.1's continued dominance in Rio despite presence of B.1.1.7



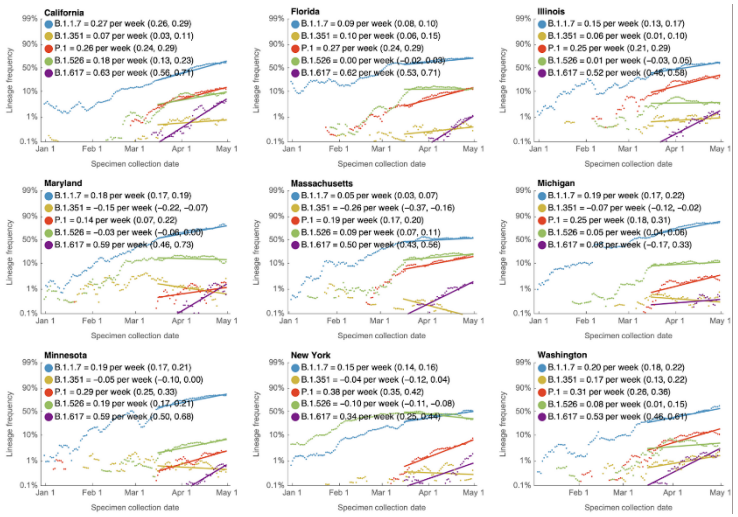
Infer that 16.9% (95% CI [9.48%, 28.5%]) of all presumed P.1 infections that were observed in 2021 were reinfections. Including probable or possible reinfections this expand to 25.8% (95% CI [16.7%, 37.4%]), and 31.0% (95% CI [21.4%, 42.5%]). medRxiv

Delta δ - Lineage B.1.617.2 and related subvariants

- Continues to drive outbreak in India and neighbors, with immeasurable numbers of cases surpassing healthcare capacities in many regions
- Categorized as VoC by Public Health England, WHO, expect CDC to follow
- Strain shows continued growth in UK, Europe and in US
- Several studies estimate B.1.617.2 to have 100% faster growth than B.1.1.7, and UK study suggests a 13% advantage over B.1.1.7
- More studies show limited immune escape similar to B.1.351, however, still suggest protection remains for vaccinated
- PHE study shows limited efficacy of Astra-Zeneca with only one dose, efficacy returns following 2nd dose



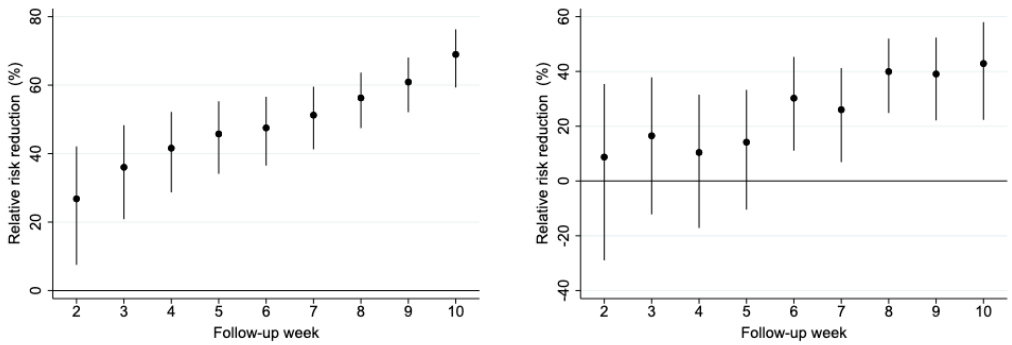
B.1.617.2 shows rapid growth throughout England and increases severity rating for vaccine escape after one dose. B.1.617.2 is reported as having an increased growth rate relative to B.1.1.7. PHE report 1 and report 2



Growth in US continues in the 0.5-0.6 growth rate range, eclipsing most other strains, remains at low levels, but is growing Nextrstrain ananlsysis

SARS-CoV2 Immunology Updates

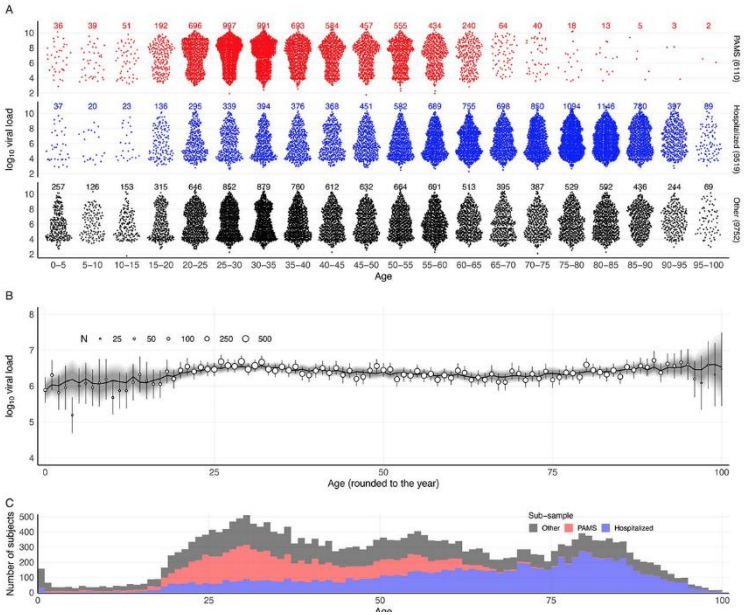
Salo et al. preprint on Medrxiv from study in Finland suggest that mRNA-based vaccines prevent infections in the vaccinated, as well in the unvaccinated household members, demonstrating indirect effects of vaccination and possible strategy for resource scarce areas.



(a) Vaccine effectiveness on vaccinated individuals (b) Vaccine effectiveness on unvaccinated spouse

Vaccine effectiveness on vaccinated individuals and unvaccinated spouses living in the same household Medrxiv

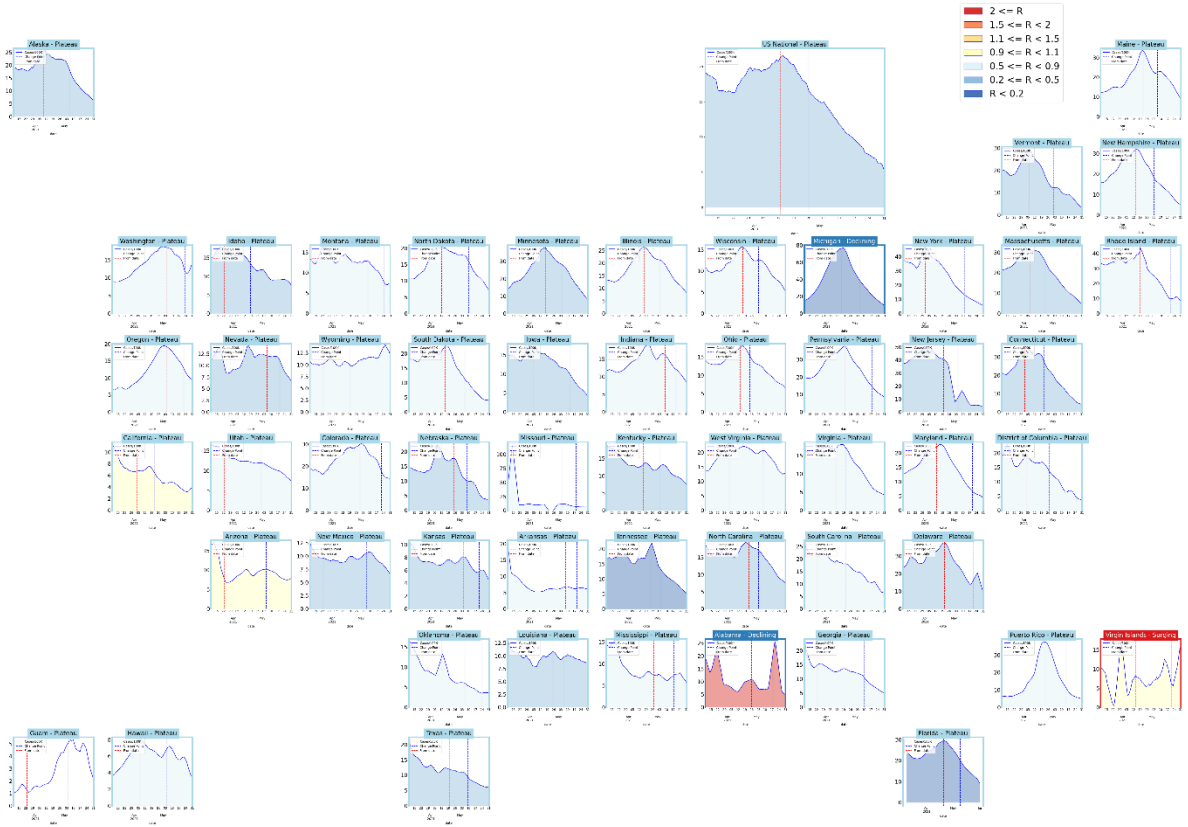
Jones et al. study in Science conducted in Germany with extensive testing reveals that “PAMs” (pre-symptomatic, asymptomatic, and mildly-symptomatic individuals) can be expected to be as infectious as hospitalised patients at the time of detection (including children). Has implications for vaccination requirements and design of surveillance systems.



(**A**) Distribution of observed first-positive viral loads for 25,381 subjects according to clinical status (6110 PAMS, 9519 Hospitalised, 9752 Other) and age group. (**B**) Age-viral load association with observed viral loads and confidence intervals as circles (with size indicating subject count) with vertical lines, and model-predicted viral loads and credible intervals as a black roughly-horizontal line with grey shading. (**C**) Overlapping age histograms according to subject clinical status. Because inclusion in the study required a positive RT-PCR test result, and testing is in many cases symptom-dependent, the study may have a proportion of PAMS cases that differs from the proportion in the general population. Science

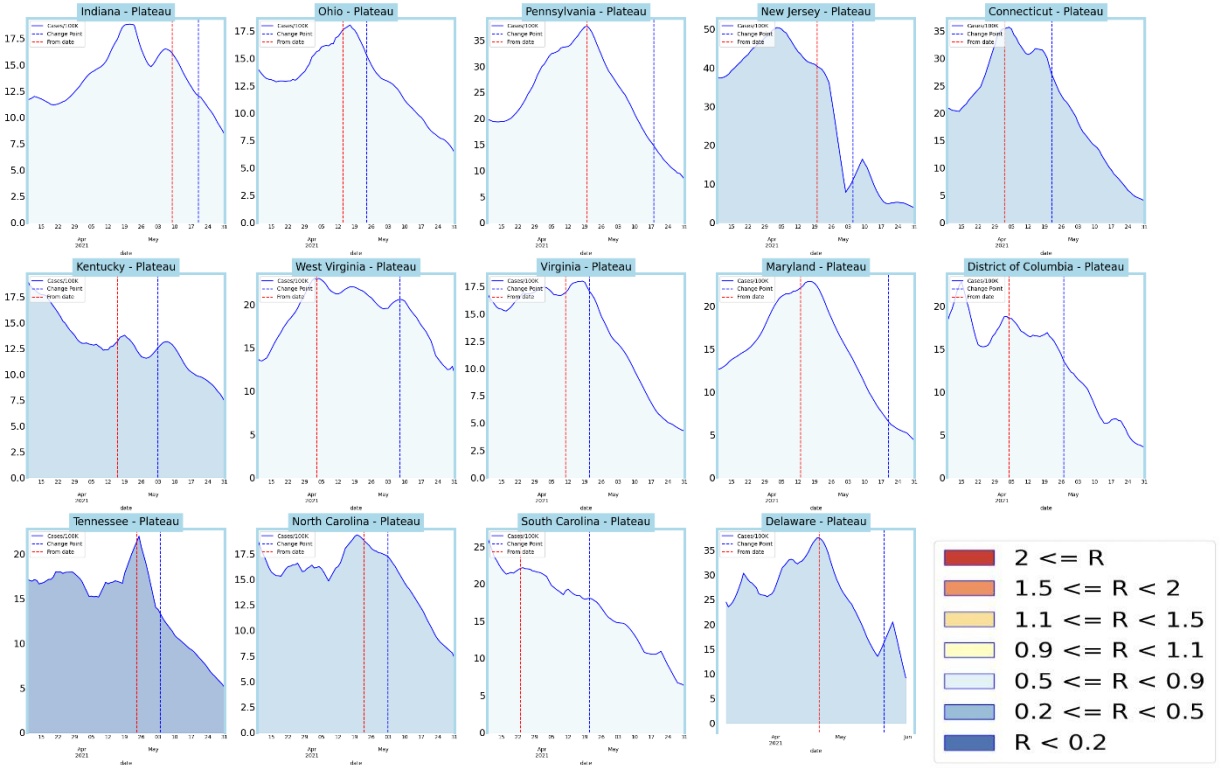
Other State Comparisons

Trajectories of States



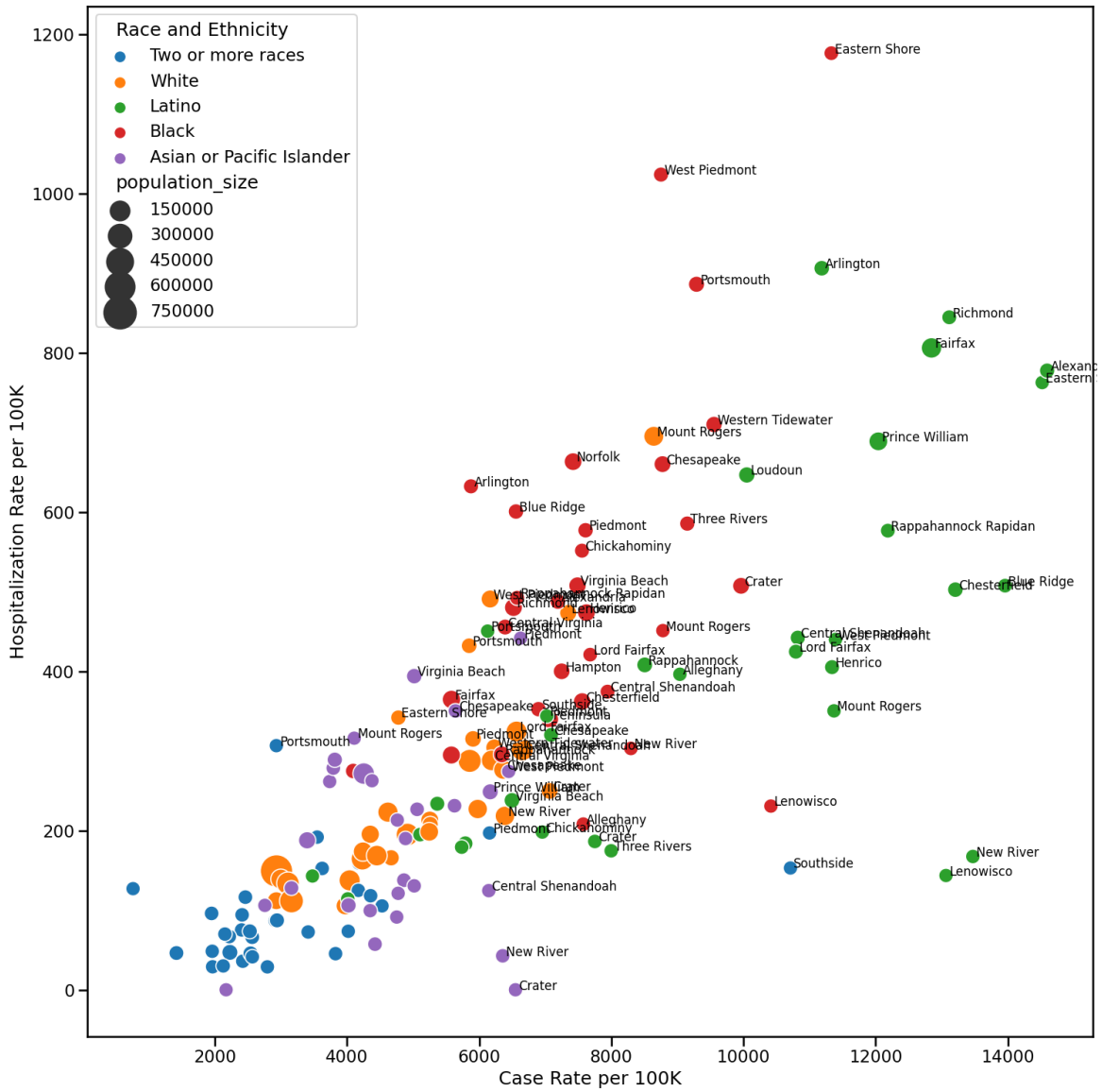
- Nearly all states are declining
- Growth out west has slowed, recent reporting artifacts in some states perturb the otherwise calm picture

Virginia and her neighbors



- VA and neighbors are all declining with steady pace
- Most neighbors are now below 10/100K level

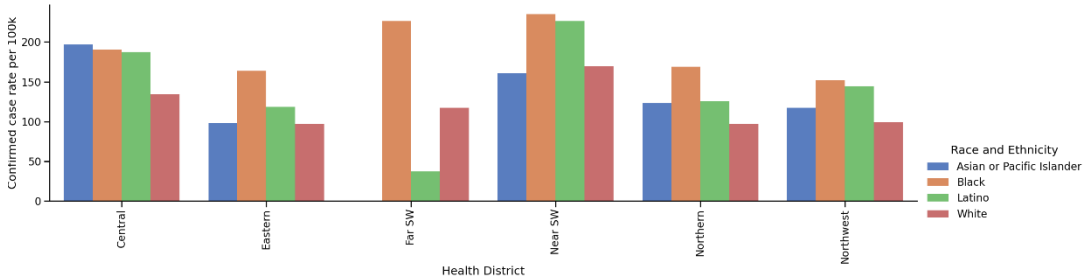
Race and Ethnicity cases per 100K



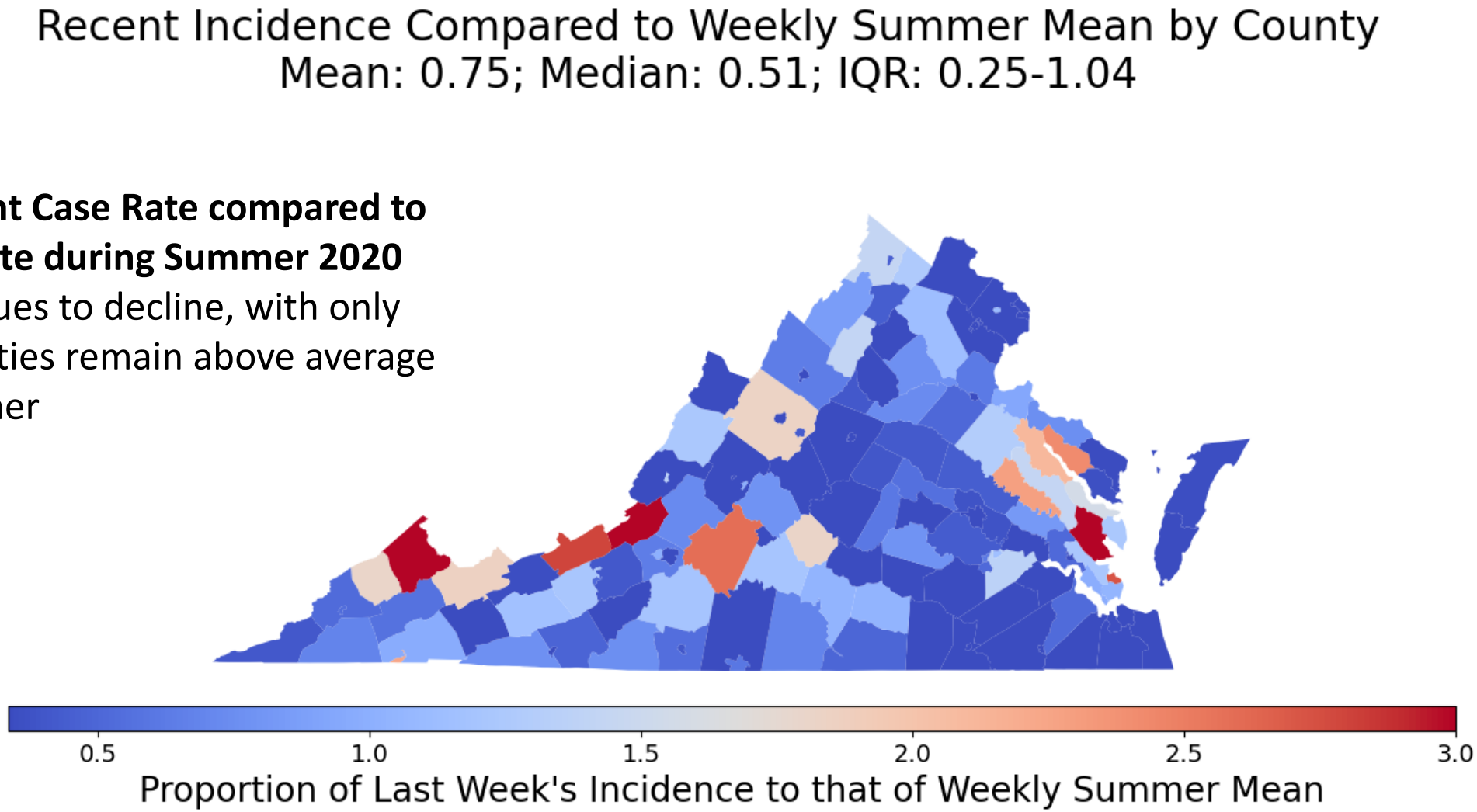
Rates per 100K of each Racial-Ethnic population by Health District

- Each Health District's Racial-Ethnic population is plotted by their Hospitalization and Case Rate
- Points are sized based on their overall population size (overlapping labels removed)
- Change in rates over the last 2 weeks

Case Rate Change in last 14 days



Recent Incidence Compared to Summer 2020



Ratio of Recent Case Rate compared to mean Case Rate during Summer 2020

- Ratio continues to decline, with only 28% of counties remain above average of last summer

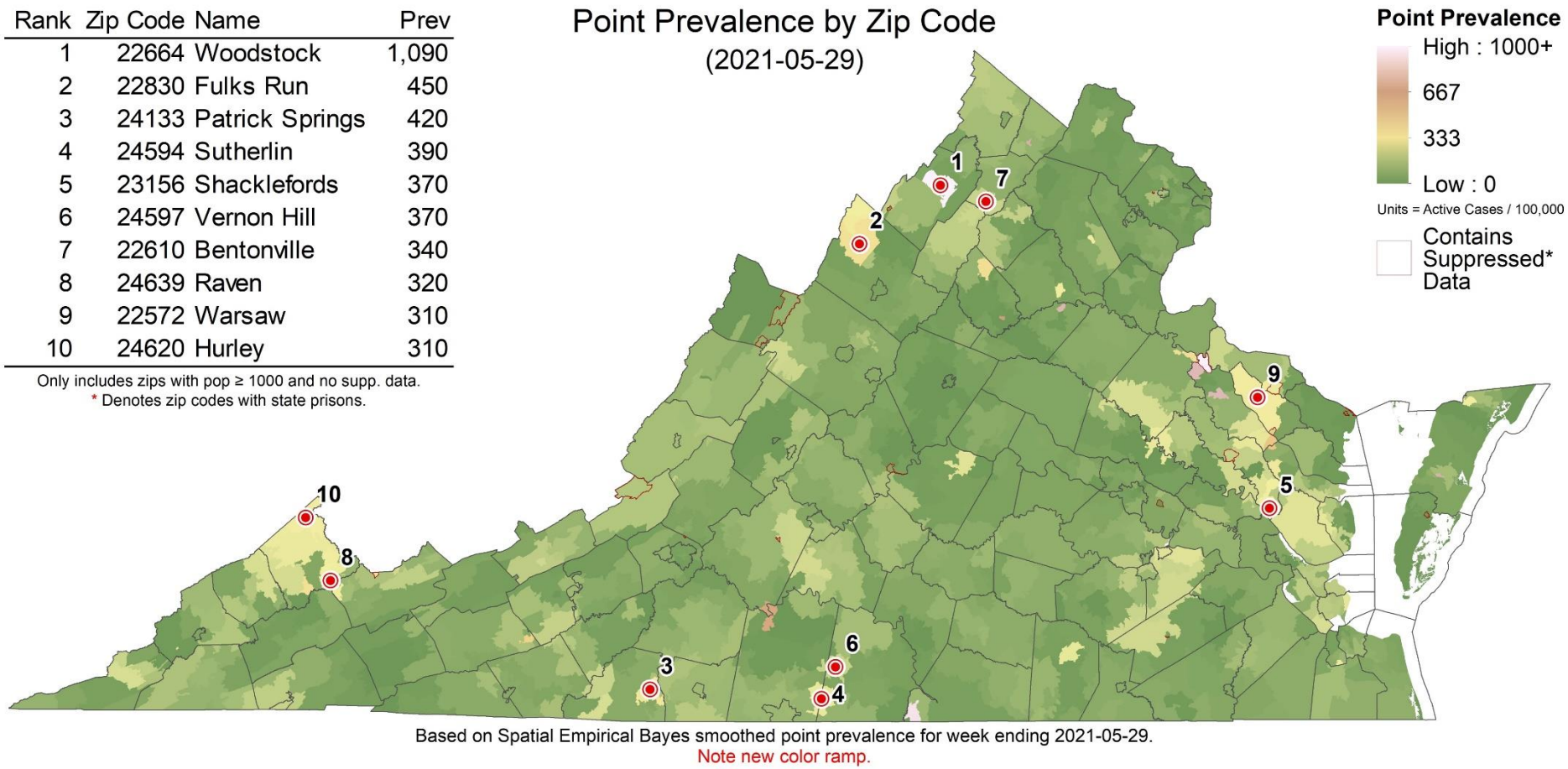
Zip code level weekly Case Rate (per 100K)

Case Rates in the last week by zip code

- Adjusted Color gradient to lower rates, thus red is a lower prevalence
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code	Name	Prev
1	22664	Woodstock	1,090
2	22830	Fulks Run	450
3	24133	Patrick Springs	420
4	24594	Sutherlin	390
5	23156	Shacklefords	370
6	24597	Vernon Hill	370
7	22610	Bentonville	340
8	24639	Raven	320
9	22572	Warsaw	310
10	24620	Hurley	310

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 2021-05-29.
Note new color ramp.

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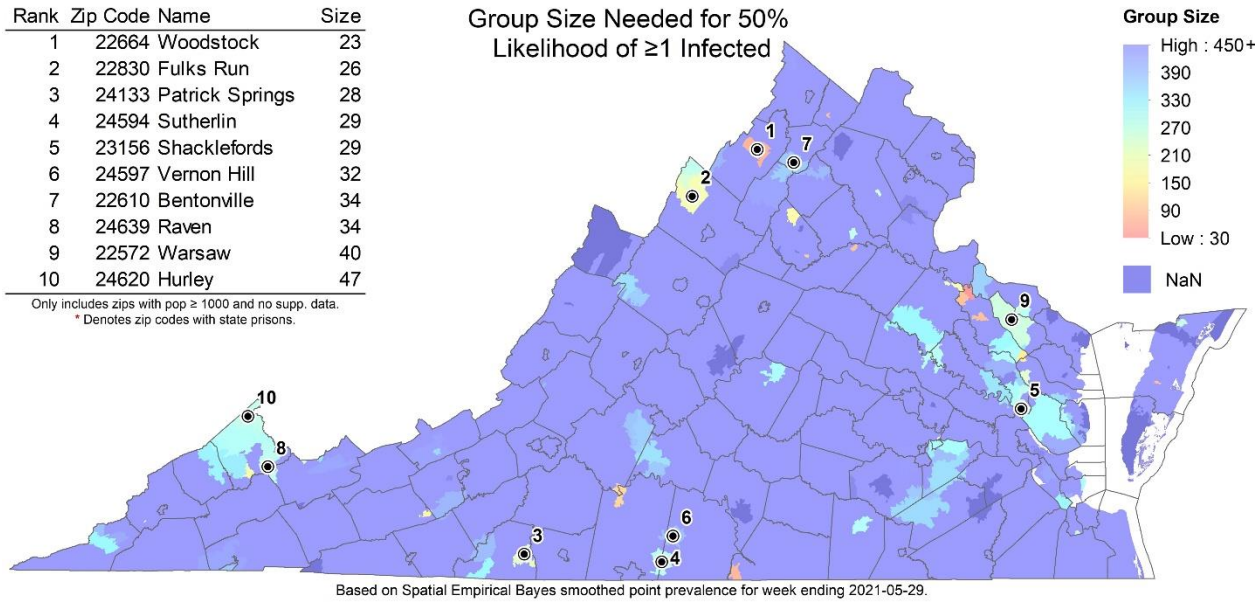
Risk of Exposure by Group Size and HCW prevalence

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)

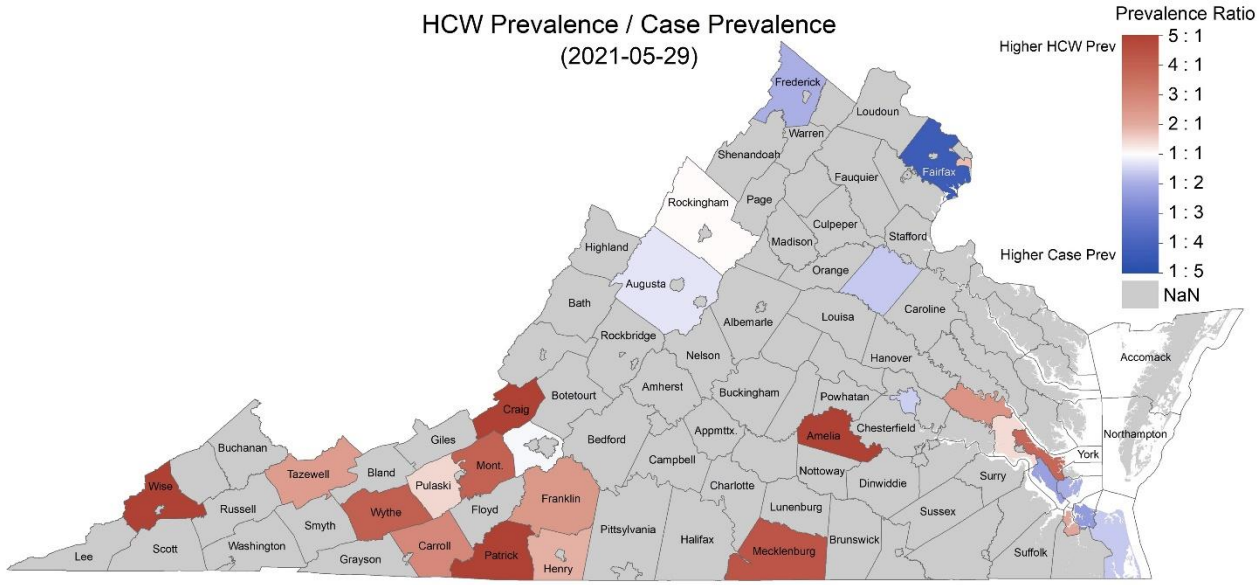
- **Group Size**: Assumes 2 undetected infections per confirmed case (ascertainment rate from recent seroprevalence survey), and shows minimum size of a group with a 50% chance an individual is infected by zip code (eg in a group of 23 in Woodstock, there is a 50% chance someone will be infected)
- **HCW prevalence**: Case rate among health care workers (HCW) in the last week using patient facing health care workers as the denominator

Rank	Zip Code	Name	Size
1	22664	Woodstock	23
2	22830	Fulks Run	26
3	24133	Patrick Springs	28
4	24594	Sutherlin	29
5	23156	Shacklefords	29
6	24597	Vernon Hill	32
7	22610	Bentonville	34
8	24639	Raven	34
9	22572	Warsaw	40
10	24620	Hurley	47

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 2021-05-29.



Current Hot-Spots

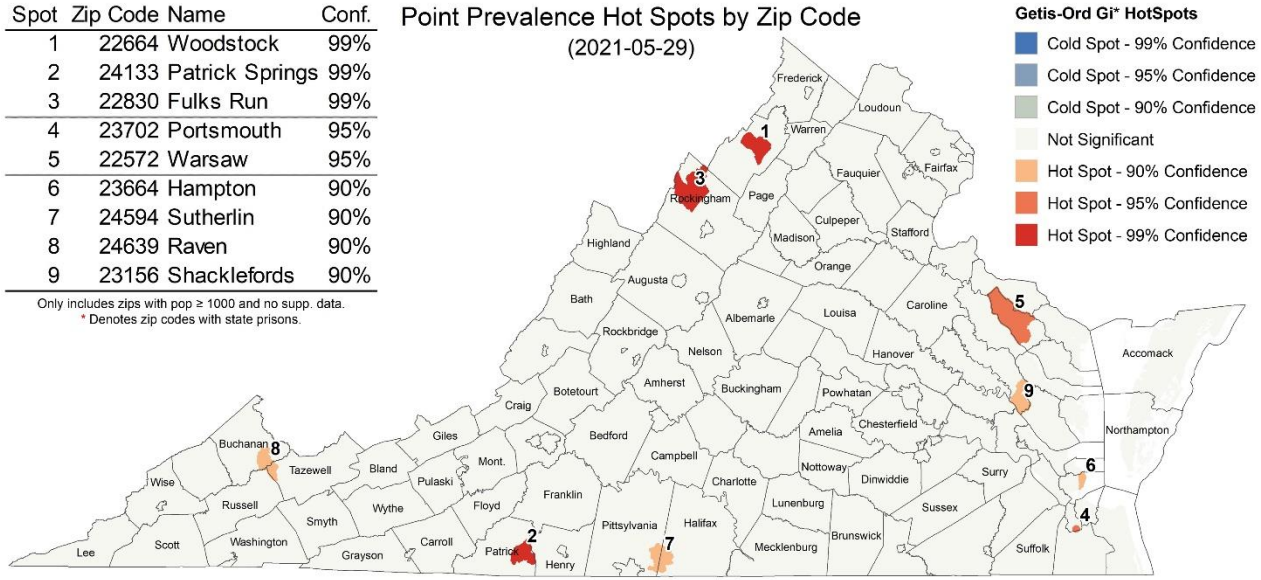
Case rates that are significantly different from neighboring areas or model projections

- **Spatial**: SaTScan 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

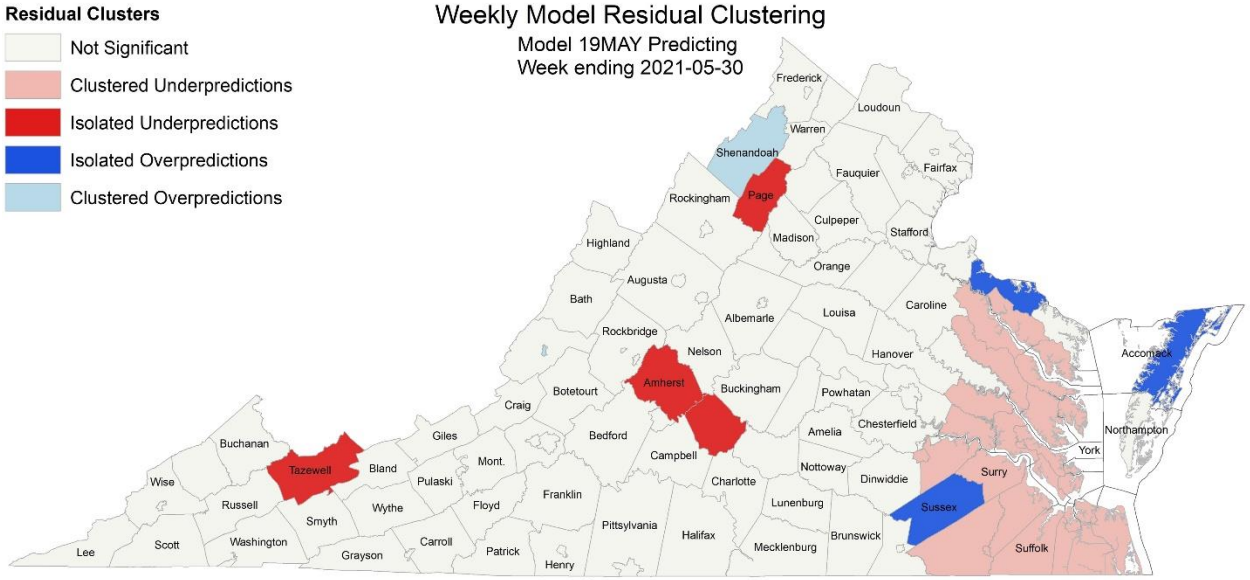
Spot	Zip Code	Name	Conf.
1	22664	Woodstock	99%
2	24133	Patrick Springs	99%
3	22830	Fulks Run	99%
4	23702	Portsmouth	95%
5	22572	Warsaw	95%
6	23664	Hampton	90%
7	24594	Sutherlin	90%
8	24639	Raven	90%
9	23156	Shacklefords	90%

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 2021-05-29.

Clustered Temporal Hotspots

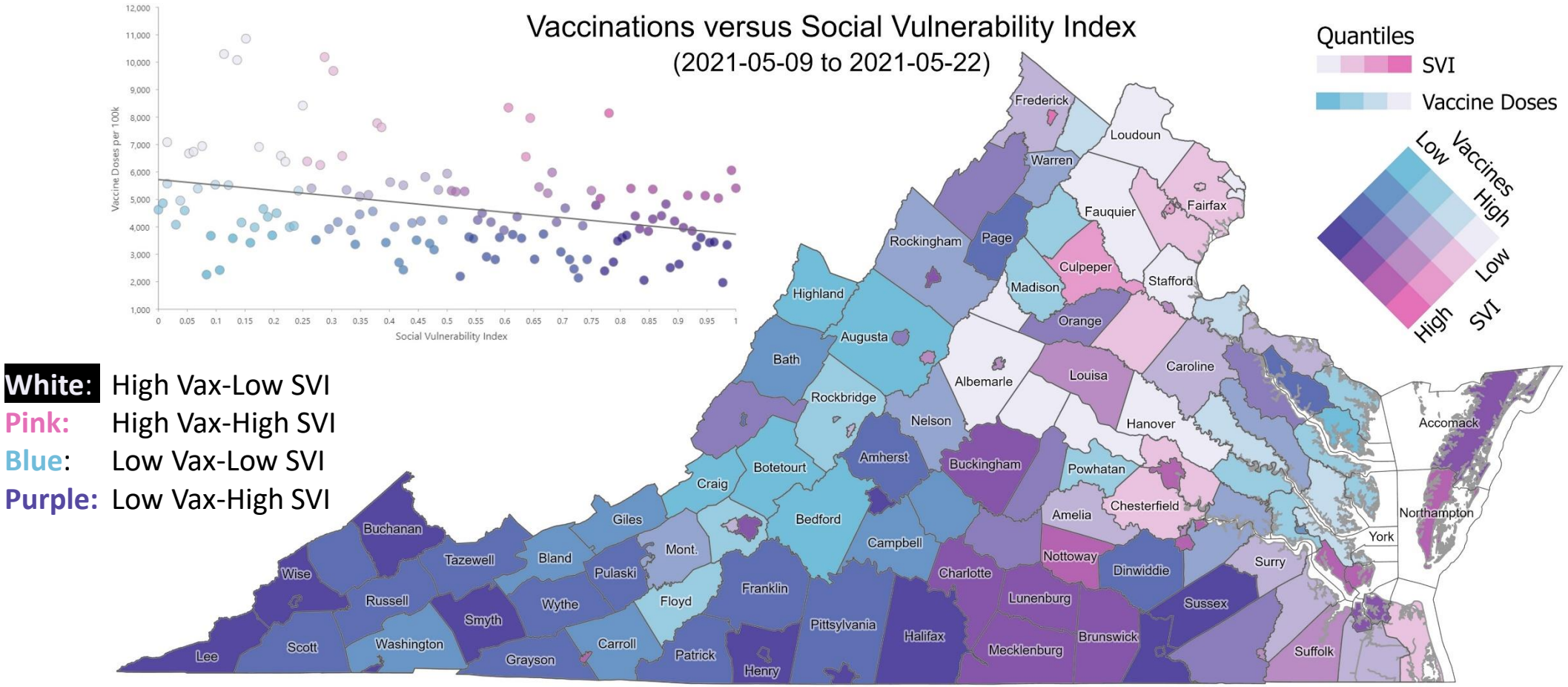


Moran's I = 0.259959, Z-Score = 3.38398, P-Value = 0.000714
Residual Autocorrelation Detected

Social Vulnerability and Recent Vaccination Rates

Comparison of social vulnerability and vaccination rate in last 2 weeks by county

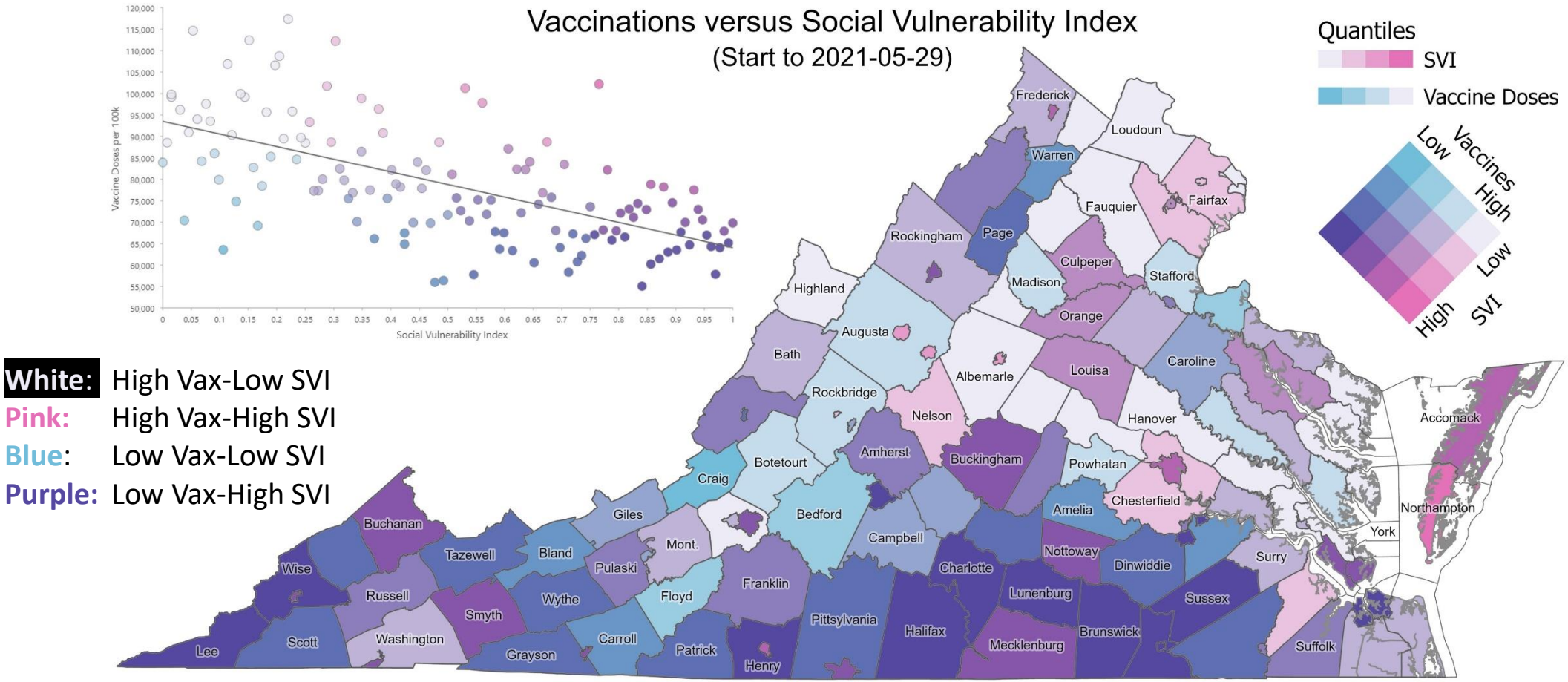
- **Social Vulnerability:** Each county's Social Vulnerability Index (CDC) compared with the level of vaccination



Social Vulnerability and Total Vaccination Rates

Comparison of social vulnerability and total vaccination rate since the start of vaccination

- **Social Vulnerability:** Each county's Social Vulnerability Index (CDC) compared with the level of vaccination



Model Update – Adaptive Fitting

Adaptive Fitting Approach

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

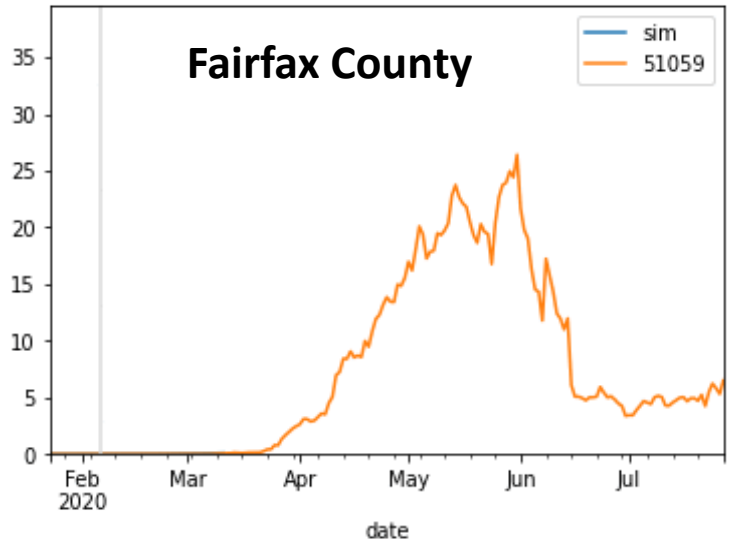
- Allows history to be precisely captured, and used to guide bounds on projections

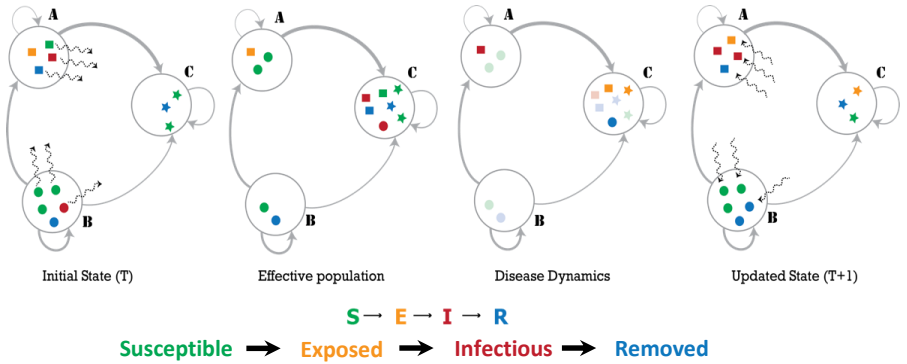
Model: An alternative use of the same meta-population model, PatchSim

- Allows for future "what-if" Scenarios to be layered on top of calibrated model
- Eliminates connectivity between patches, to allow calibration to capture the increasingly unsynchronized epidemic

External Seeding: Steady low-level importation

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





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Using Ensemble Model to Guide Projections

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

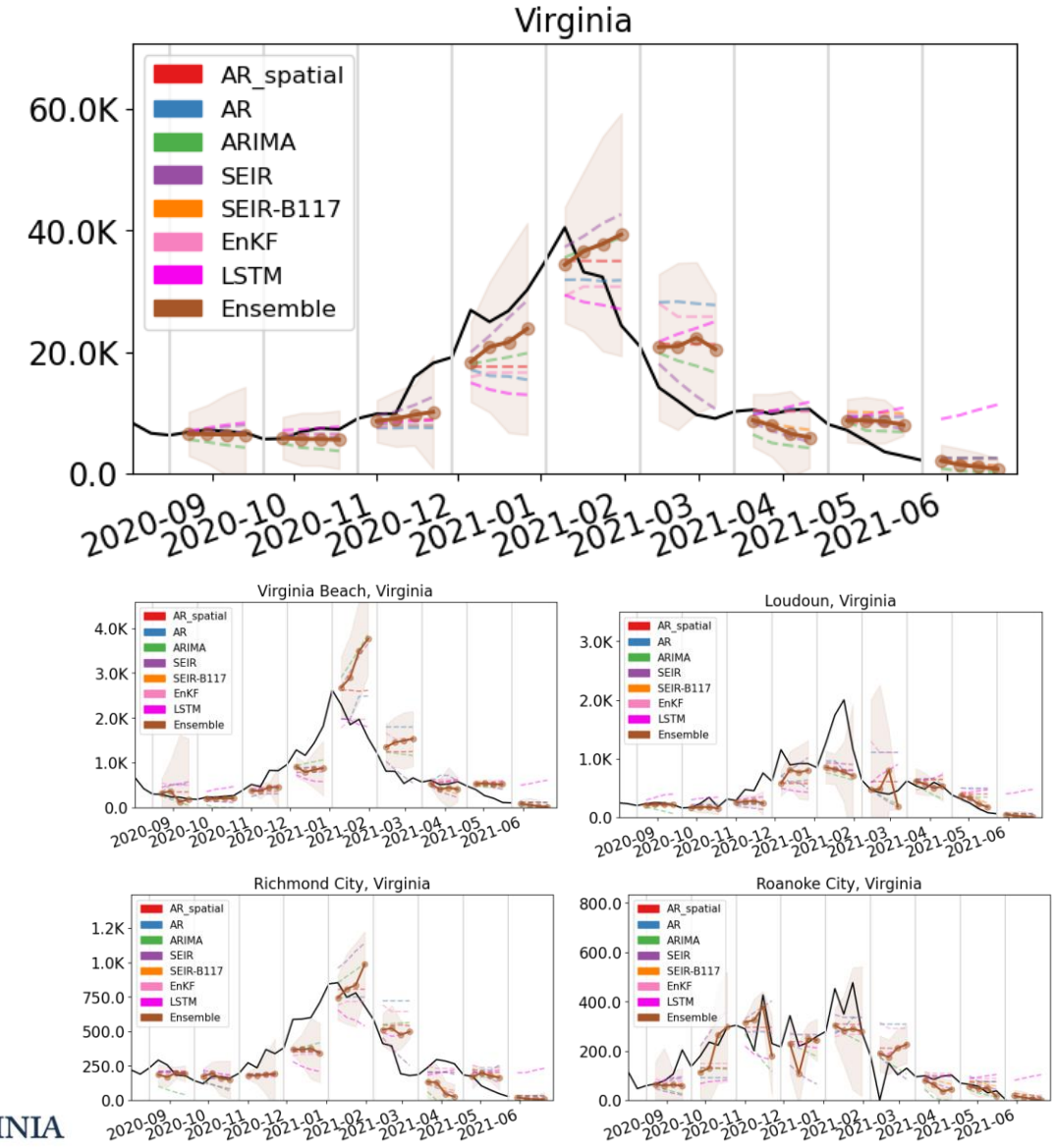
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

<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.



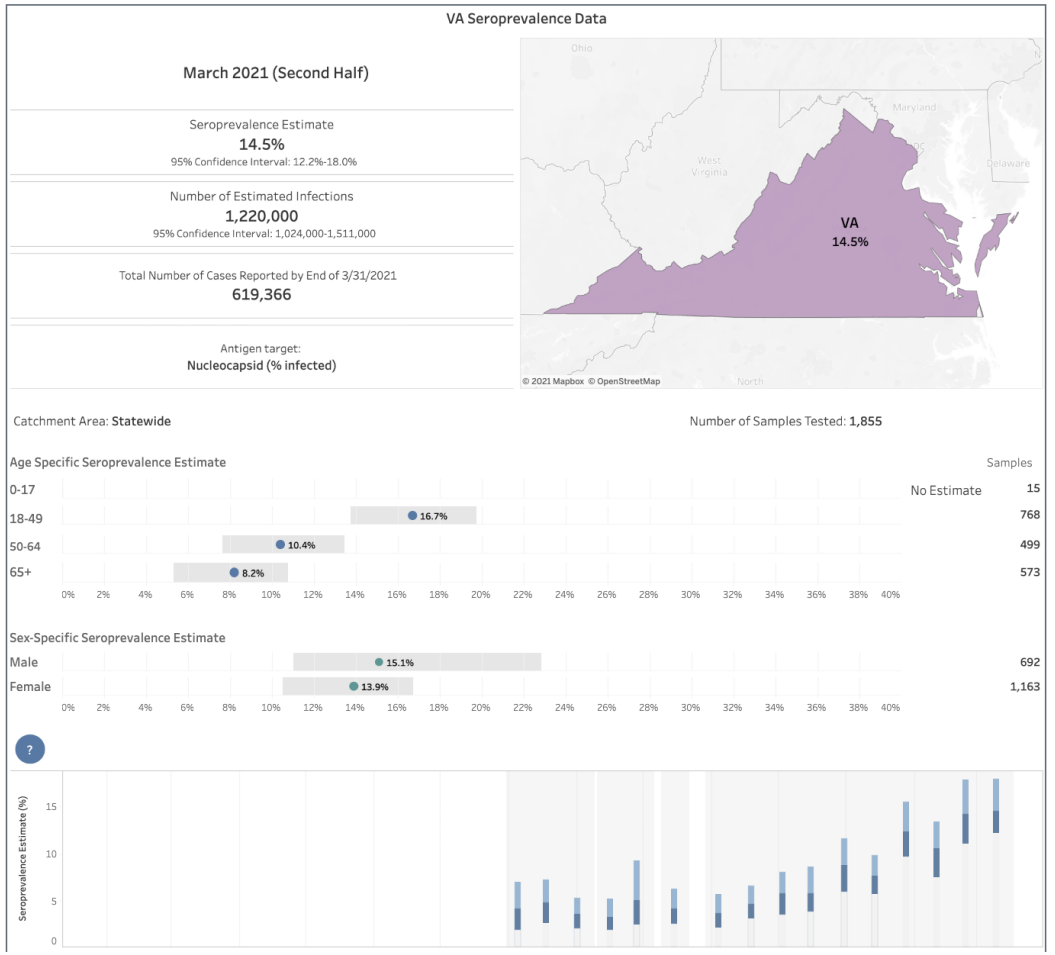
Seroprevalence updates to model design

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

- CDC Nationwide Commercial Laboratory Seroprevalence Survey estimated 14.5% [12% – 18%] seroprevalence as of March 4th – 17th up from 10.5% a month earlier

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

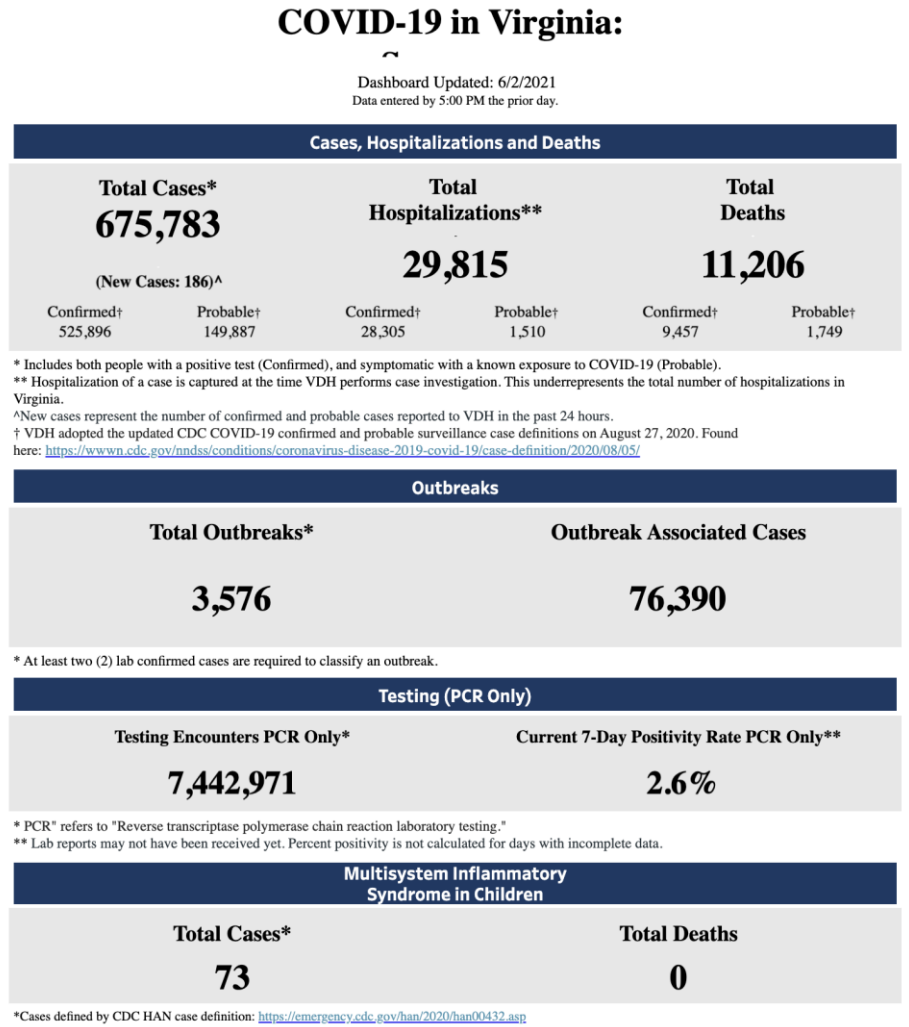
- Thus for 2x there are 2 total infections in the population for every confirmed case recently
- This measure now fully tracks the estimated ascertainment over time
- Uncertainty design has been shifted to these bounds (previously higher ascertainments as was consistent earlier in the pandemic were being 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



COVID-19 in Virginia:

Dashboard Updated: 6/2/2021
Data entered by 5:00 PM the prior day.

Cases, Hospitalizations and Deaths

Total Cases*	Total Hospitalizations**	Total Deaths
675,783	29,815	11,206
(New Cases: 186)^		
Confirmed† 525,896 / Probable† 149,887	Confirmed† 28,305 / Probable† 1,510	Confirmed† 9,457 / Probable† 1,749

* Includes both people with a positive test (Confirmed), and symptomatic with a 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 confirmed and probable surveillance case definitions on August 27, 2020. Found here: https://wwwn.cdc.gov/nndss/conditions/coronavirus-disease-2019-covid-19/case-definition/2020/08/05/

Outbreaks

Total Outbreaks*	Outbreak Associated Cases
3,576	76,390

* 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**
7,442,971	2.6%

* 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
73	0

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

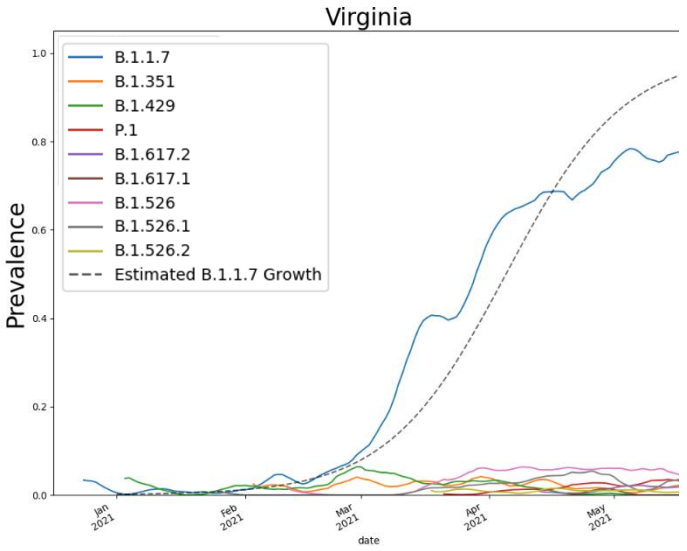
Accessed 9:00am June 2, 2021
https://www.vdh.virginia.gov/coronavirus/

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
- Plausible levels of transmission can be bounded by past experience
  - Assess transmission levels at the county level from May 1, 2020 – Sept 1, 2020 or current, whichever is highest
- Projection Scenario:
  - **Adaptive:** Control remains as is currently experienced into the future
  - **Fatigued Control**:
    - Highest level of transmission (95th percentile) increased by additional 5%
    - Transition to this level over 4 weeks, remain at this level for the summer, then return to Adaptive
- Additional study scenarios with Fall Resurgence:
  - **Fall:** Resurgence to worst of Fall 2020 starting in September and ramping up quickly

Scenarios – Mixed Variants Condition

- Variant B.1.1.7 has reached dominance in Virginia but no longer is growing at a predictable pace as variants compete
- Other variants with differing levels of transmissibility, immune escape, and impacts on severity also exist, to varying degrees
- Transmissibility boosting effects and growth of variants are no longer predictable
  - Rely on adaptive fitting to find transmissibility trends for projection
- Immune Escape
  - Many variants demonstrate the ability to evade immunity, both natural and vaccine-induced, uncertainty remains high thus this is not factored into the model
- Impact on Severity
  - Assume current variant prevalence remains relatively stable into future
  - Severity increases:
    - B.1.1.7= 1.6 times hospitalization and death
    - P.1 = 1.5 times hospitalization and death
    - B.1.351 = 1.5 times hospitalization and death



outbreak.info

Outbreak Info

GISAID

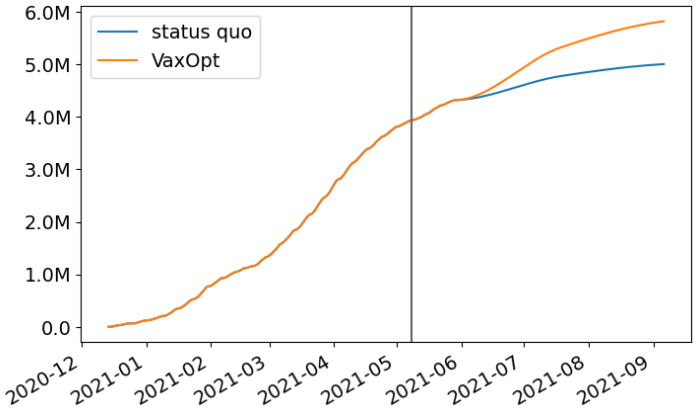
Scenarios – Vaccination Conditions

Vaccine Characteristics

- **Pfizer/Moderna**: 50% after first dose, 95% after second dose (3.5 week gap)
- **J & J** : 67% efficacy after first (and only) dose
- Delay to efficacy from doses is 14 days, immunity lasts at least 7m (NEJM study)

Vaccine Administration Scenarios

- **Status quo (no label):** COVIDcast corrected acceptance estimates (statewide mean is ~65%) reached by Labor Day.
- **Optimistic (VaxOpt):** Expand VA mean acceptance to ~80% (with all counties reaching a minimum of 65%, max of 95%).
- Acceptance at county level = regional acceptance +/- relative current vax
- Front-loaded rollout (two-thirds of the remaining in half the time)

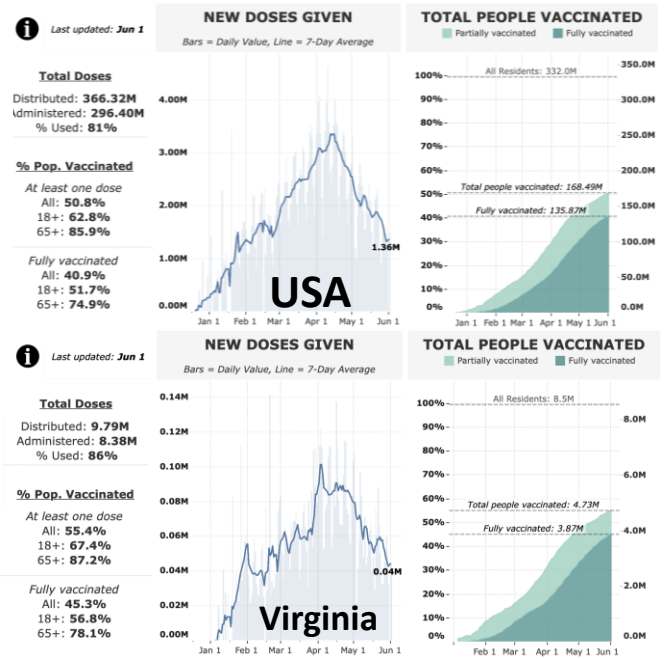


Monthly first doses

Date	status quo	VaxOpt
2020-12-31	114.3K	114.3K
2021-01-31	654.1K	654.1K
2021-02-28	564.7K	564.7K
2021-03-31	1.3M	1.3M
2021-04-30	1.1M	1.1M
2021-05-31	533.5K	534.3K
2021-06-30	274.1K	594.4K
2021-07-31	253.7K	565.2K
2021-08-31	138.4K	303.5K
2021-09-30	16.1K	35.2K

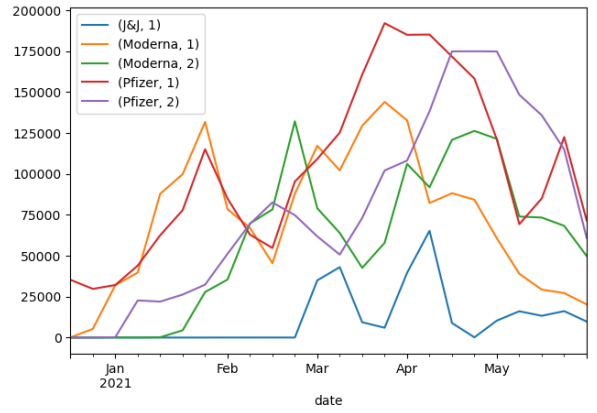
Cumulative

Date	status quo	VaxOpt
2020-12-31	114.3K	114.3K
2021-01-31	768.5K	768.5K
2021-02-28	1.3M	1.3M
2021-03-31	2.6M	2.6M
2021-04-30	3.8M	3.8M
2021-05-31	4.3M	4.3M
2021-06-30	4.6M	4.9M
2021-07-31	4.9M	5.5M
2021-08-31	5.0M	5.8M
2021-09-30	5.0M	5.8M



Source: https://ckelly17.github.io/vaccine_dashboard.html

Weekly VA doses administered by manufacturer



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Scenarios – Combined Conditions

Name	Txm Controls	Variant Boosting	Vax	Description
Adaptive	C	Mixed	SQ	Likely trajectory based on conditions remaining similar to how they are now
Adaptive-FatigueControl	F	Mixed	SQ	Worst case trajectory if control conditions deteriorate to highest transmission rates of the past
Adaptive-VaxOpt	C	Mixed	VO	Likely trajectory based on conditions remaining similar to now, but with improvements to vaccine acceptance
Adaptive-FatigueControl-VaxOpt	F	Mixed	VO	Worst case trajectory if control conditions deteriorate to worst of the past, with improvements to vax acceptance

Transmission Controls: C = Current levels persist into the future
F = Fatiguing controls drift to worst levels of last summer and persist

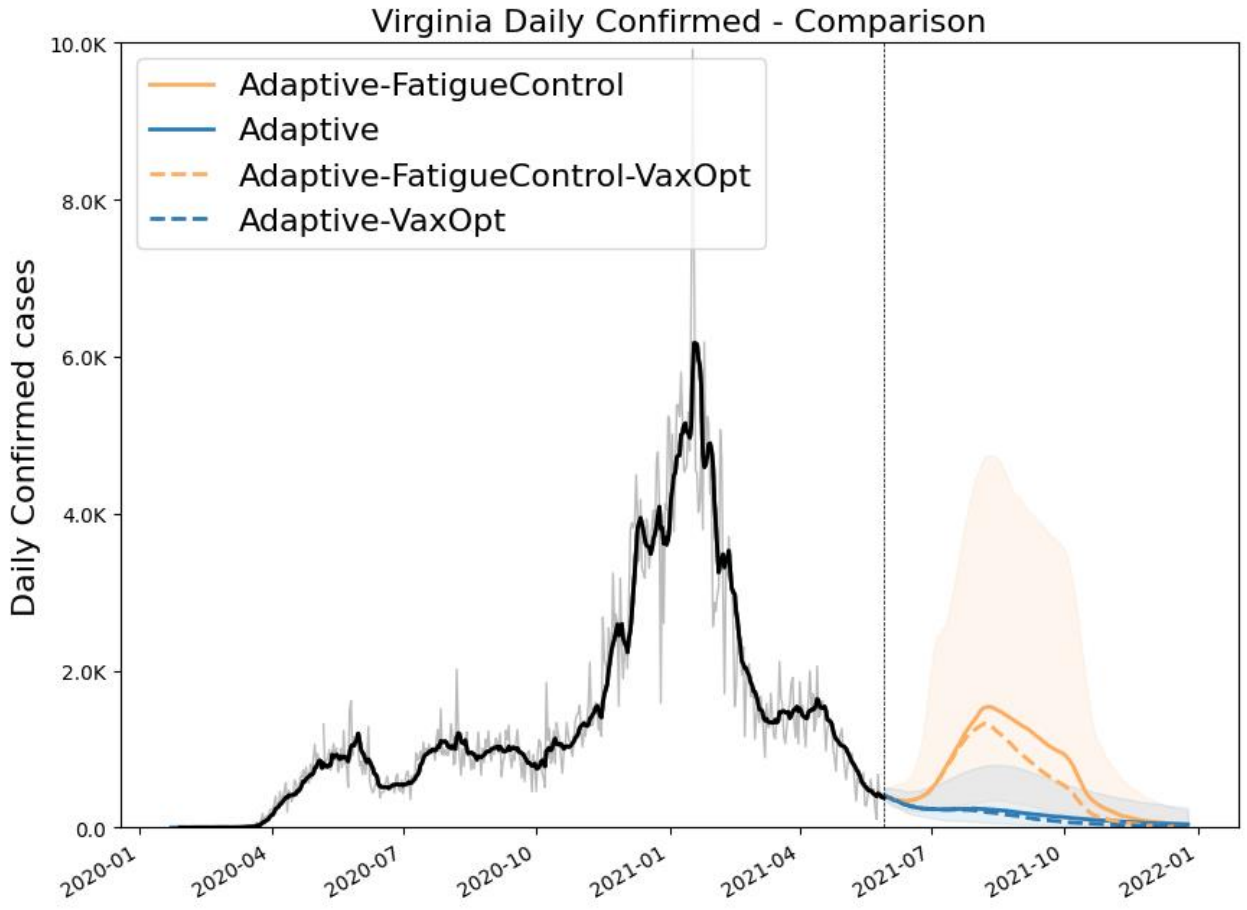
Variant Boosting: Mixed = Variety of variants, no future txm boosting, but with severity impacts from current levels

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

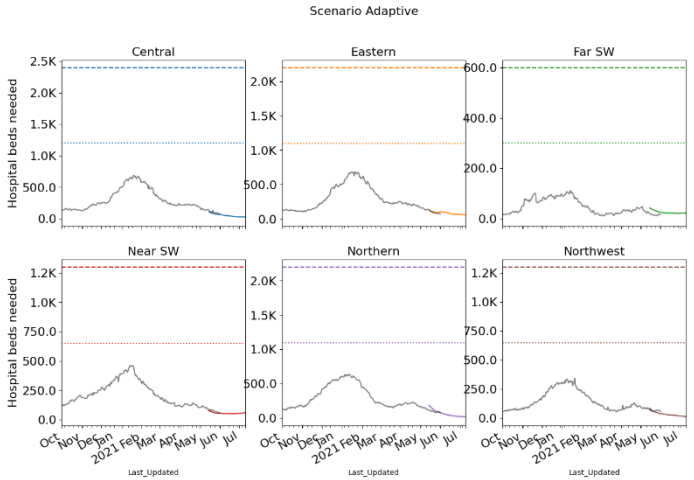
Model Results

Outcome Projections

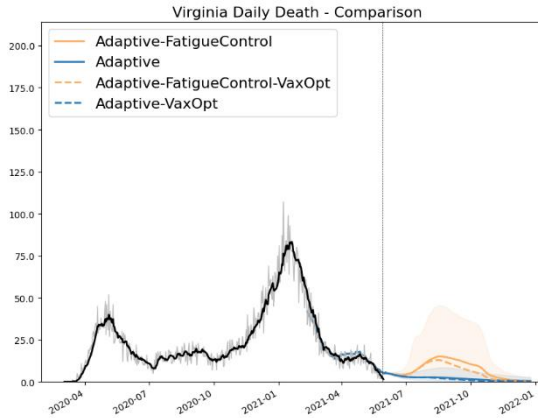
Confirmed cases



Estimated Hospital Occupancy

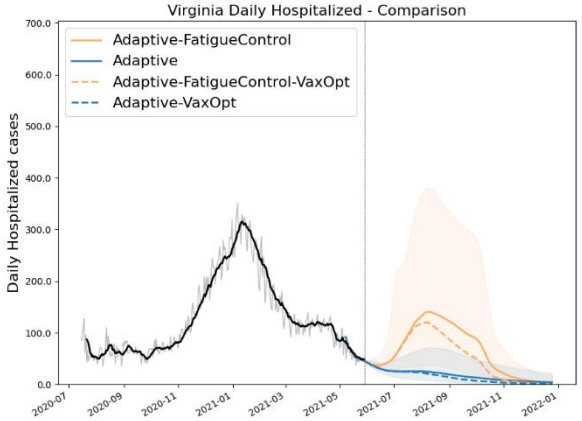


Daily Deaths



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

Daily Hospitalized



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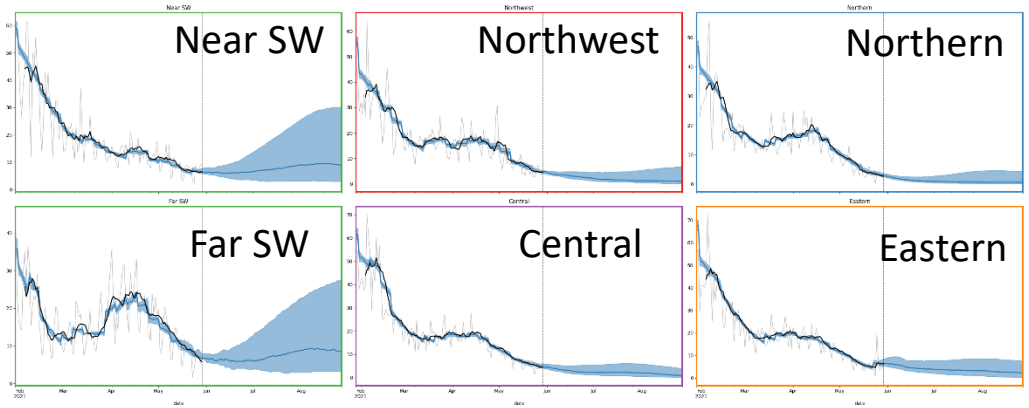
District Level Projections: Adaptive

Projections by Region



Projections by District

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

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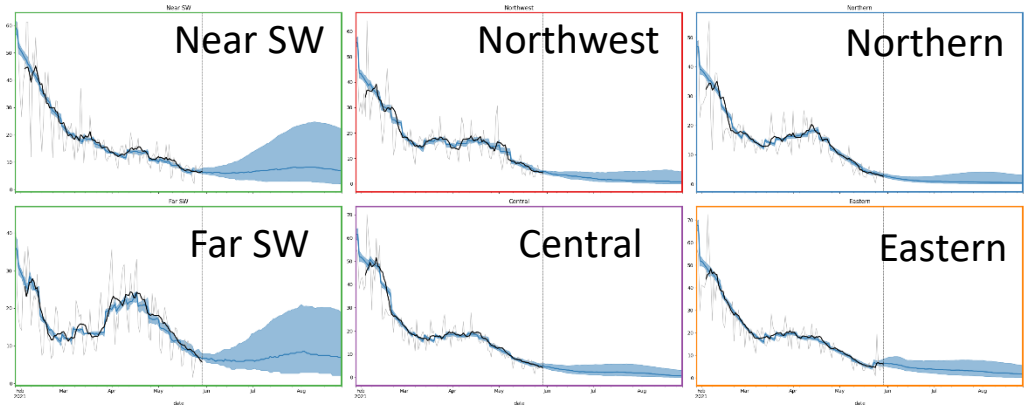
District Level Projections: Adaptive-VaxOpt

Projections by Region



Projections by District

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

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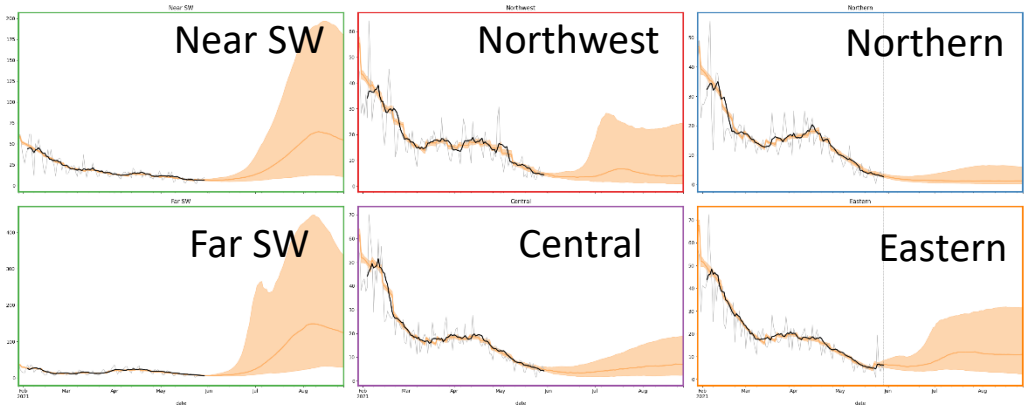
District Level Projections: Adaptive-FatigueControl

Projections by Region



Projections by District

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

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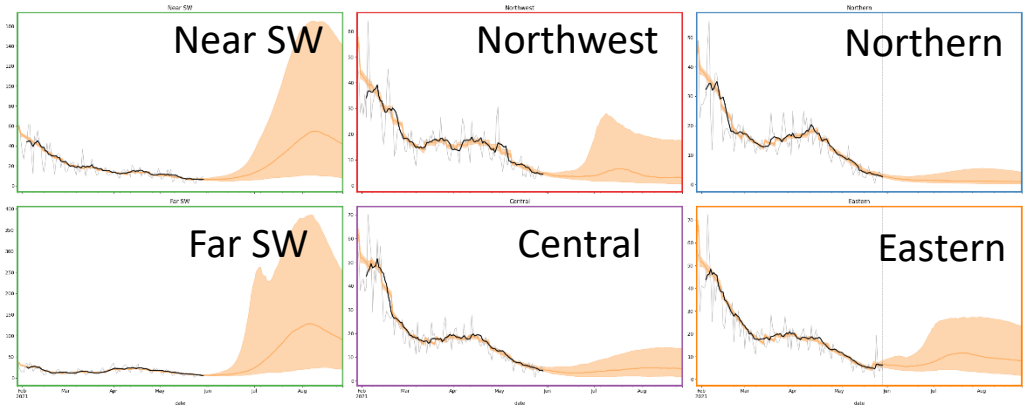
District Level Projections: Adaptive-FatigueControl-VaxOpt

Projections by Region



Projections by District

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

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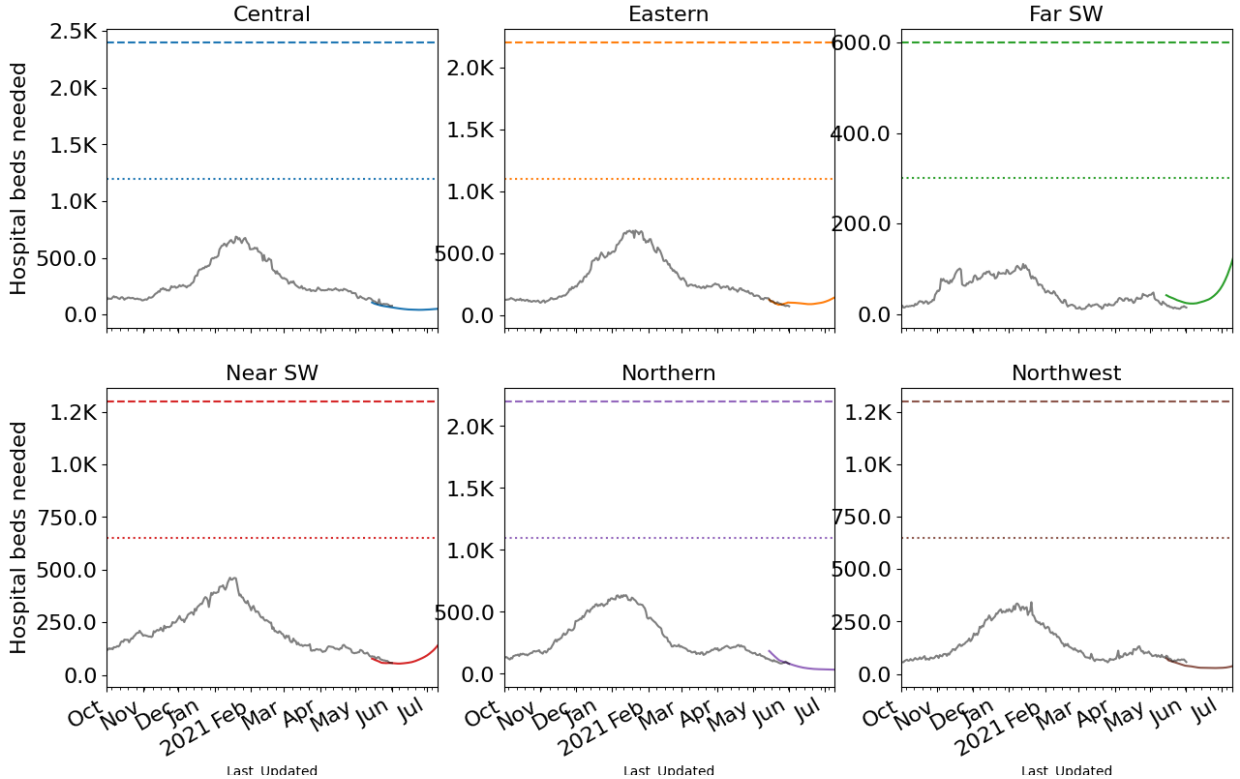
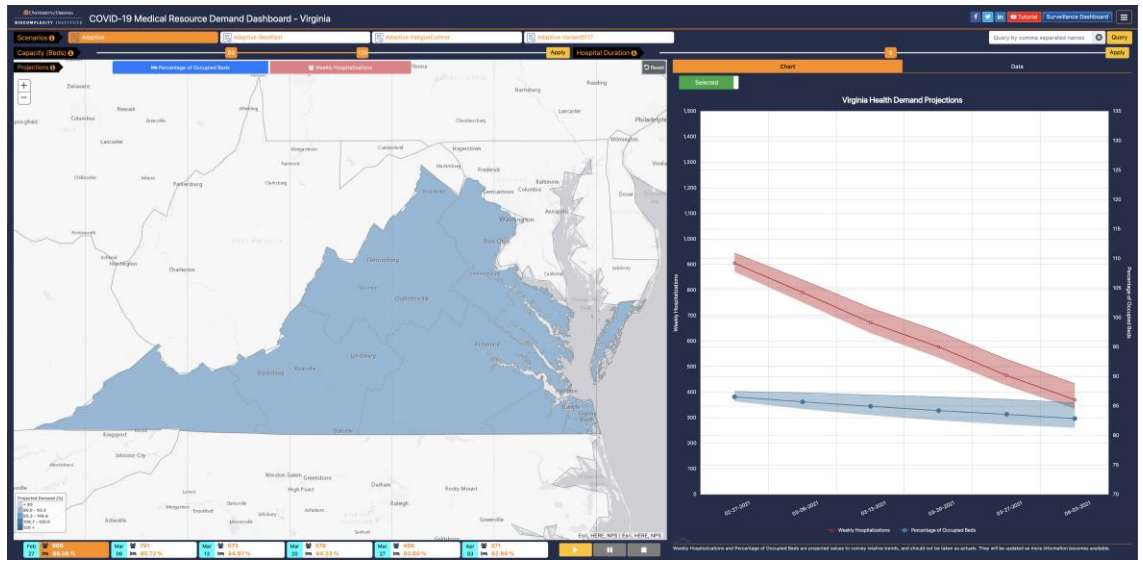
Hospital Demand and Bed Capacity by Region

Capacities* by Region – Adaptive-FatigueControl

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





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

The Adaptive-FatigueControl scenario shows it remains possible to generate more hospitalizations:

- Far Southwest and Near Southwest could generate some more hospitalizations

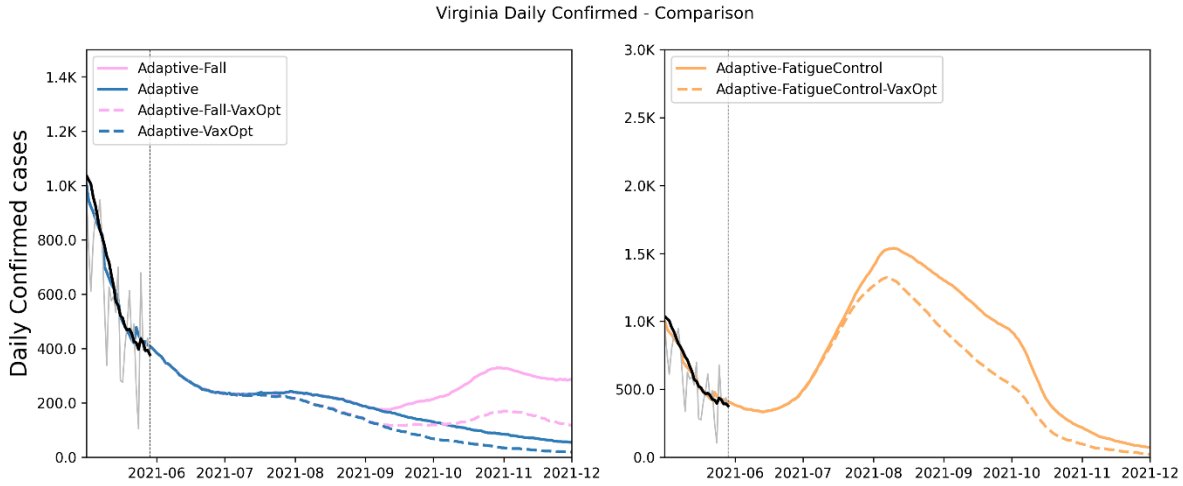
* Assumes average length of stay of 8 days

Impact of Expanded Vaccination Levels

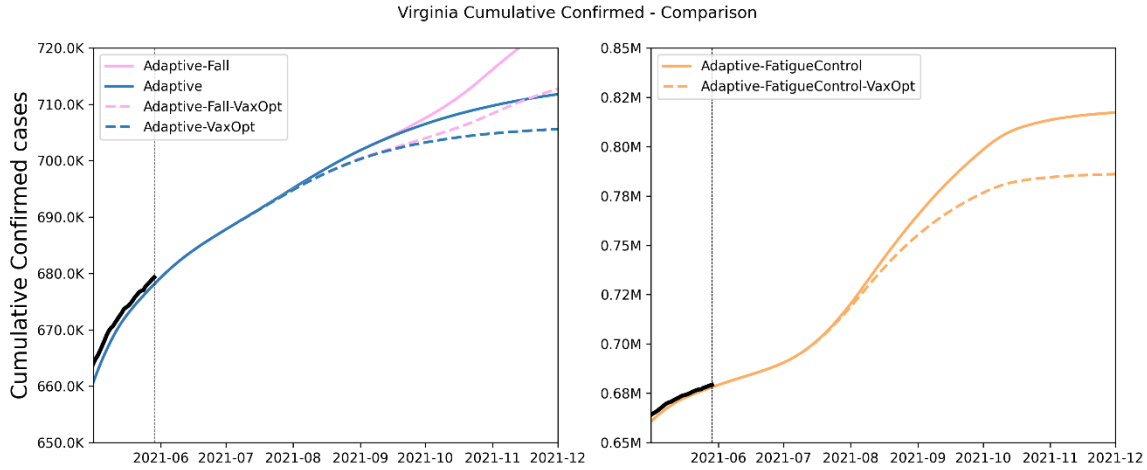
Impact of expanded vaccine acceptance against a Fall Surge

- Use a Fall Surge scenario to test resilience to new transmission surges
  - Surge to highest rate from Fall 2020, boosted 20%, over two weeks starting on Sept 1st 2021
- Achieving the optimistic levels of vaccination could prevent 17K cases over the fall
- In worst case of sustained Fatigue Control 32K+ cases averted

Daily Infections



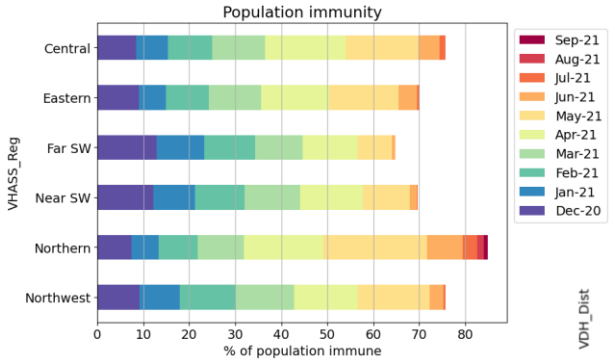
Cumulative Infections

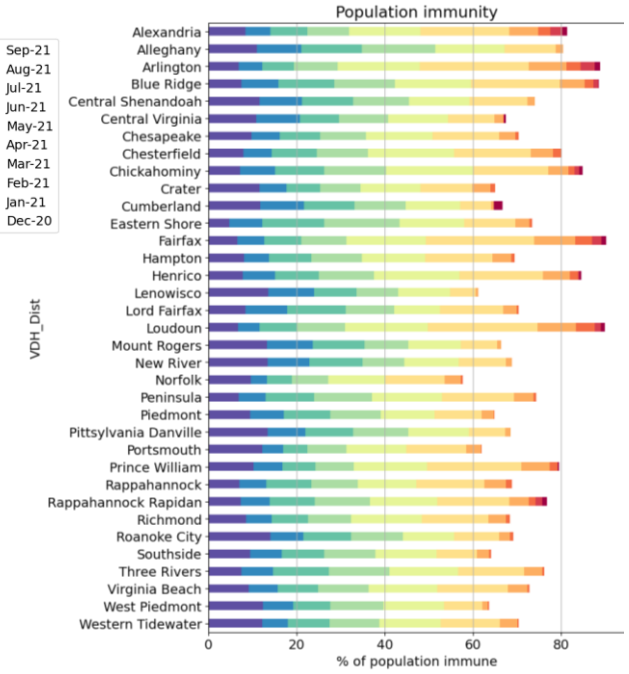


Virginia's Progress on Population Immunity

Natural Immunity and Vaccines combine to produce a population level of immunity

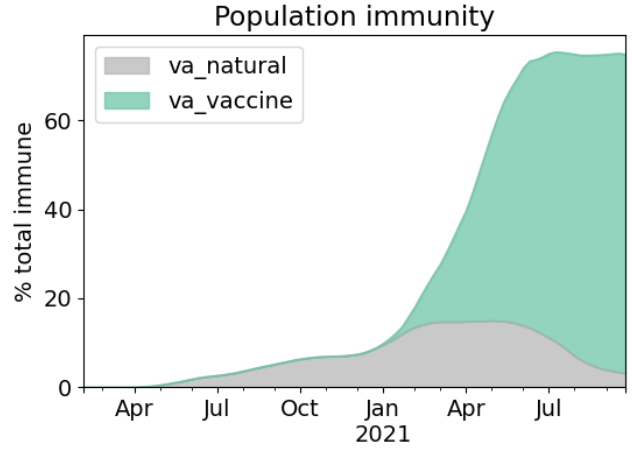
- Duration of immunity from infection with SARS-CoV2 still not well understood
  - We assume a conservative 6 month period of protection for these calculations
  - Natural immunity is well calibrated to recent seroprevalence surveys
- Vaccine induced immunity is likely to last longer, we assume indefinite protection
  - This also assumes that all administered vaccines remain protective against current and future novel variants
- Population immunity depends on a very high proportion of the population getting vaccinated
  - Using regional vaccine acceptance





Region	% immune (est.)*
Central	70%
Eastern	65%
Far SW	64%
Near SW	68%
Northern	72%
Northwest	72%
Virginia	69%

* As of May 30, 2021



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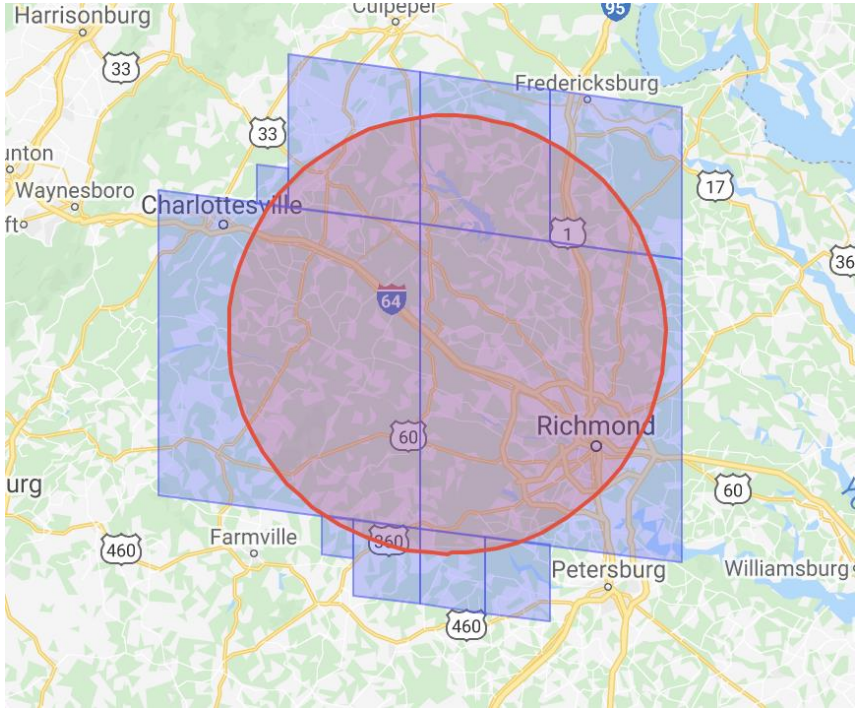
Mobile CVC Placement - Approach

Geographical Units

- Google's S2 Geometry is an approach for representing a geographical area using cells (polygons)
- Divides the world map into nested cells of decreasing size (L0 - L30)
  - Each L1 cell contains four L2 cells, each L2 contains four L3s, and so on
  - Typical sizes: L8 = 500 sq mi; L10 = 31 sq mi; L14 = 0.12 sq mi or 79 acres; see all cell statistics here
- Each cell has a unique token that can be used to locate that area (eg, 89b14 = L7 cell that includes Richmond)
- Any geographical area can be represented in S2 cells of varying size
- You can visualize cells of any size using this interface



Mobile CVC Placement - Approach

Measuring mobility

- SafeGraph: anonymized geolocation data aggregated from numerous cell phone apps
- Daily and hourly number of visits to points-of-interest (POIs), i.e., non-residential locations such as restaurants, bars, gas stations, malls, grocery stores, churches, etc.
- Weekly reports per POI of *where visitors are coming from* (at the census block group level)
- One of the most fine-grained and high-coverage mobility data sources available: 6.4 million POIs in the US; 158,869 POIs in VA
- Has been utilized by hundreds of researchers, governments, and the CDC to aid COVID-19 efforts (Chang, Pierson, Koh, et al., *Nature* 2020; Chang et al, KDD 2021)
- Still has limitations to be aware of (e.g., less representation among children and seniors)

SAFEGRAPH

Mobile CVC Placement - Approach

Provide a ranked list, per **region** and day of week, of the highest-mobility **areas**

Region = L8 cells

- Approximately county-magnitude (since there are 133 counties + independent cities in VA)

Area = L14 cells

- Busiest L14s usually contain 10-30 POIs
- Any reasonable site can be used within this area

Output: for each L8 and day of the week, the top 10 highest-mobility L14s

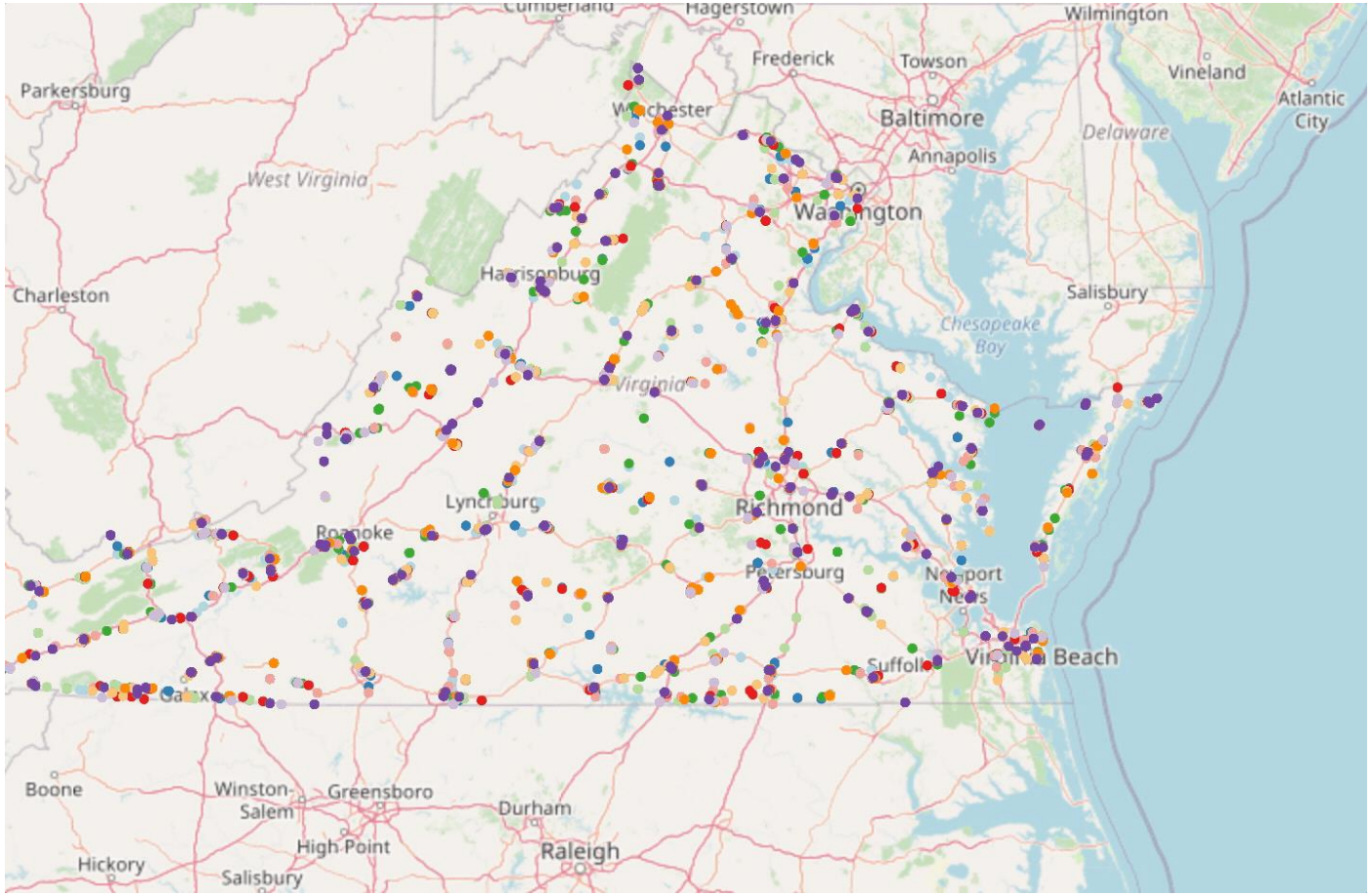
- Mobility is measured as visits to POIs
- Currently summing over the most recent 3 weeks of SafeGraph data (Apr 26 to May 16, 2021)

Cell level	# in VA*
L7	41
L8	124
L9	409
…	
L13	14718
L14	25376
L15	40215

* Only counting cells for which we have at least one SafeGraph POI

Mobile CVC Placement - Results

Interactive interface for browsing the data



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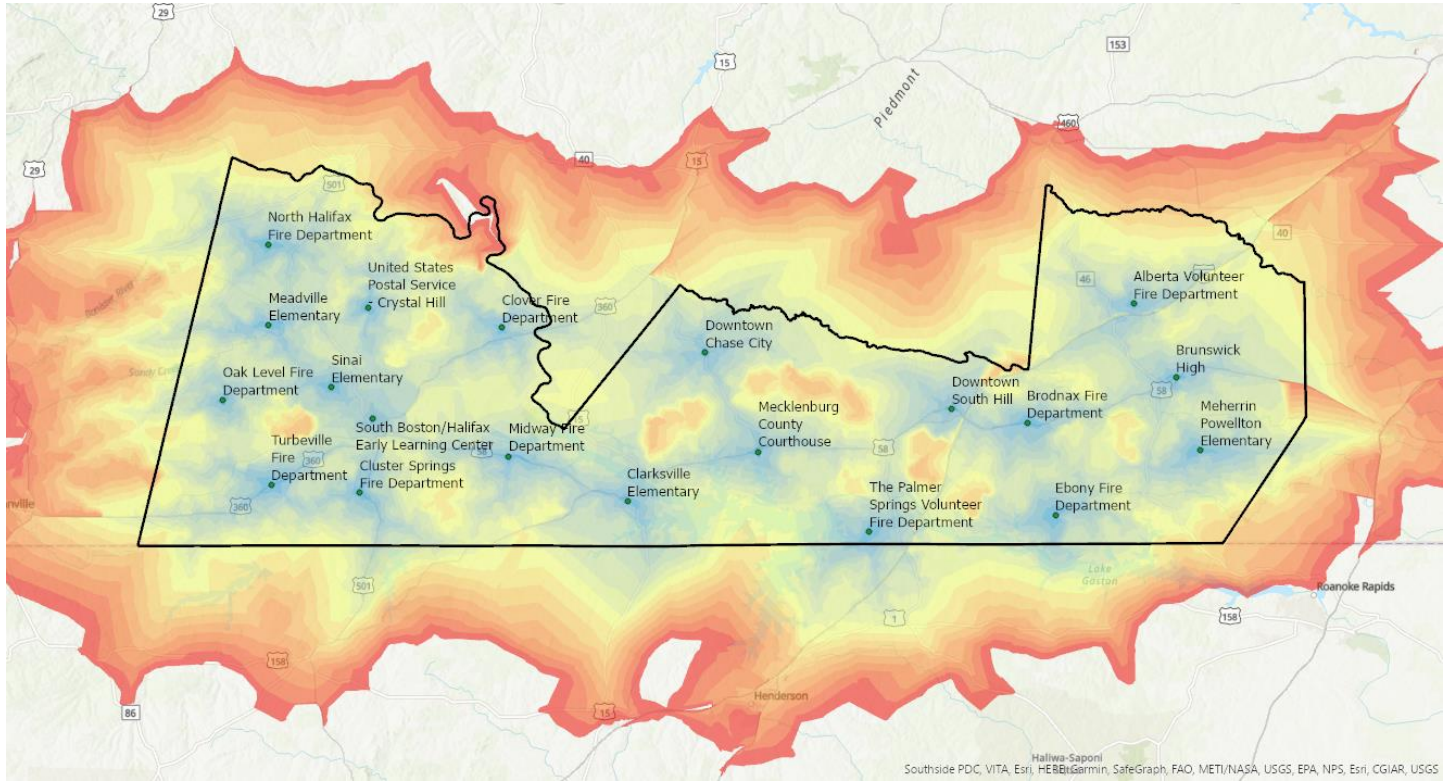
Mobile CVC Placement – Pilot Study in Southside

Goal: Find 20 locations that minimize driving distance for largest group of underserved Black and Latinx population

Results: Many of these points coincide with existing clinics or planned sites, however, others have yet to be tried.



Southside mobile unit site candidates. Color gradient represents driving time of covered population to nearest point.

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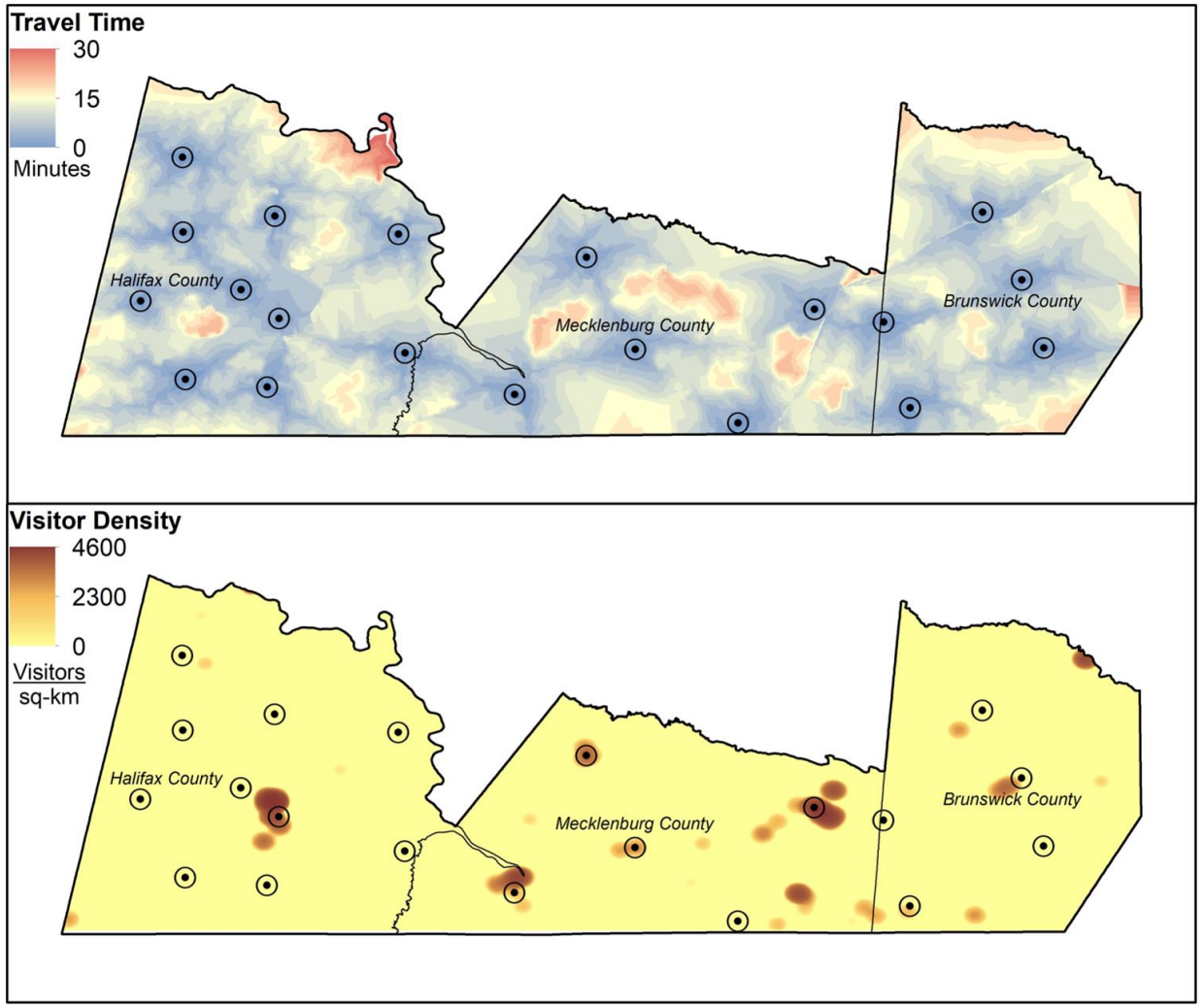
Mobile CVC Placement – Pilot Study in Southside

Top: Previously identified sites

Bottom: Most visited POIs in the Southside health district in the last week overlaid with candidates.

Some additional high yield locations identified. Some locations are places like truck stops that may not reach local residents.



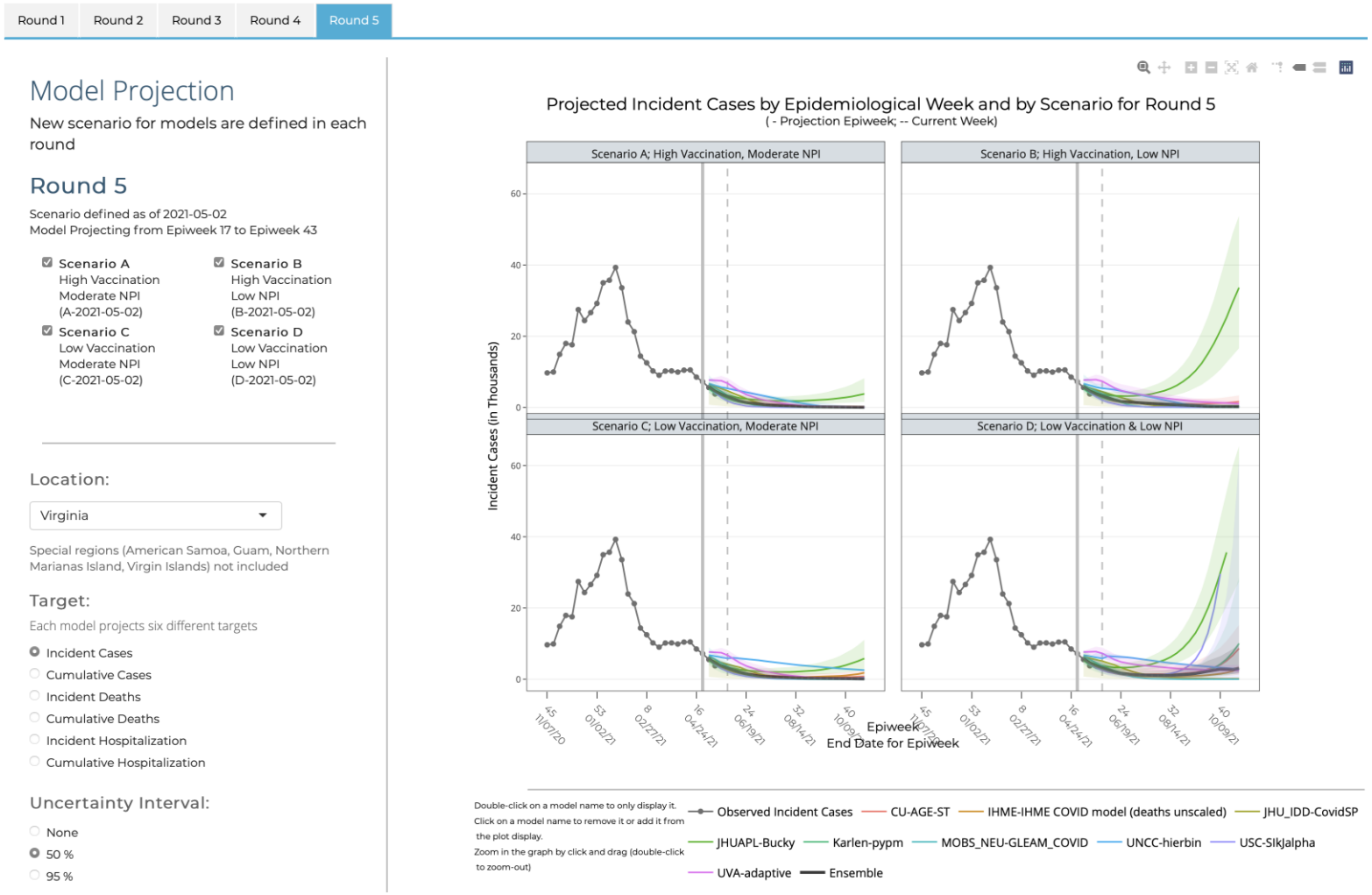
COVID-19 Scenario Modeling Hub

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 levels of control (moderate and low)

Round 5 updates now available

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

https://covid19scenariomodelinghub.org/viz.html



Key Takeaways

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

- **Case rates in Virginia continue to decline though some districts have small rebounds in rates**
- VA mean weekly incidence flat at 4/100K, US down to 5/100K from 8/100K
- Vaccination rates continue to decline after rebound from 12-16 year-olds
- Projections show declining rate overall across Commonwealth
- Recent updates:
  - Minor updates to measured acceptance levels and expanded optimistic vaccination scenario
  - Additional Fall resurgence study scenario testing resilience of population
  - Limited waning of natural immunity included in fit and projections, also with seroprevalence update
  - Mobile CVC placement side study undertaken
- The situation continues to change. Models continue to be updated regularly.

References

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

Arindam Fadikar, Dave Higdon, Jiangzhuo Chen, Bryan Lewis, Srinivasan Venkatramanan, and Madhav Marathe. Calibrating a stochastic, agent-based model using quantile-based emulation. SIAM/ASA Journal on Uncertainty Quantification, 6(4):1685–1706, 2018.

Adiga, Aniruddha, Srinivasan Venkatramanan, Akhil Peddireddy, et al. "Evaluating the impact of international airline suspensions on COVID-19 direct importation risk." *medRxiv* (2020)

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

Virginia Department of Health. COVID-19 in Virginia. http://www.vdh.virginia.gov/coronavirus/

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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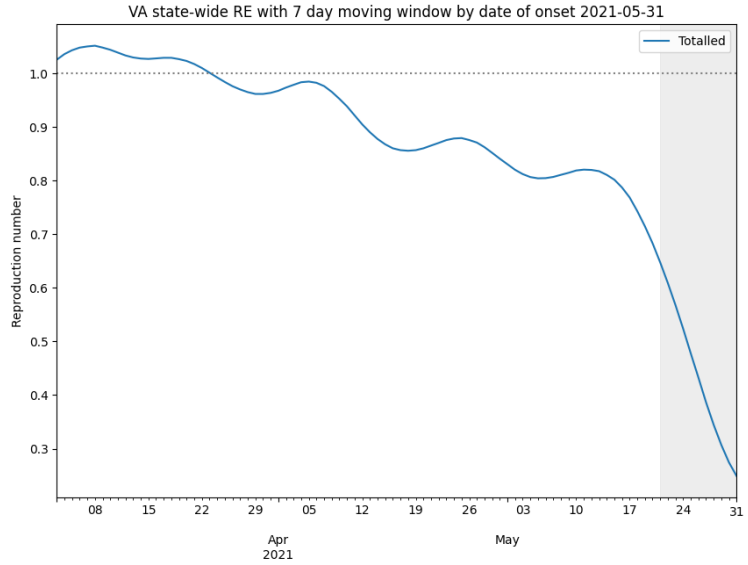
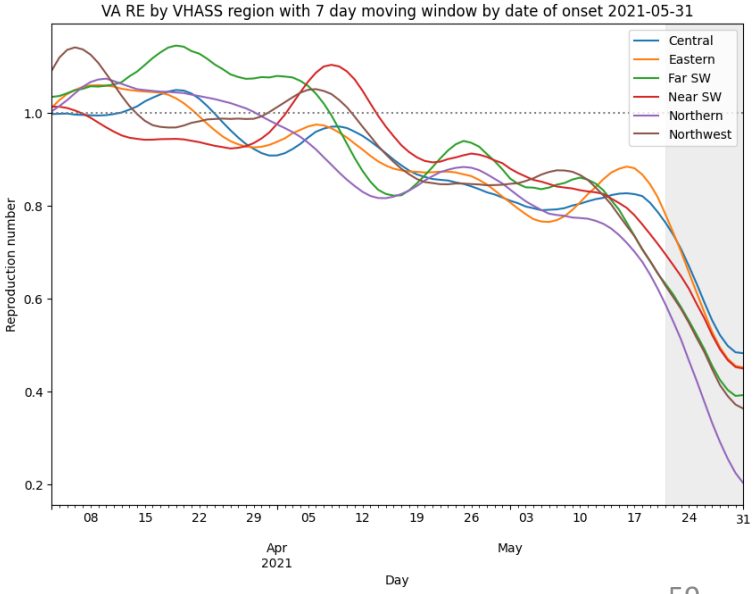
Supplemental Slides

Estimating Daily Reproductive Number

May 22nd Estimates

Region	Date of Onset R_e	Date Onset Diff Last Week
State-wide	0.934	0.276
Central	0.738	0.007
Eastern	0.742	-0.019
Far SW	0.609	-0.104
Near SW	0.673	-0.037
Northern	0.551	-0.064
Northwest	0.604	-0.055





Methodology

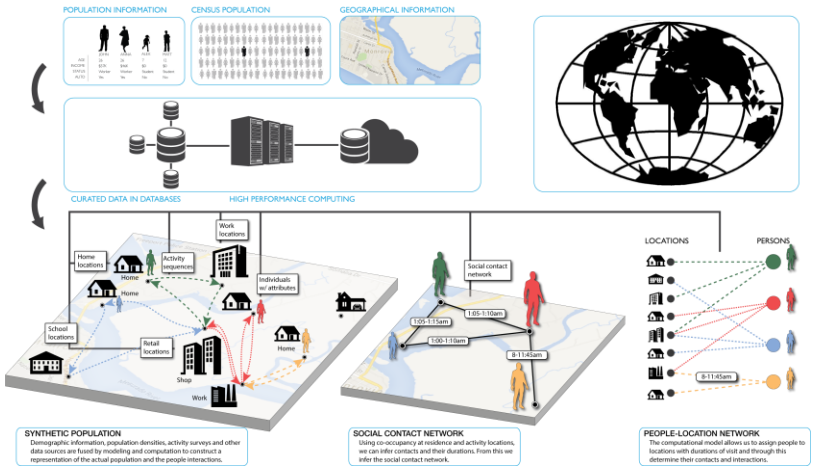
- Wallinga-Teunis method (EpiEstim[1]) for cases by **confirmation date**
- Serial interval: updated to discrete distribution from observations (mean=4.3, Flaxman et al, Nature 2020)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

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

Agent-based Model (ABM)

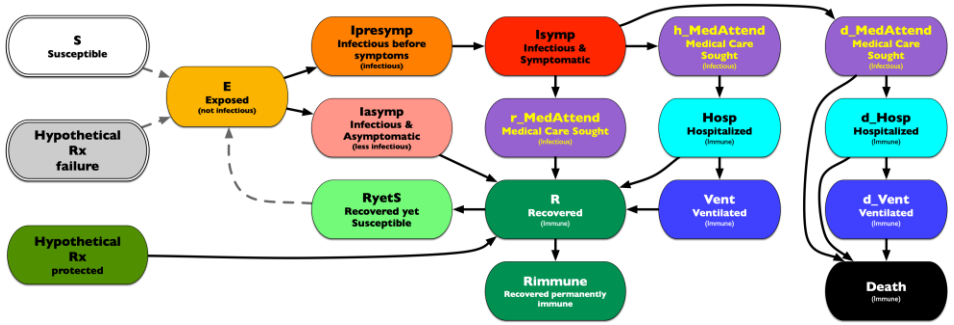
EpiHiper: Distributed network-based stochastic disease transmission simulations

- 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