Network Systems Science & Advanced Computing

Biocomplexity Institute & Initiative

University of Virginia

Estimation of COVID-19 Impact in Virginia

March 31st, 2021

(data current to March 29th – 31st)

Biocomplexity Institute Technical report: TR 2021-032

UNIVERSITY of VIRGINIA

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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

Points of Contact

Bryan Lewis
brylew@virginia.edu

Srini Venkatramanan
srini@virginia.edu

Madhav Marathe
marathe@virginia.edu

Chris Barrett
ChrisBarrett@virginia.edu

Biocomplexity COVID-19 Response Team

Aniruddha Adiga, Abhijin Adiga, Hannah Baek, Chris Barrett, Golda Barrow, Richard Beckman, Parantapa Bhattacharya, Andrei Bura, Jiangzhuo Chen, Clark Cucinell, Patrick Corbett, Allan Dickerman, Stephen Eubank, Arindam Fadikar, Joshua Goldstein, Stefan Hoops, Ben Hurt, Sallie Keller, Ron Kenyon, Brian Klahn, Gizem Korkmaz, Vicki Lancaster, Bryan Lewis, Dustin Machi, Chunhong Mao, Achla Marathe, Madhav Marathe, Fanchao Meng, Henning Mortveit, Mark Orr, Joseph Outten, Akhil Peddireddy, Przemyslaw Porebski, SS Ravi, Erin Raymond, Jose Bayoan Santiago Calderon, James Schlitt, Aaron Schroeder, Stephanie Shipp, Samarth Swarup, Alex Telionis, Srinivasan Venkatramanan, Anil Vullikanti, James Walke, Andrew Warren, Amanda Wilson, Dawen Xie

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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:

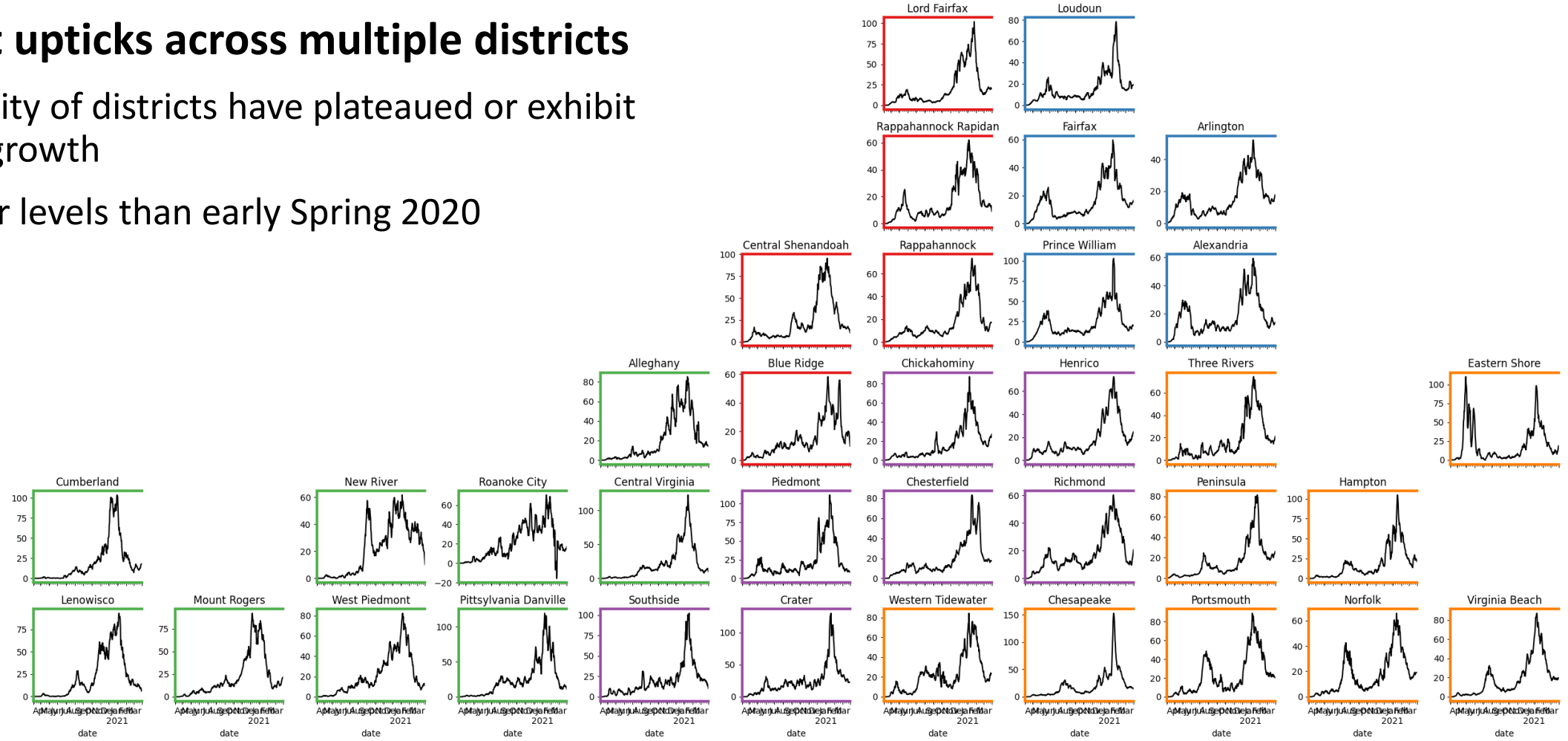
- **Case rates in Virginia have flattened and now have some growth**
- VA mean weekly incidence flat at 17.5/100K from 17/100K, US up (to 18.5 from 16.5 per 100K)
- Progress is stalling, 84% of VA counties above mean rate of Summer 2020
- Projections shifting to growth across Commonwealth, boosted by B.1.1.7
- Recent updates:
  - Currently challenged to estimate the impact on hospitalizations and deaths, as increased rates from Variant B.1.1.7 interact with decreases from vaccination of the most susceptible to these outcomes
  - Johnson & Johnson included in vaccine schedule and Seasonal Effects adjusted for spring and summer
- The situation continues to change. Models continue to be updated regularly.

Situation Assessment

Case Rate (per 100k) by VDH District

Recent upticks across multiple districts

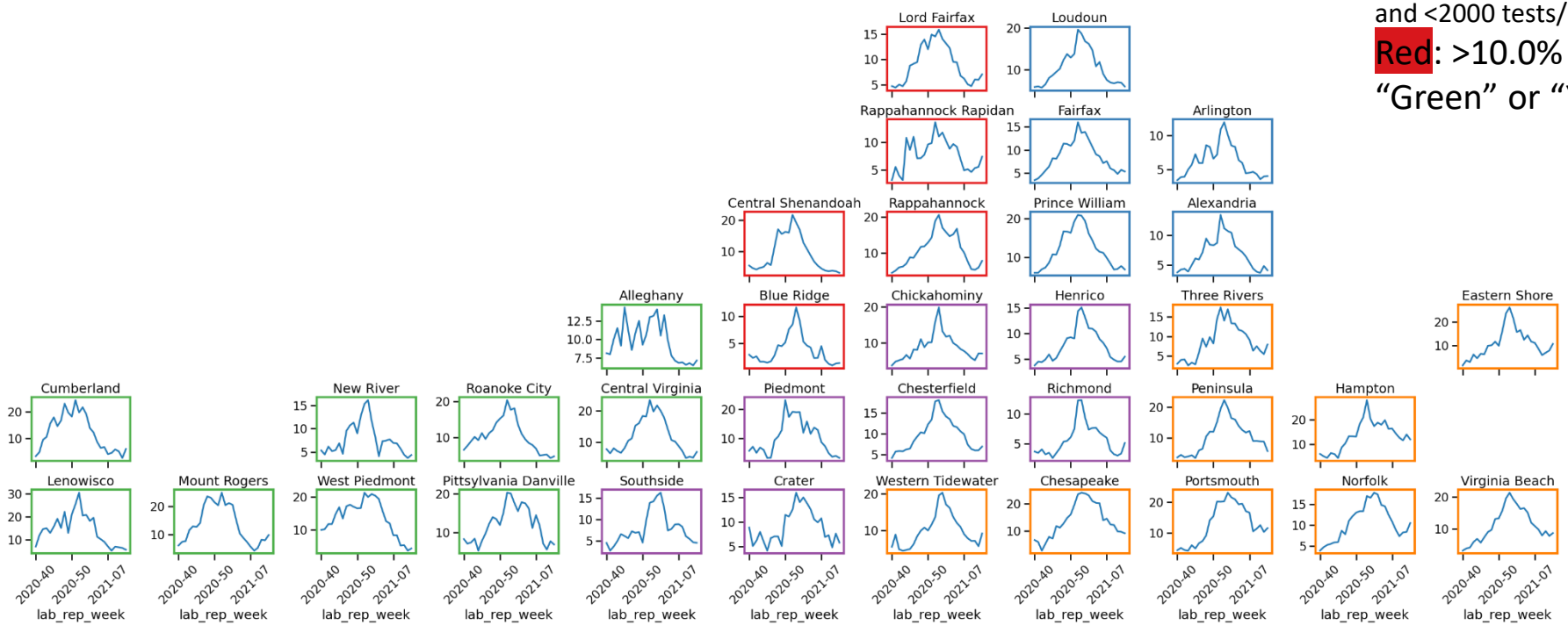
- Majority of districts have plateaued or exhibit slow growth
- Higher levels than early Spring 2020



Test Positivity by VDH District

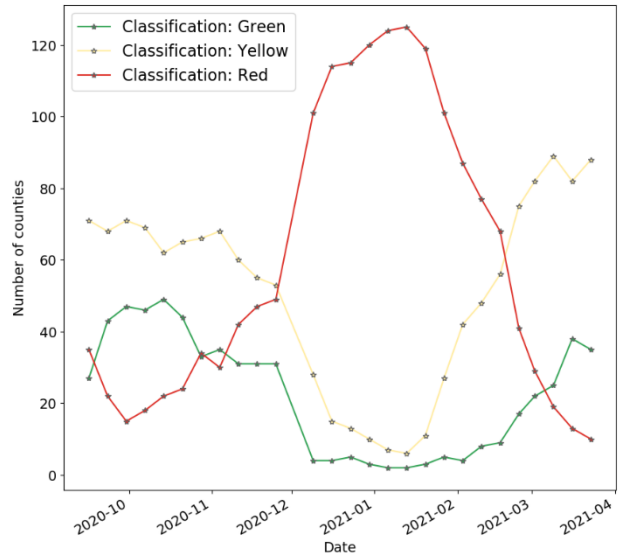
Weekly changes in test positivity by district

- Some upticks/flattening in the positivity rates
- Nearly 75% of counties still in Red or Yellow categories



County level test positivity rates for RT-PCR tests.

Green: Test positivity <5.0%
(or with <20 tests in past 14 days)
Yellow: Test positivity 5.0%-10.0% (or with <500 tests and <2000 tests/100k and >10% positivity over 14 days)
Red: >10.0% and not meeting the criteria for "Green" or "Yellow"



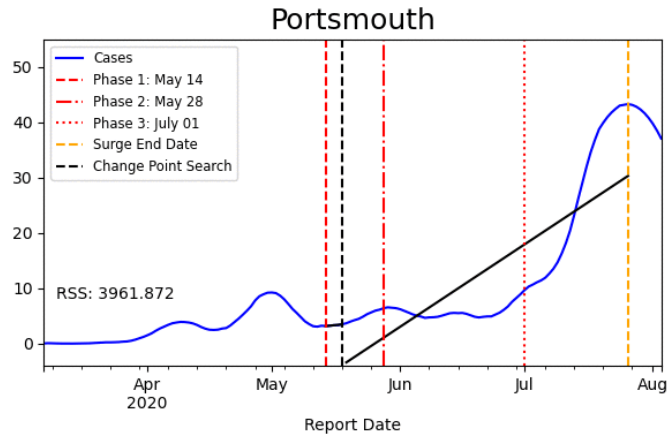
https://data.cms.gov/stories/s/q5r5-gjyu

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

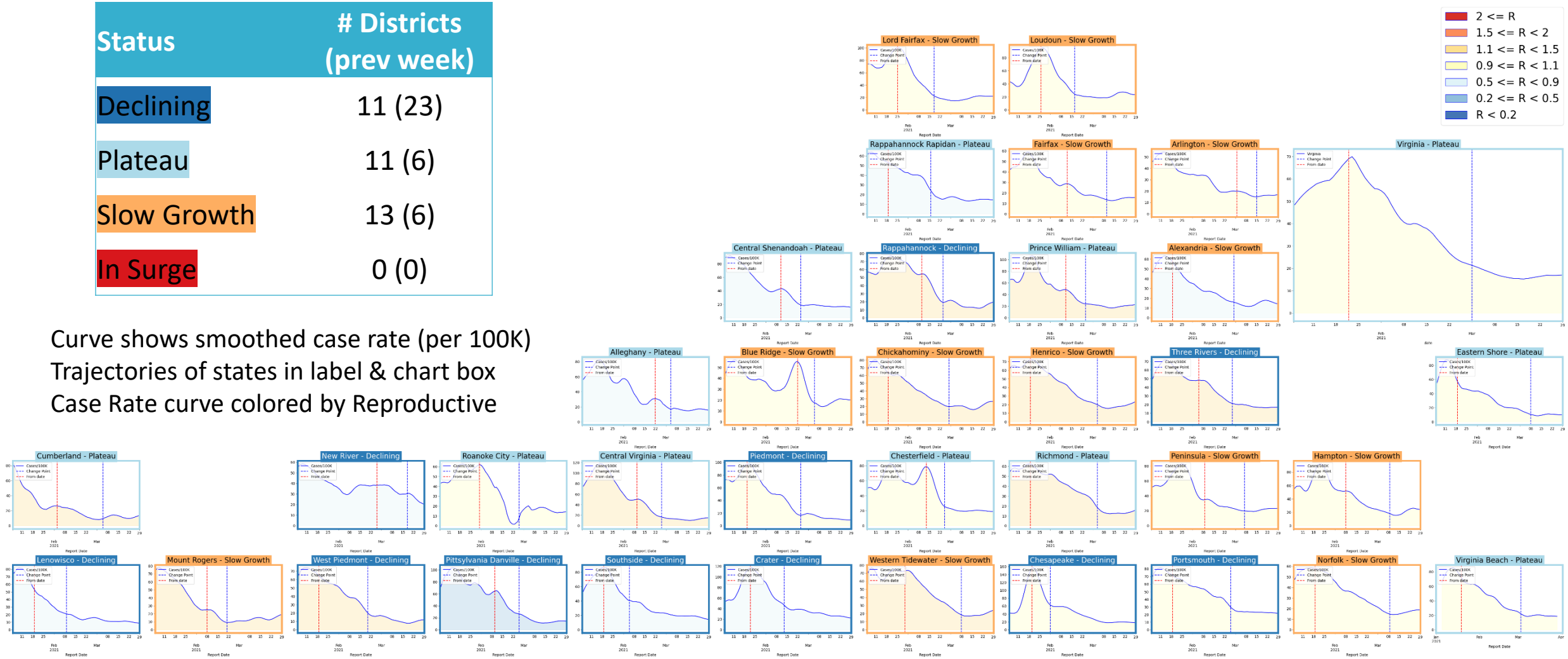


Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	11 (23)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	11 (6)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	13 (6)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	0 (0)

District Trajectories – last 10 weeks

Status	# Districts (prev week)
Declining	11 (23)
Plateau	11 (6)
Slow Growth	13 (6)
In Surge	0 (0)

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



SARS-CoV2 Variants of Concern

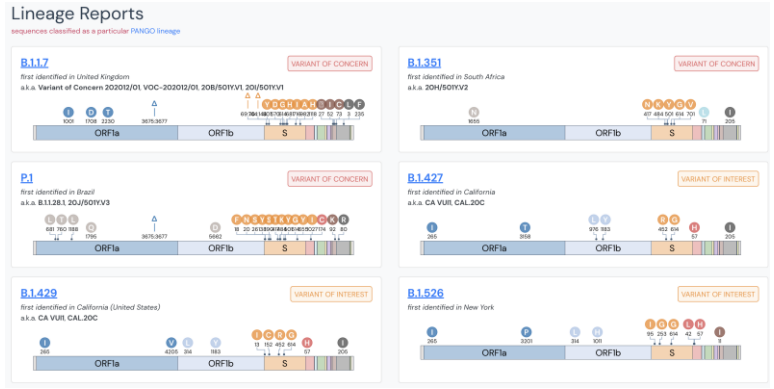
Emerging new variants will alter the future trajectories of pandemic and have implications for future control

- Current evidence supports that new 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
  - B.1.1.7 is most frequent and well studied

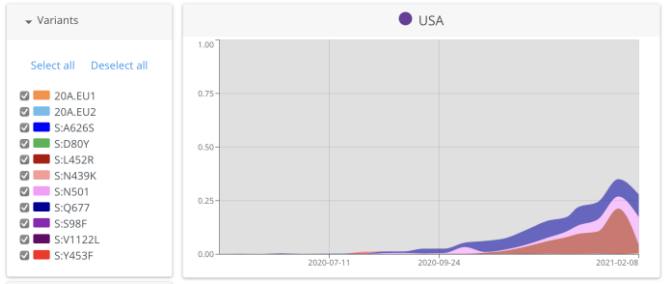
Lineages Of Concern

LoC name	PANGO lineage	NextStrain lineage	Other synonyms	Emergence date	Emergence location	Key AA substitutions in spike protein	Impact
B.1.1.7	B.1.1.7	20I/501Y.V1	VOC 202012/01, UK variant	September 2020	Southeast England	H69-, V70-, N501Y, D614G, P681H	Increased transmissibility; S gene target failure (SGTF)
B.1.351	B.1.351	20H/501Y.V2	South African variant	October 2020	Nelson Mandela Bay, South African	L241-, L242-, A243-, K417N, E484K, N501Y, D614G	loss of serum antibody neutralization
P.1	B.1.1.28	20J/501Y.V3	Brazilian variant	July 2020	Brazil	K417T, E484K, N501Y, D614G	Increased transmissibility; loss of serum antibody neutralization
CAL.20C	B.1.429			July 2020	Southern California, USA	W152C, L452R, D614G	loss of monoclonal antibody binding
B.1.375	B.1.375			September 2020	Massachusetts, USA	H69-, V70-, D614G	S gene target failure (SGTF)

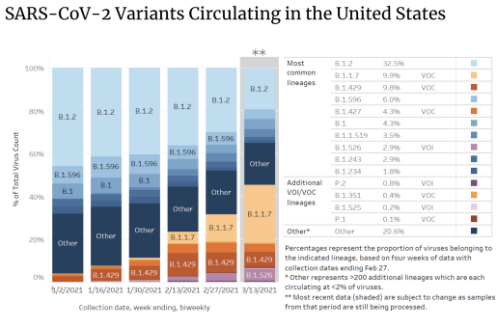
[NIH-NIAID Bacterial-Viral Bioinformatics Resource Center]



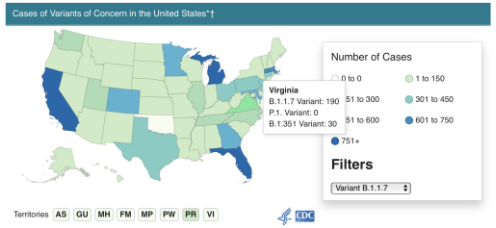
outbreak.info [Outbreak Info]



CoVariants [CoVariants.org]



Variant	Reported Cases	States
B.1.1.7	11,569	51
B.1.351	312	31
P.1	172	22

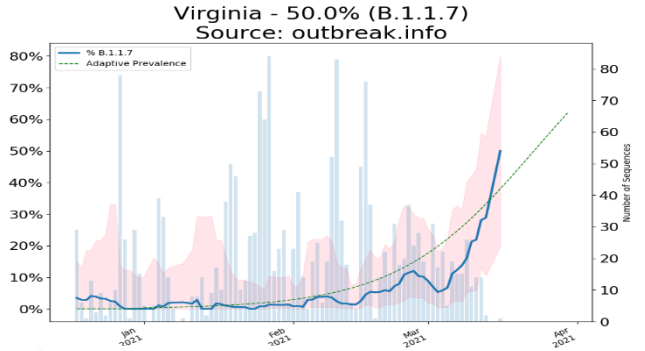


CDC [CDC Variant Tracking]

SARS-CoV2 Variants of Concern

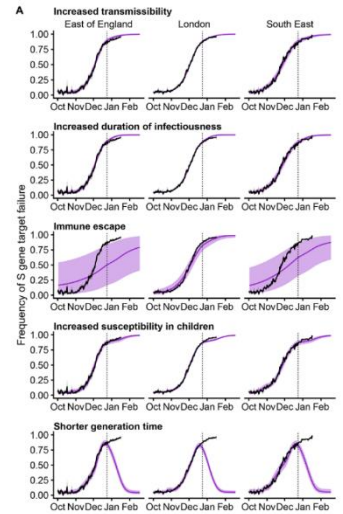
Lineage B.1.1.7

- B.1.1.7 has been detected in Virginia and has continued to rapidly grow. Current estimates suggest VA may be at 50% (national frequency at ~45%)
- Virginia seems to keep pace with estimates based on growth rates indicating B.1.1.7 now predominates (eg reach 50% frequency) in late March
- Science study using two-strain model supports that increased transmissibility, duration of infectiousness, or increased transmission in children best fit the epi data observed in the UK across regions. Some combination of all also likely.
- A recent study finds B.1.1.7 to have longer duration which may be the source of increased transmissibility and has implications for isolation durations
- Evidence continues to mount supporting increased risks of hospitalization and mortality for B.1.1.7 infected individuals



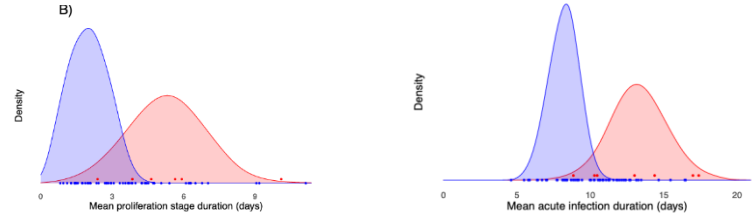
GISAID outbreak.info

Outbreak Info



A fitted two-strain dynamic transmission model shows that B.1.1.7 will lead to large resurgences of COVID-19 cases. Without stringent control measures, including limited closure of educational institutions and a greatly accelerated vaccine roll-out, COVID-19 hospitalisations and deaths across England in 2021 will exceed those in 2020.Hypotheses 2 (longer infectious period) and 4 (increased susceptibility in children) also fitted the data well, although hypothesis 4 is not well supported by household secondary attack rate data.

Science

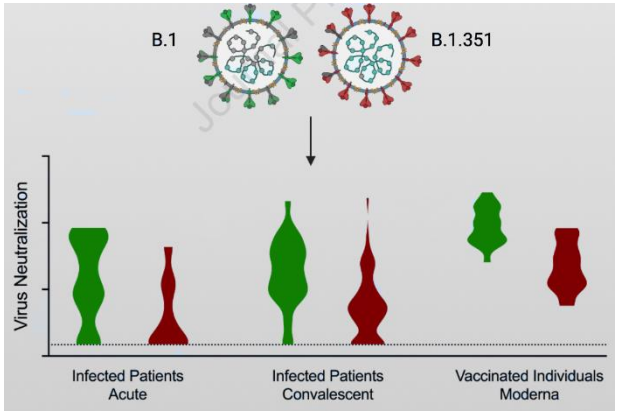


Variant B.1.1.7 may cause longer infections with similar peak viral concentration compared to non-B.1.1.7 May contribute to B.1.1.7's increased transmissibility.
https://dash.harvard.edu/handle/1/37366884

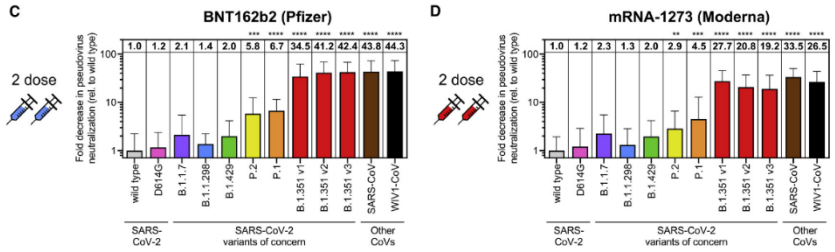
SARS-CoV2 Variants of Concern

Lineage B.1.351

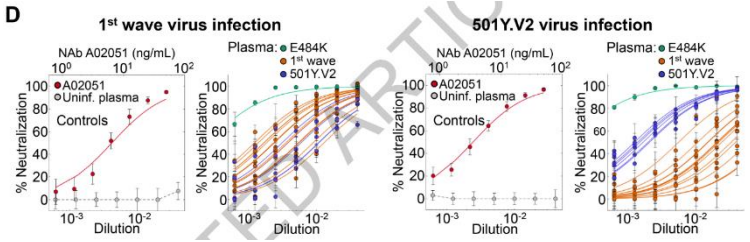
- Emerging strain initially identified in South Africa shows signs of vaccine escape, currently 312 reported cases in 31 states (including 30 now in Virginia)
- Nature study shows that plasma from the 2nd wave of infections in South Africa (with B.1.351 circulating) neutralized non-B.1.351 virus, suggesting targeted B.1.351 vaccines or treatments may remain effective against other variants
- An additional study corroborates recent study based on clinical trial data shows that convalescent serum neutralization is highly predictive of actual immune protection for infection, thus B.1.351 may require booster vaccinations, and provides estimates for timing
- Another study in Cell supports previous report that demonstrated that despite reduced antibody binding the Moderna vaccinated individuals able to neutralize the B.1.351 variant



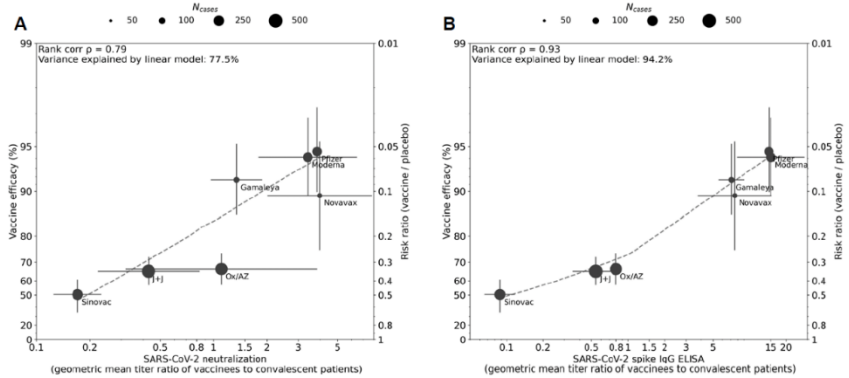
Despite reduced antibody binding to the B.1.351 RBD, sera from infected (acute and convalescent) and Moderna (mRNA-1273) vaccinated individuals were still able to neutralize the SARS-CoV-2 B.1.351 variant. Cell



Update: several recent reports and preprints, including studies conducted by Pfizer as well as Moderna, have produced similar findings in terms of vaccine potency against B.1.1.7 and B.1.1.298 variants but substantially less neutralization resistance by B.1.351 than we measured. Cell



In cross-neutralization, 501Y.V2 virus was poorly neutralized by first wave plasma, with a 15.1-fold drop relative to 501Y.V2 neutralization by second wave plasma across participants. In contrast, second wave plasma cross-neutralization of first wave virus was more effective, showing only a 2.3-fold decline relative to first wave plasma neutralization of first wave virus. Nature

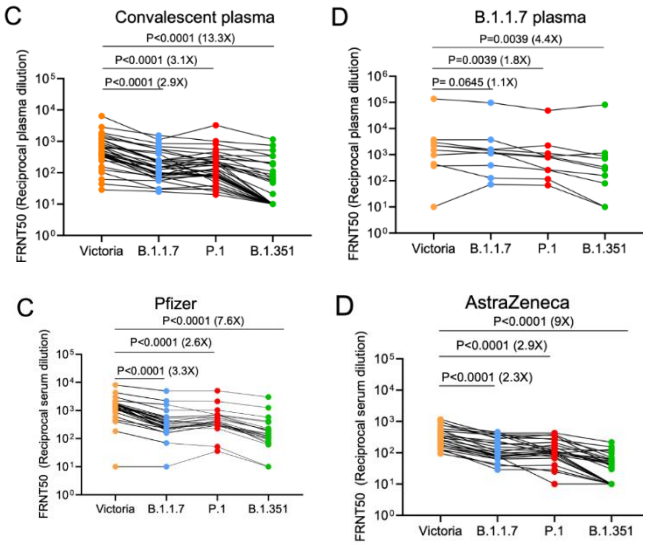


Corroborating: calibrated to titers of human convalescent sera reported in each study, a robust correlation was seen between neutralizing titer and efficacy (ρ= 0.79) and binding antibody titer and efficacy (ρ = 0.93) MedArxiv

SARS-CoV2 Variants of Concern

Lineage P.1

- Present in at least 172 cases in 22 states, shows signs of increased transmissibility and ability to evade immunity
- Caused a resurgence of hospitalizations in Manaus, Brazil which has now caused more deaths in last 3 months than all of 2020
- Study in Cell shows P.1 may be less resistant to neutralization than B.1.351



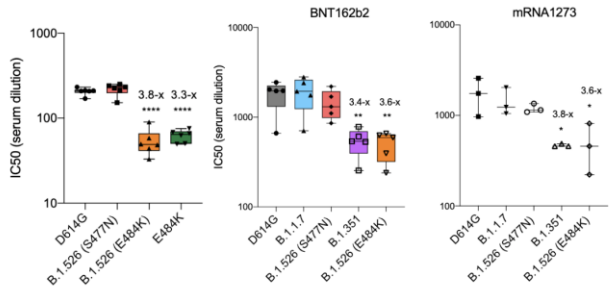
P.1 and B.1.351 having a virtually identical triplet: E484K, K417N/T and N501Y, confer similar increased affinity for ACE2. Despite this, P.1 is significantly less resistant to naturally acquired or vaccine induced antibody responses than B.1.351 suggesting that changes outside the RBD impact neutralization. Cell

Lineage B.1.429

- Recently officially recognized as variant of concern, estimates of ~20% increase in transmission and some evasion of immunity
- Initially found in Southern California, coincided with surge in Nov and Dec, found in over half of sequenced samples in LA

Lineage B.1.526

- Initially identified in NY and found increasingly as cases in NY / NJ increase
- Recent study finds vaccine-elicited plasma neutralizes B.1.526 but less efficiently than other variants

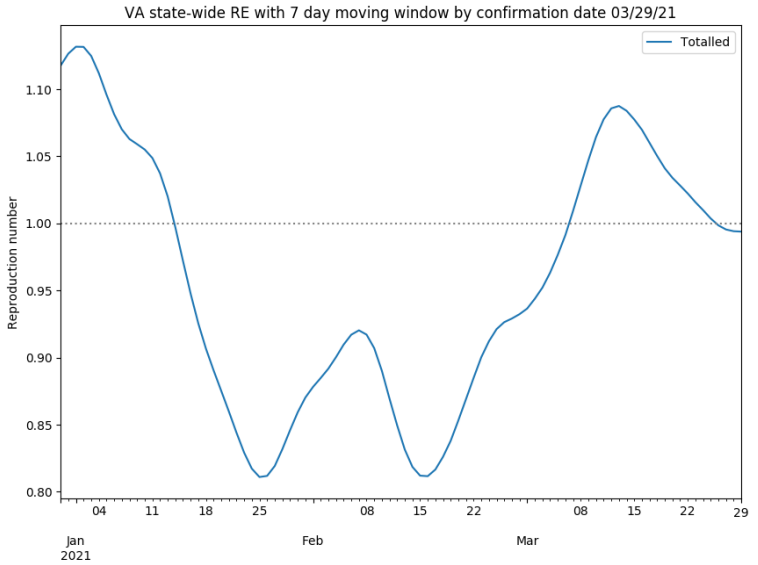


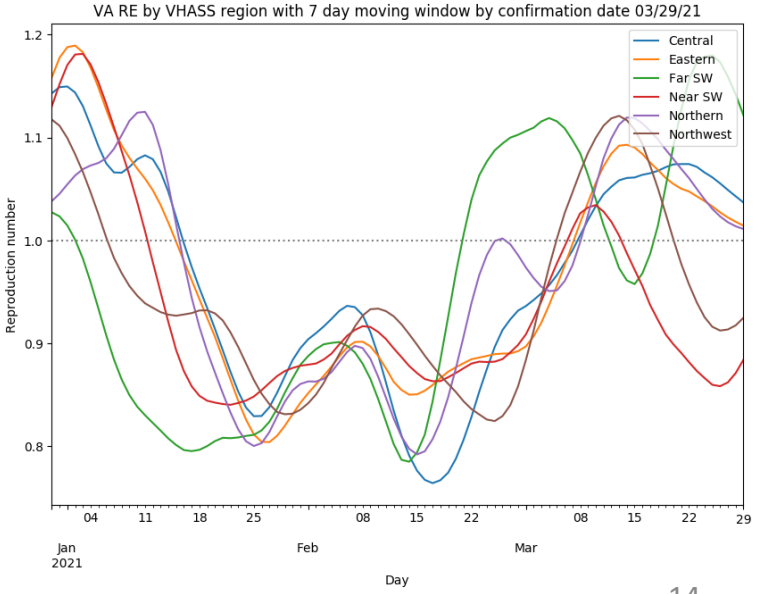
B.1.526 SARS-CoV-2 variants identified in New York City are neutralized by vaccine-elicited and therapeutic monoclonal antibodies. BioRxiv

Estimating Daily Reproductive Number

March 29th Estimates

Region	Date Confirmed R_e	Date Confirmed Diff Last Week
State-wide	0.994	-0.013
Central	1.037	0.014
Eastern	1.014	-0.030
Far SW	1.122	0.273
Near SW	0.884	-0.021
Northern	1.011	-0.034
Northwest	0.925	-0.115





Methodology

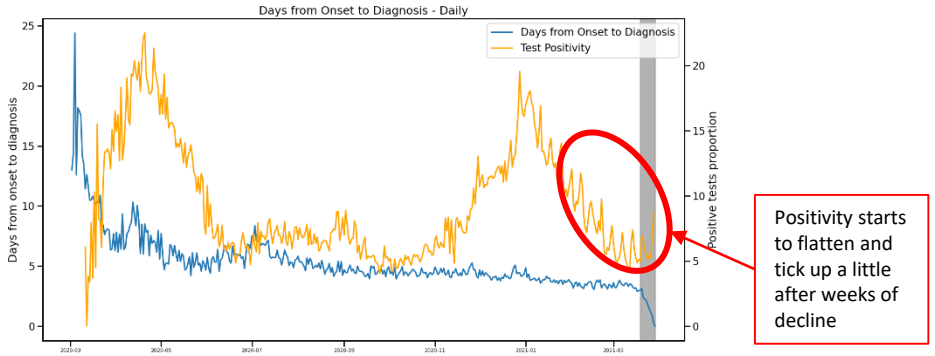
- Wallinga-Teunis method (EpiEstim[1]) for cases by **confirmation date**
- Serial interval: updated to discrete distribution from observations (mean=4.3, Flaxman et al, Nature 2020)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

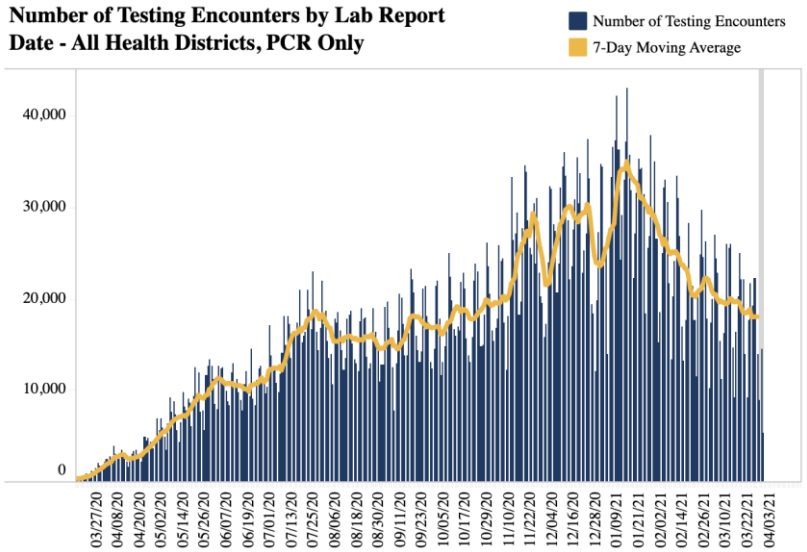
1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, https://doi.org/10.1093/aje/kwt133

Changes in Case Detection

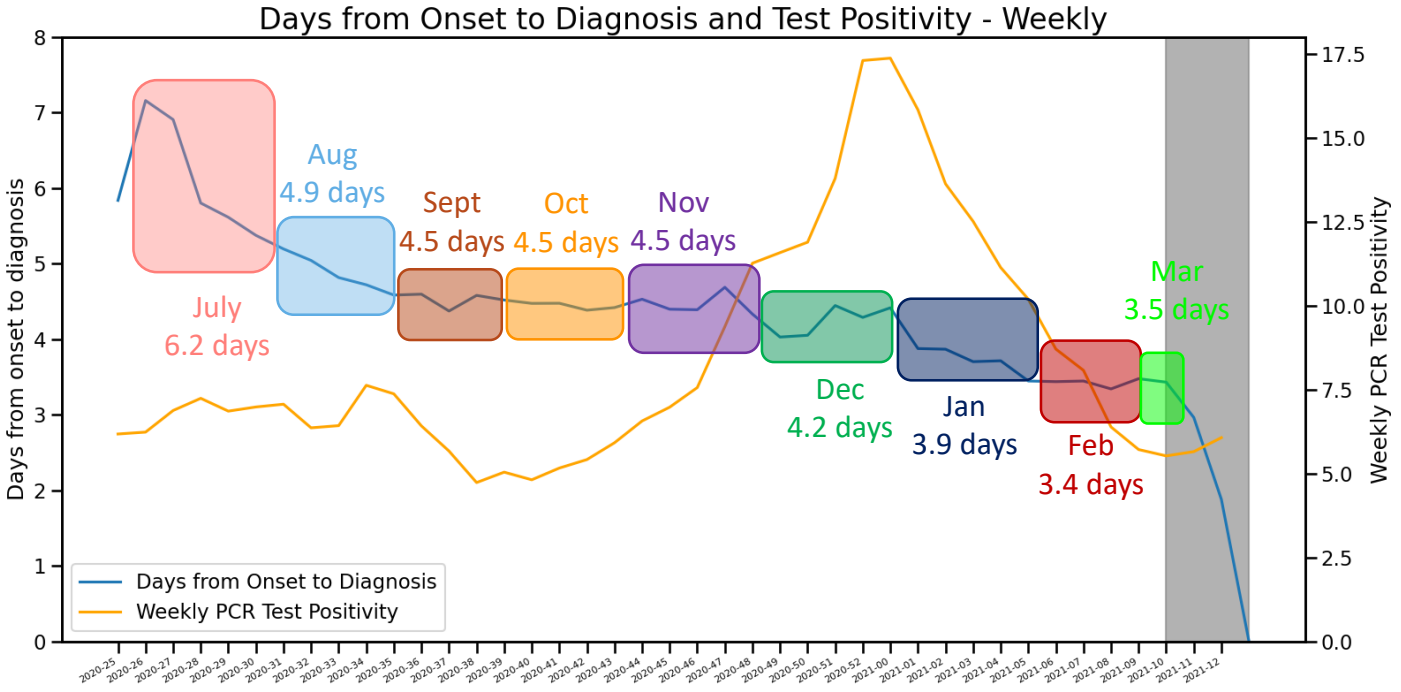
Timeframe (weeks)	Mean days	% difference from overall mean
July (26-30)	6.2	-8%
Aug (31-34)	4.9	-26%
Sept (35-38)	4.5	-32%
Oct (39-43)	4.5	-33%
Nov (44-47)	4.5	-33%
Dec (48-49)	4.2	-37%
Jan (00-04)	3.9	-41%
Feb (05-08)	3.4	-49%
Mar (09)	3.5	-48%
Overall (13-09)	6.7	--

Test positivity vs. Onset to Diagnosis

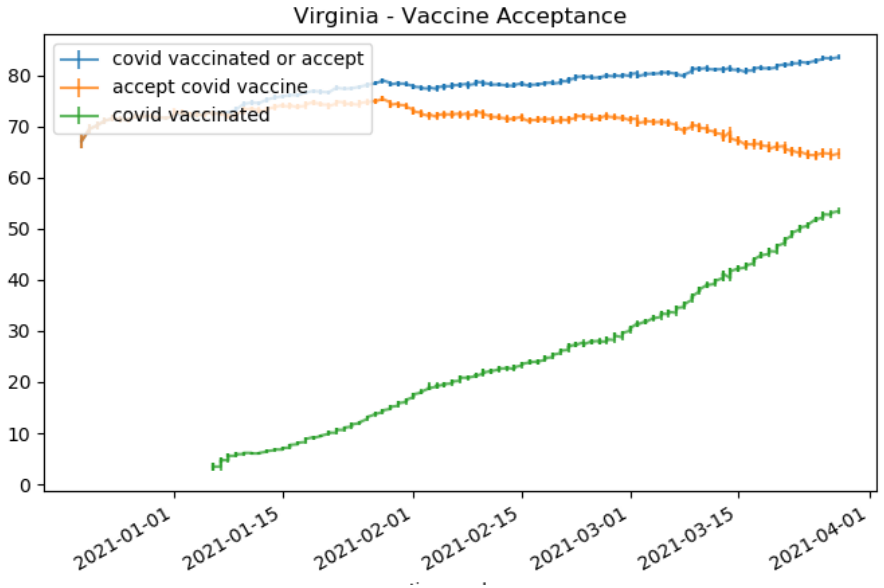


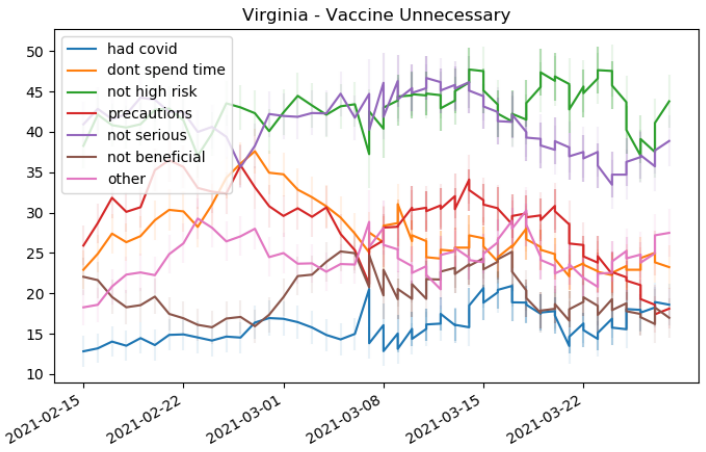


Accessed 9:00am March 31, 2021
https://www.vdh.virginia.gov/coronavirus/



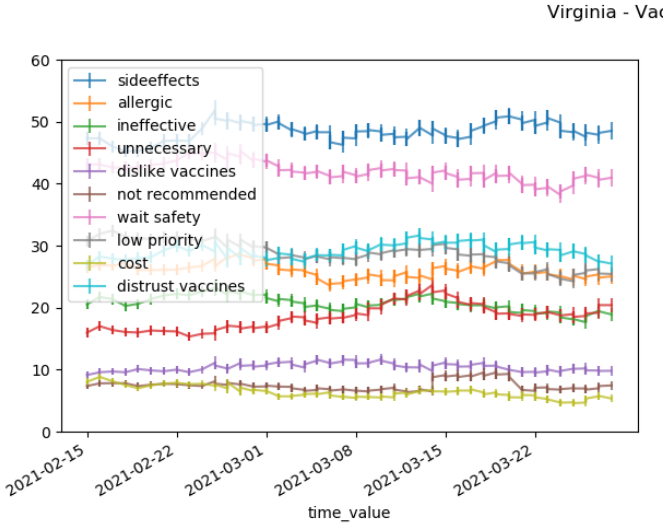
Vaccine Acceptance in Virginia

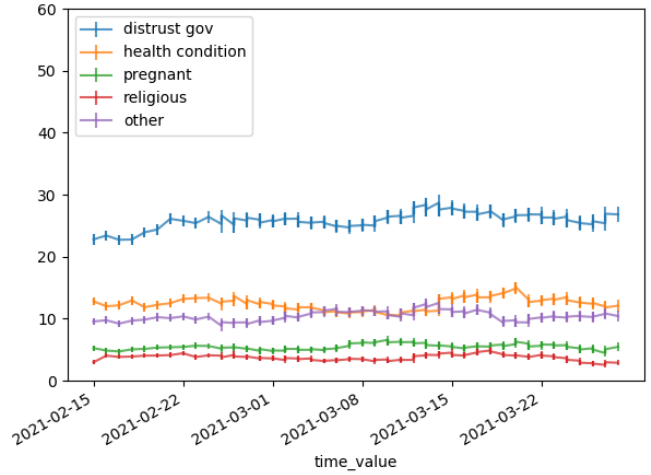




Acceptance remains high:

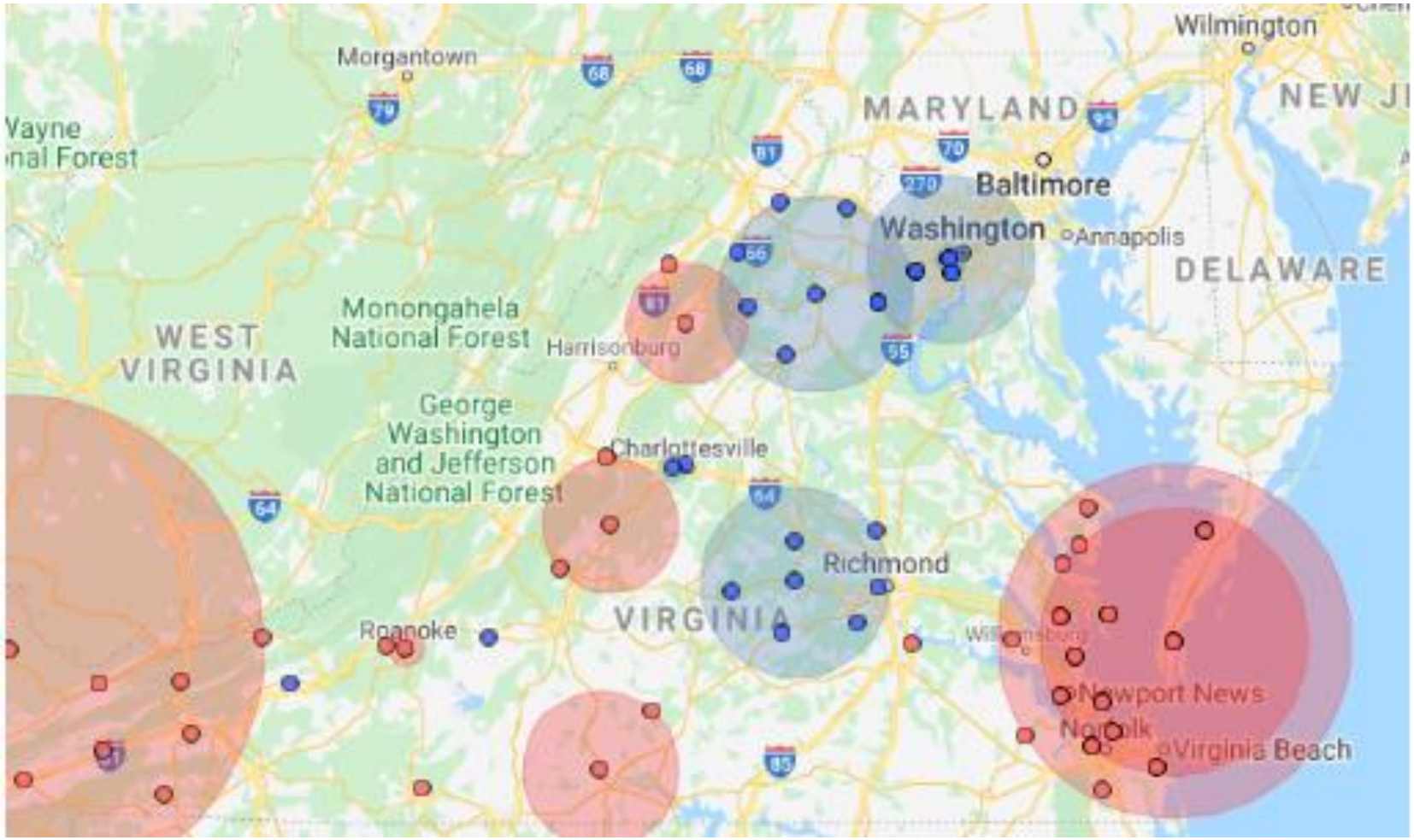
- Proportion of Virginians that have already or would definitely or probably accept vaccination if offered today
- Survey respondents are reporting high levels of vaccination of ~50% reflecting some bias of the the mechanism
- Nearly 80% Virginians have already or will choose to be vaccinated
- Top reasons for hesitancy: side effects, safety, distrust





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

Vaccine Hesitancy in Virginia



Geographic distribution of Hesitancy clusters in Virginia:

- Rate of hesitancy assessed by those saying they would probably not, or definetly not take the vaccine if offered today
- Total of 111 locations covering ~8.2M residents

Red Clusters: High hesitancy rate

Blue Clusters: Low hesitancy rate

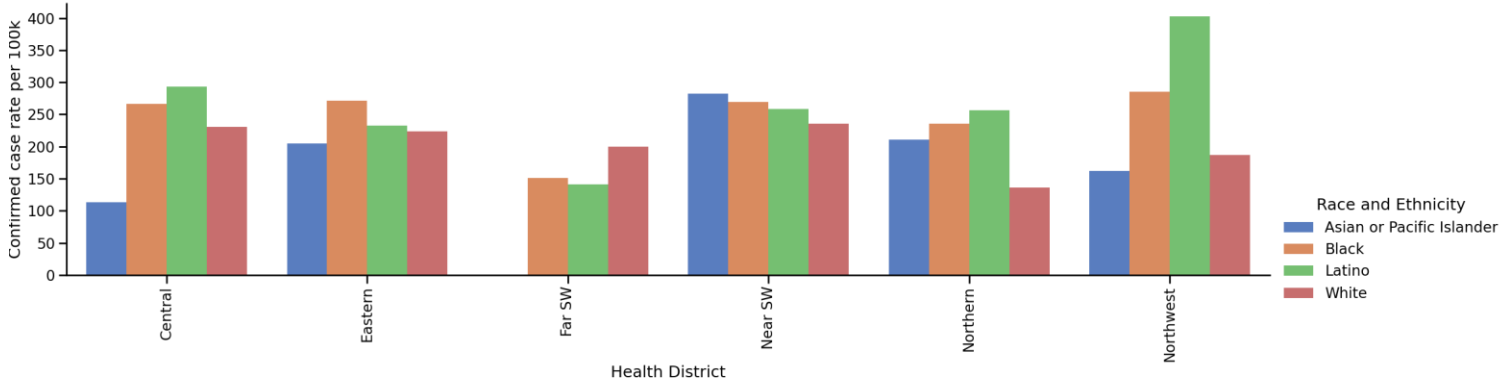
Data Source: https://covidcast.cmu.edu

Race and Ethnicity – Recent Rate Changes (per 100K)

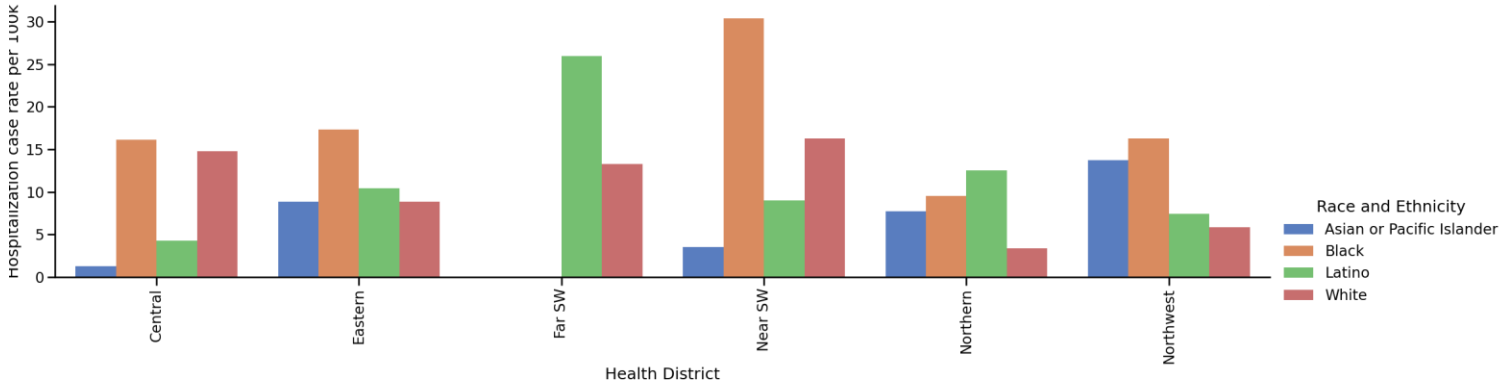
Changes in Race and Ethnicity Rates (per 100k) in past two weeks

- Two week change in population level rates
- Black, Latinx and 2 or more races populations have much higher changes in rates; disparity is more pronounced in some regions than others
- Based on 2019 census race-ethnicity data by county

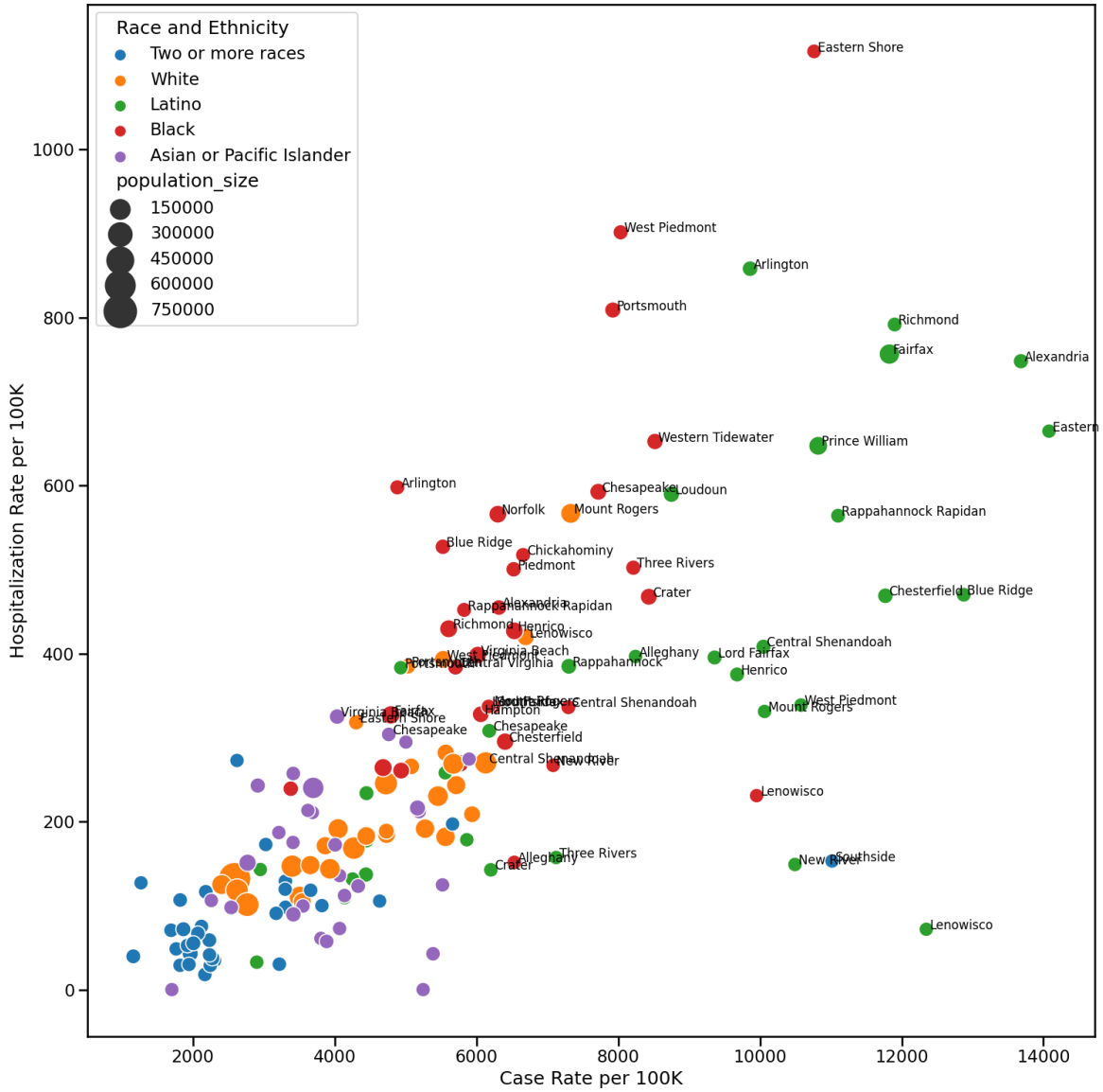
Case Rate



Hospitalization Rate



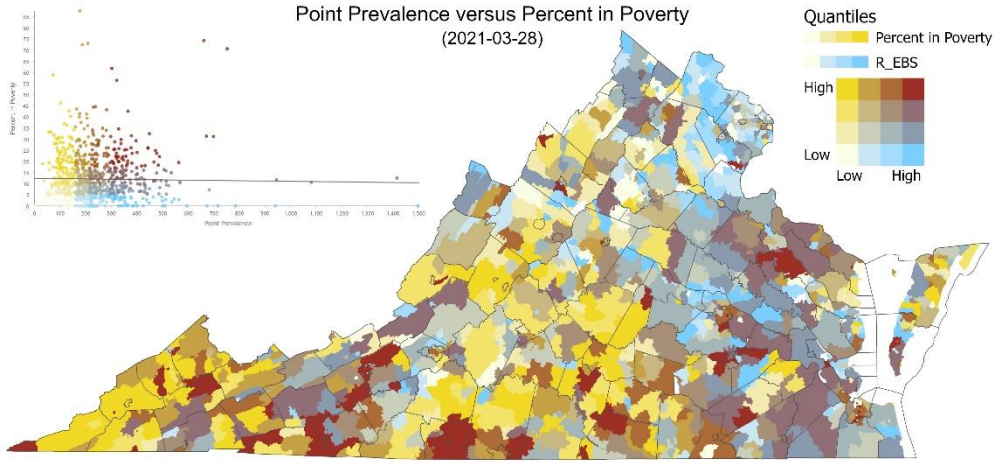
Race and Ethnicity cases per 100K



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)

Correlations between Infection Rates and Poverty

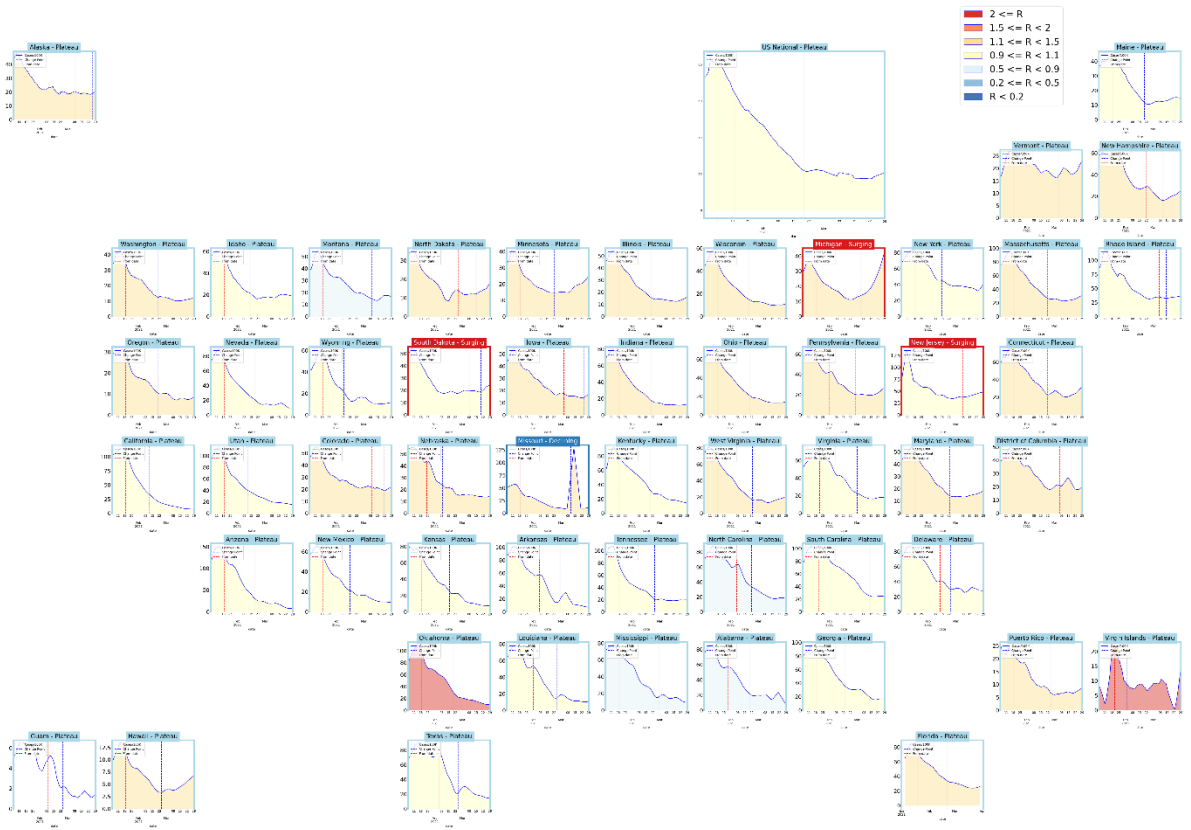


Based on Global Empirical Bayes smoothed point prevalence for week ending 2021-03-28.

High poverty and high case rates overlap in southside (red), but high rates occur with low poverty in Northern and Richmond area (light blue)

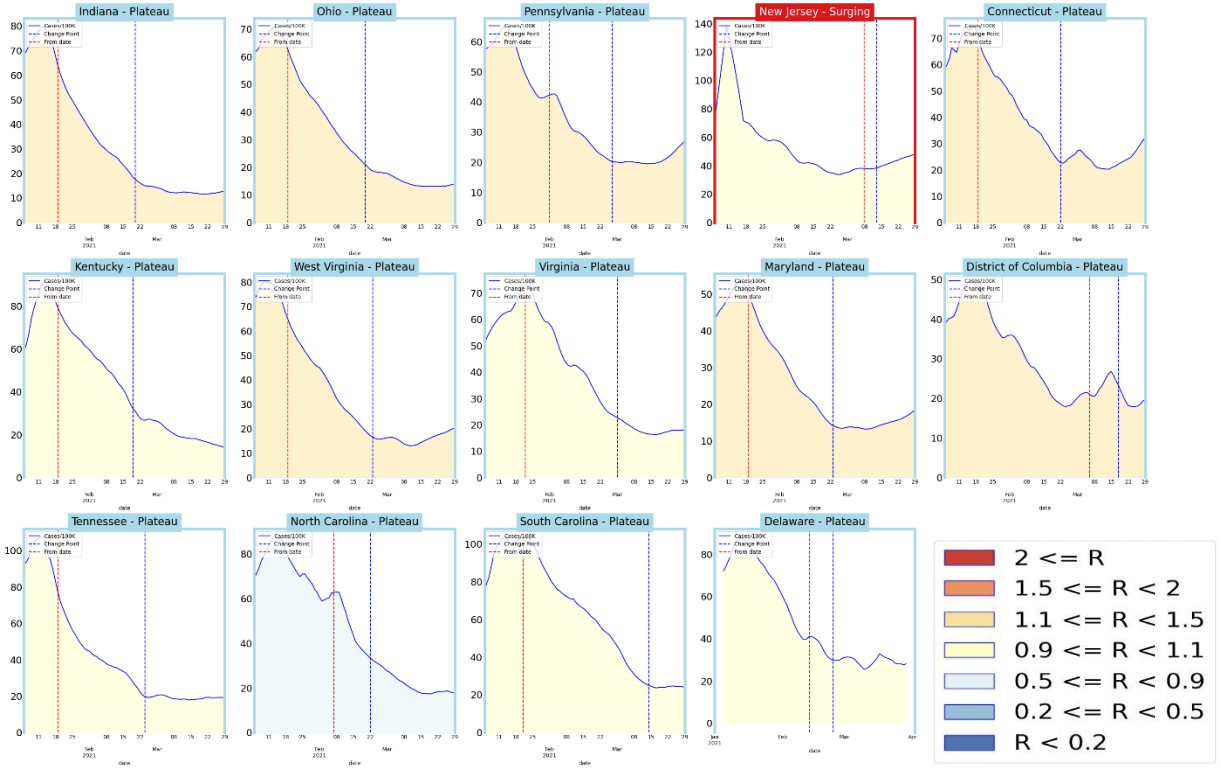
Other State Comparisons

Trajectories of States



- Nearly all states are plateaued, with 3 states in surge, most plateaued states show signs of growth
- Missouri in decline only because of data artifact in reporting

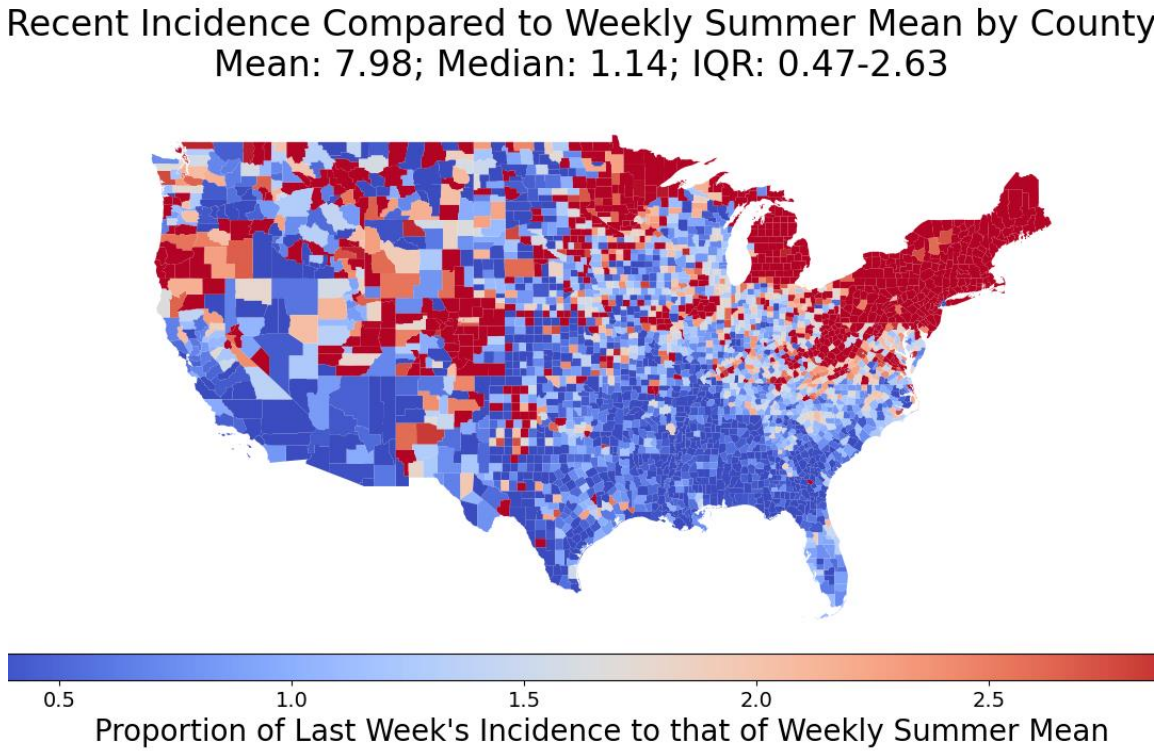
Virginia and her neighbors

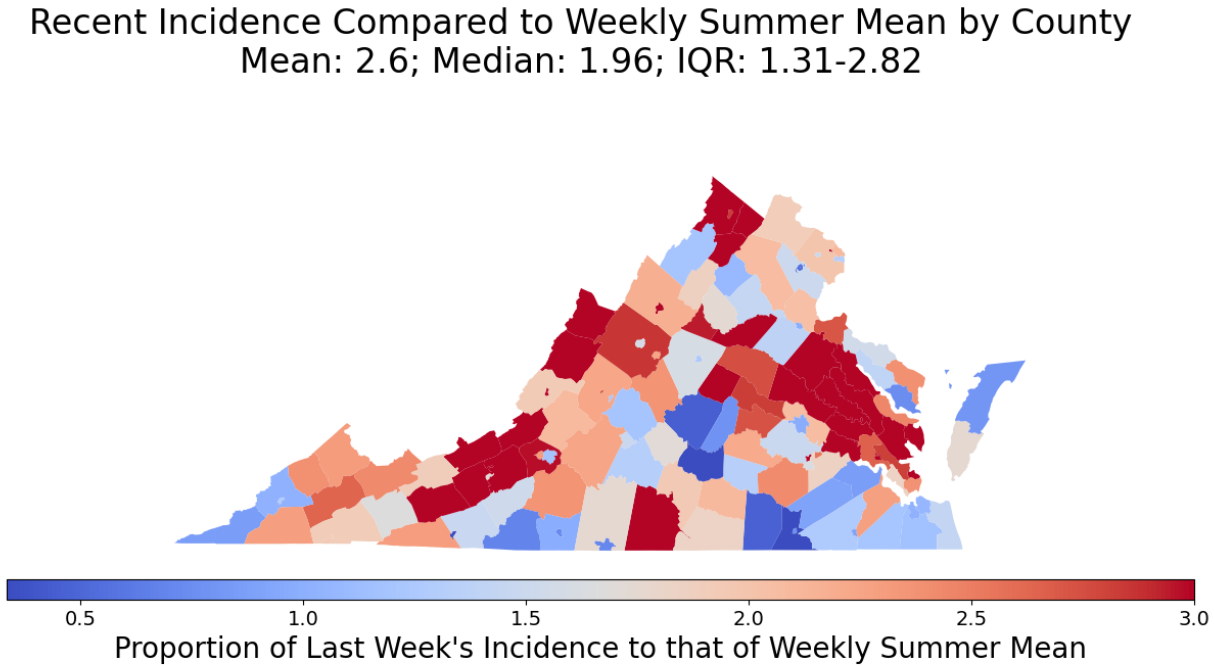


- VA and nearly all in plateau with upward trends
- Rates remain elevated, but significantly down from peaks in Jan

Current Week vs. Summer Mean (June-Aug 2020)

Still some way to go to return to rates experienced during the summer of 2020 (June through August)





- 54% of US counties are above the summer mean case rate compared to 53% last week, slightly up

- 84% of VA counties are above the average rate for the summer compared to 81% last week, slightly up

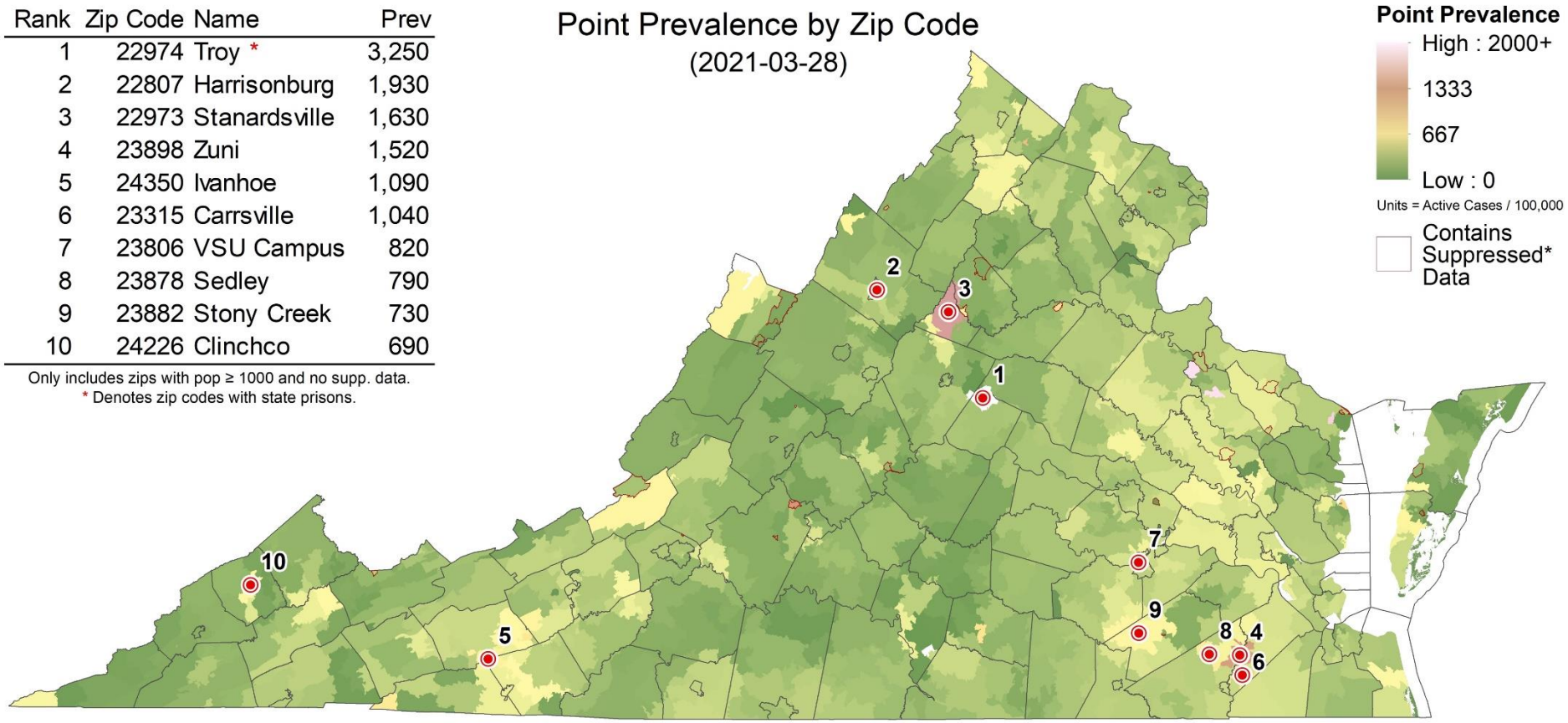
Zip code level weekly Case Rate (per 100K)

Case Rates in the last week by zip code

- Universities still dominate the top 10 list
- Concentrations of high rates scattered across the Commonwealth
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code	Name	Prev
1	22974	Troy *	3,250
2	22807	Harrisonburg	1,930
3	22973	Stanardsville	1,630
4	23898	Zuni	1,520
5	24350	Ivanhoe	1,090
6	23315	Carrsville	1,040
7	23806	VSU Campus	820
8	23878	Sedley	790
9	23882	Stony Creek	730
10	24226	Clinchco	690

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 2021-03-28.
Note: New color ramp scale and new ascertainment ratio of 2:1.

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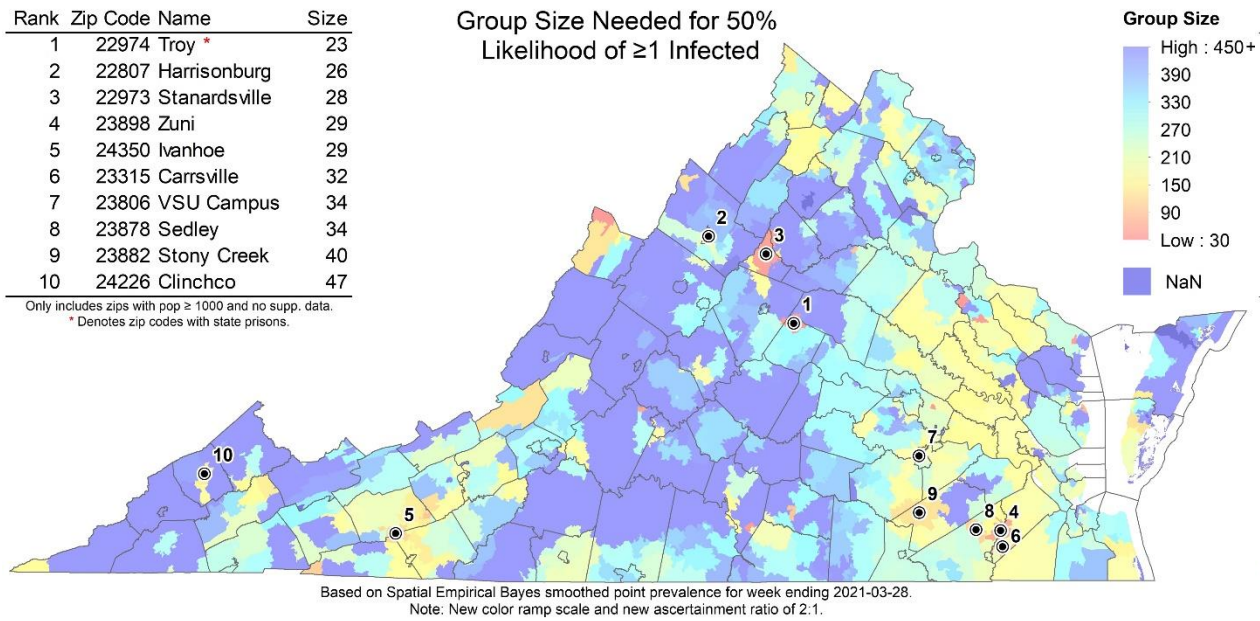
Risk of Exposure by Group Size and HCW prevalence

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 26 in Harrisonburg, 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

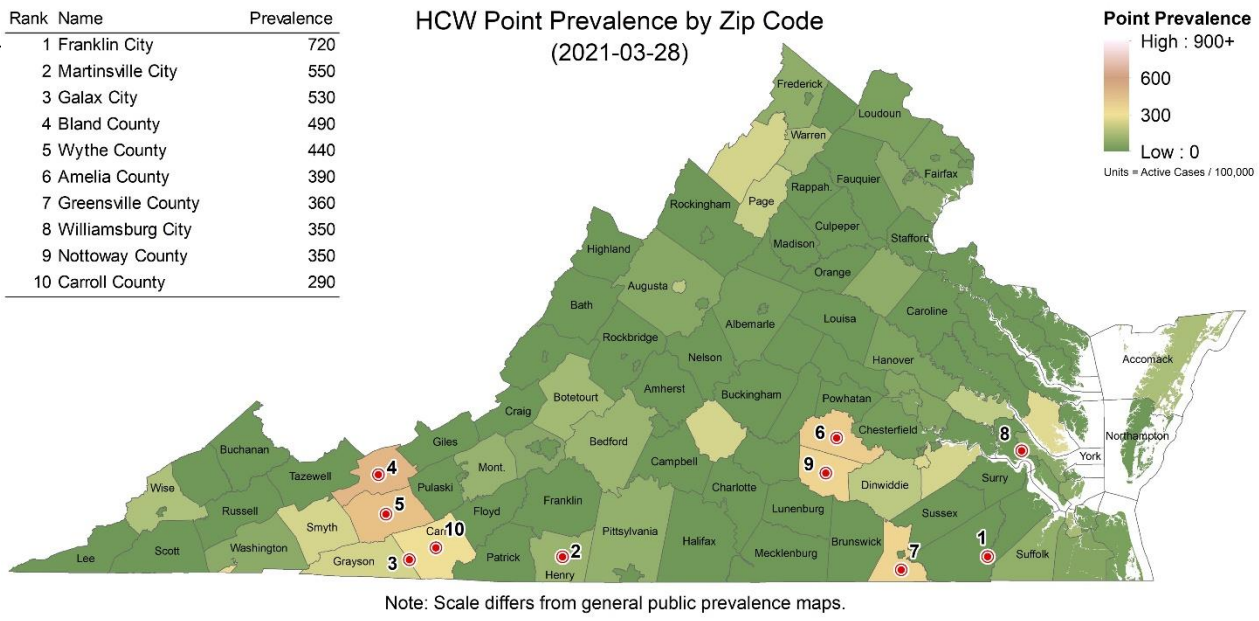
Rank	Zip Code	Name	Size
1	22974	Troy *	23
2	22807	Harrisonburg	26
3	22973	Stanardsville	28
4	23898	Zuni	29
5	24350	Ivanhoe	29
6	23315	Carrsville	32
7	23806	VSU Campus	34
8	23878	Sedley	34
9	23882	Stony Creek	40
10	24226	Clinchco	47

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 2021-03-28.
Note: New color ramp scale and new ascertainment ratio of 2:1.

Rank	Name	Prevalence
1	Franklin City	720
2	Martinsville City	550
3	Galax City	530
4	Bland County	490
5	Wythe County	440
6	Amelia County	390
7	Greensville County	360
8	Williamsburg City	350
9	Nottoway County	350
10	Carroll County	290



Note: Scale differs from general public prevalence maps.

Current Hot-Spots

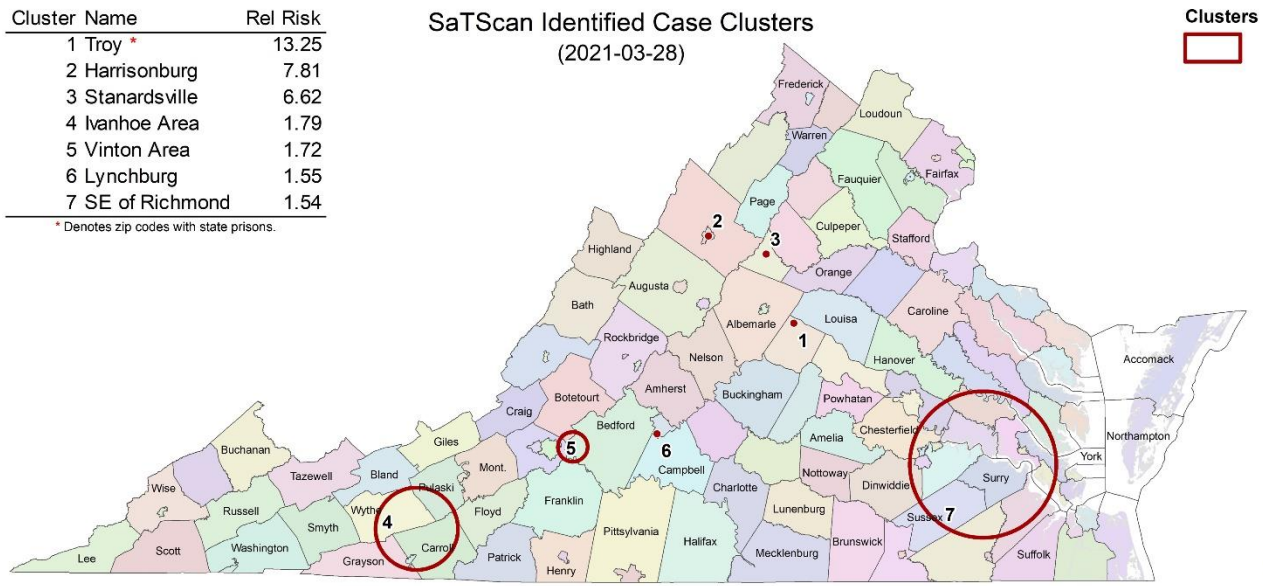
Case rates that are significantly different from neighboring areas or model projections

- **Spatial**: SaTScan based hot spots compare clusters of zipcodes 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

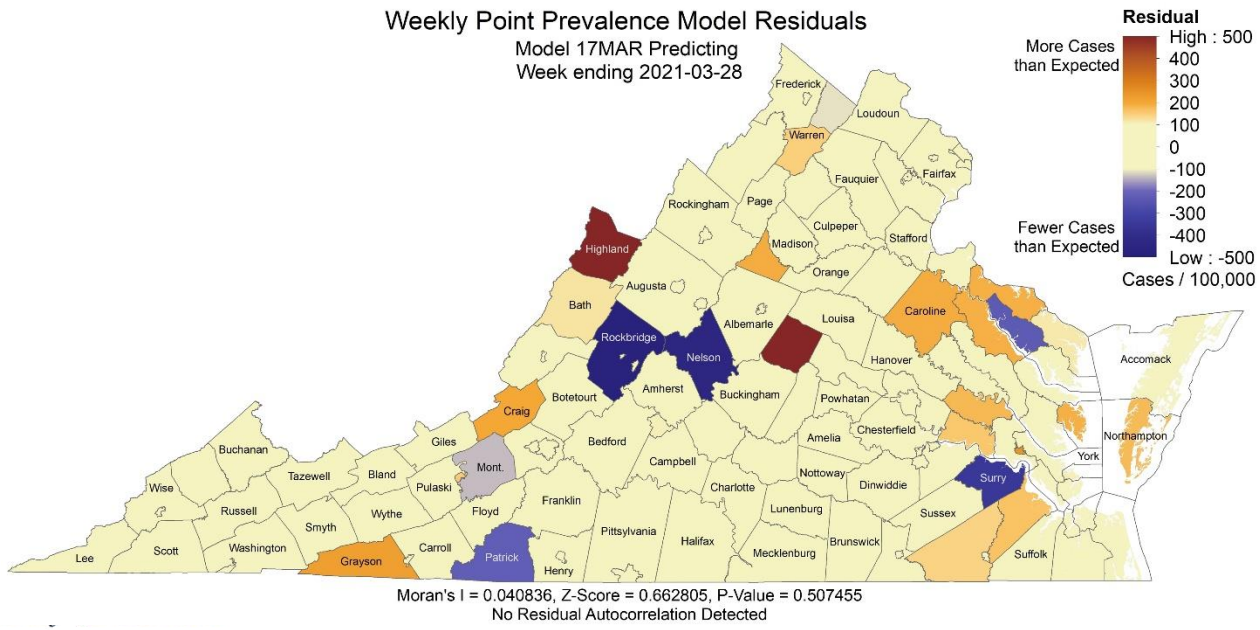
Spatial Hotspots

Cluster	Name	Rel Risk
1	Troy *	13.25
2	Harrisonburg	7.81
3	Stanardsville	6.62
4	Ivanhoe Area	1.79
5	Vinton Area	1.72
6	Lynchburg	1.55
7	SE of Richmond	1.54

* Denotes zip codes with state prisons.



Temporal Hotspots



Moran's I = 0.040836, Z-Score = 0.662805, P-Value = 0.507455
No Residual Autocorrelation Detected

Model Update – Adaptive Fitting

Adaptive Fitting Approach

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

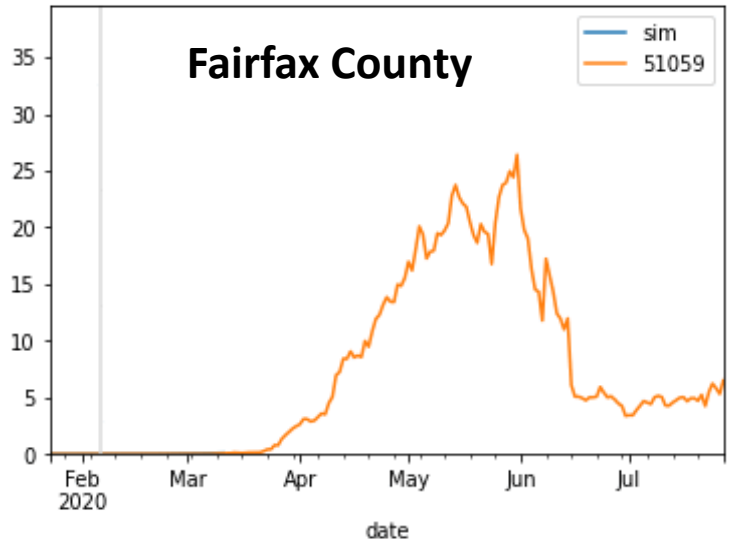
- Allows history to be precisely captured, and used to guide bounds on projections

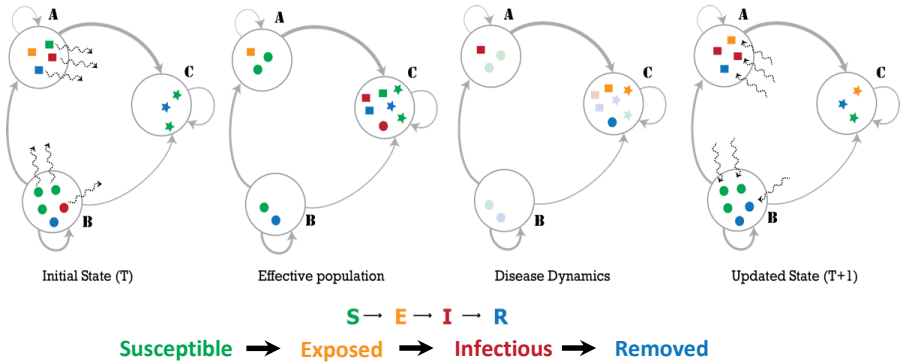
Model: An alternative use of the same meta-population model, PatchSim

- 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:

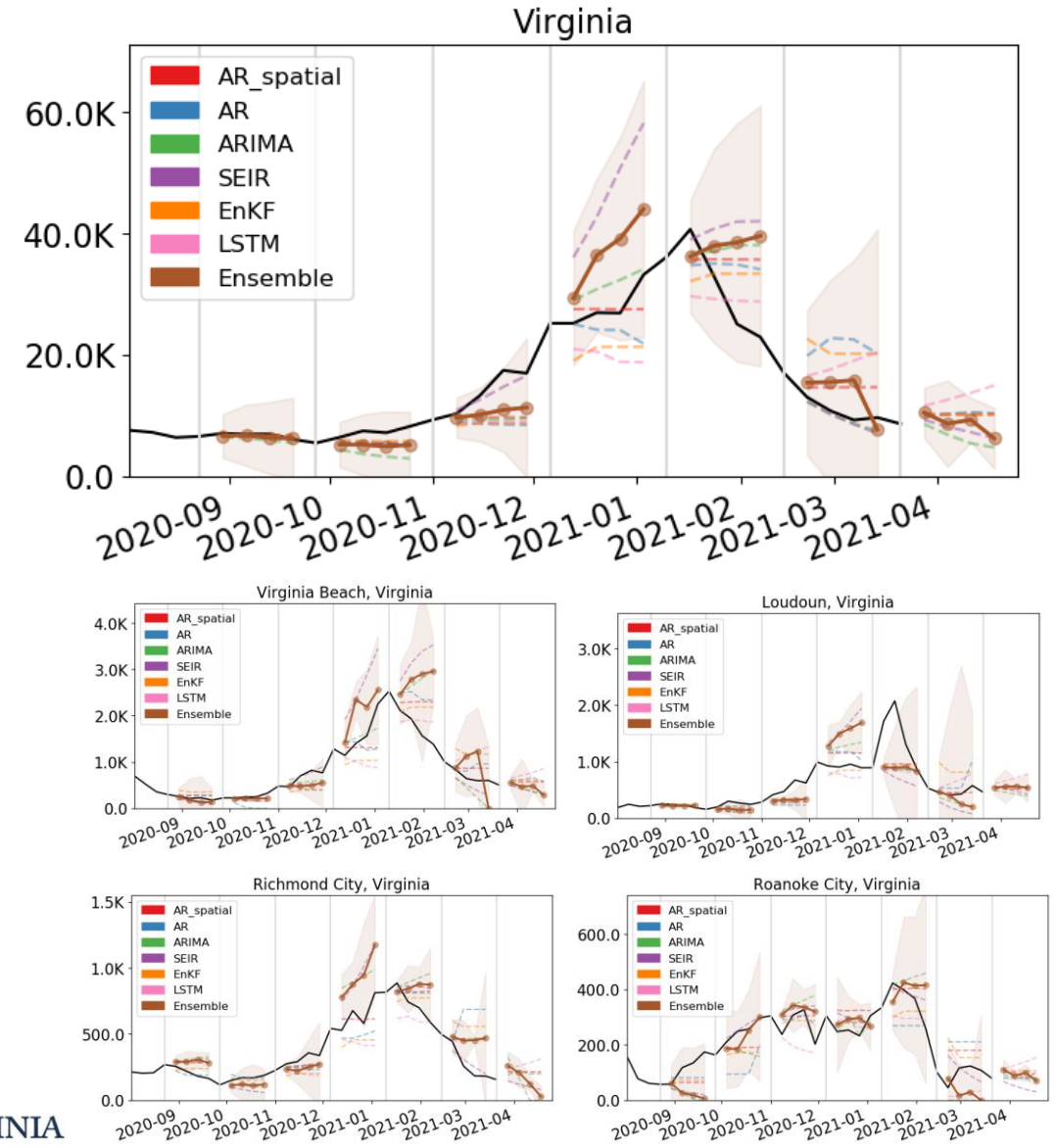
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

<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.



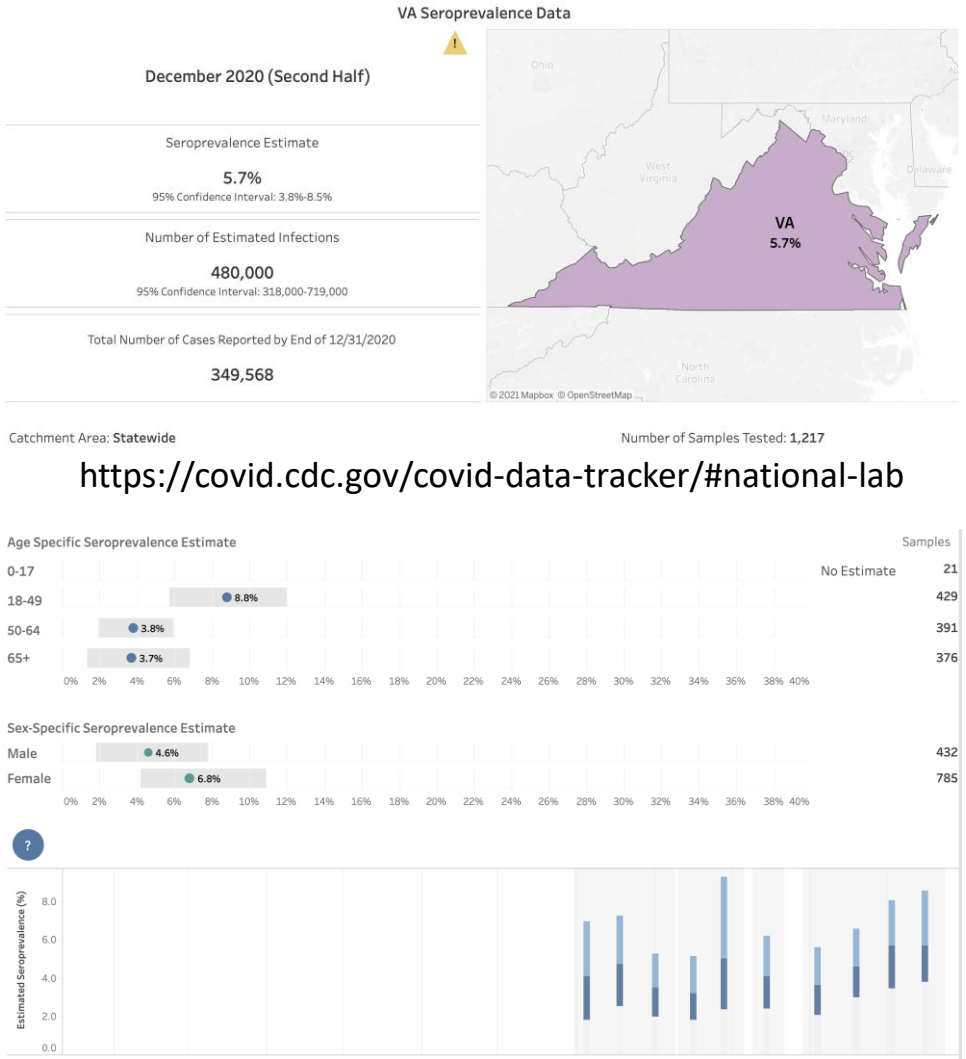
Seroprevalence updates to model design

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

- CDC Nationwide Commercial Laboratory Seroprevalence Survey estimated 7.6% [5.6% – 9.8%] seroprevalence as of Jan 7th – 21st up from 5.7% a month earlier

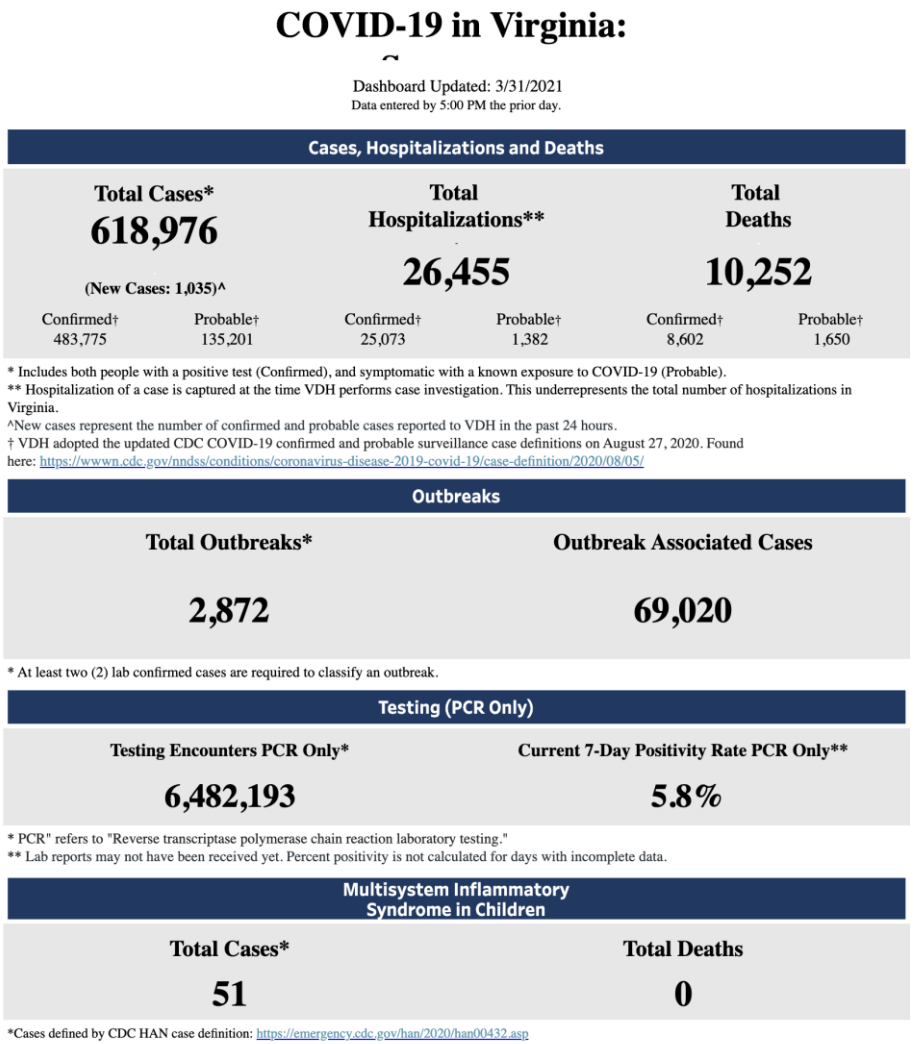
These findings are equivalent to an ascertainment ratio of ~2x in the future, with bounds of (1.3x to 3x)

- 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)



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: 3/31/2021
Data entered by 5:00 PM the prior day.

Cases, Hospitalizations and Deaths

Total Cases*		Total Hospitalizations**		Total Deaths	
618,976		26,455		10,252	
(New Cases: 1,035)^					
Confirmed†	Probable†	Confirmed†	Probable†	Confirmed†	Probable†
483,775	135,201	25,073	1,382	8,602	1,650

* 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
2,872	69,020

* 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**
6,482,193	5.8%

* 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
51	0

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

Accessed 9:00am March 31, 2021

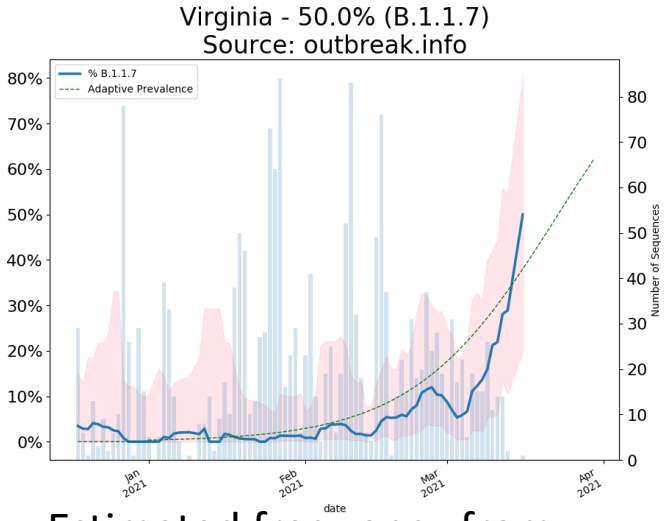
https://www.vdh.virginia.gov/coronavirus/

Scenarios – Seasonal Effects

- 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 since May 1, 2020 through September 30, 2020
  - Use the highest and lowest levels experienced (excluding outliers) as plausible bounds for levels of control achievable
  - Transition from current levels of projection to the new levels over 2 months
- Projection Scenario:
  - **Fatigued Control**: Highest level of transmission (95th percentile) increased by additional 5%

Scenarios – Variant B.1.17

- New Variant B.1.1.7 is best understood and is in Virginia
  - **Transmission increase**: Several different studies have estimated the increase in transmission to be 30-55%, we use 50% increase from the current baseline projection
  - **Increased Severity**: Not included in this scenario yet. B.1.1.7 is known to cause more hospitalizations and deaths compared to previous SARS-CoV2 variants (see previous variant slides) however, evidence in US still sparse
  - **Emergence timing:** Gradual frequency increase reaching 50% frequency on March 30th, one week after the national estimate in MMWR report from CDC and refined by Andersen et al.
- Variant planning Scenario:
  - **VariantB117**: Current projected transmissibility continues to increase through June to a level 50% more transmissible



Estimated frequency from public genome repository with added analysis: 50%
Current frequency used in model: 50%

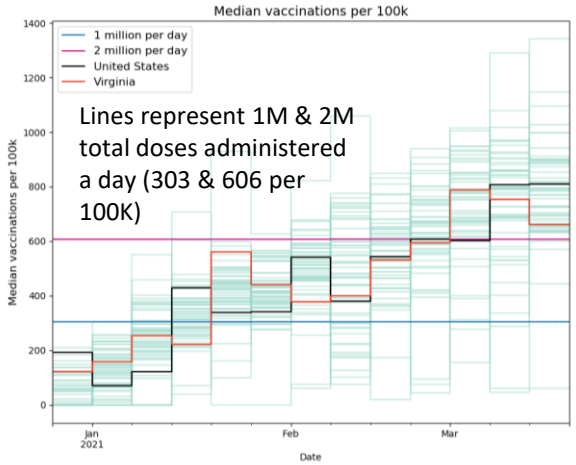
outbreak.info

Outbreak Info

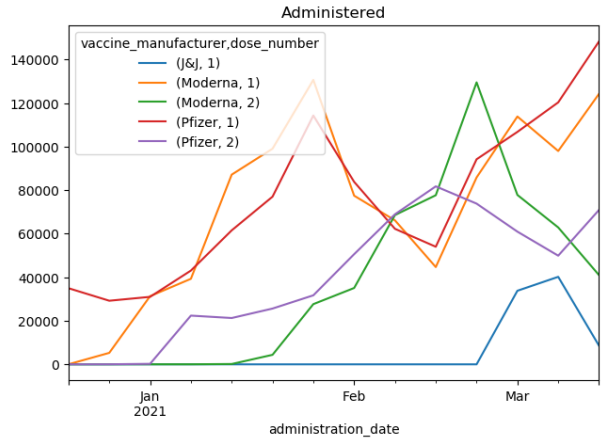
GISAID

Scenarios – Vaccines

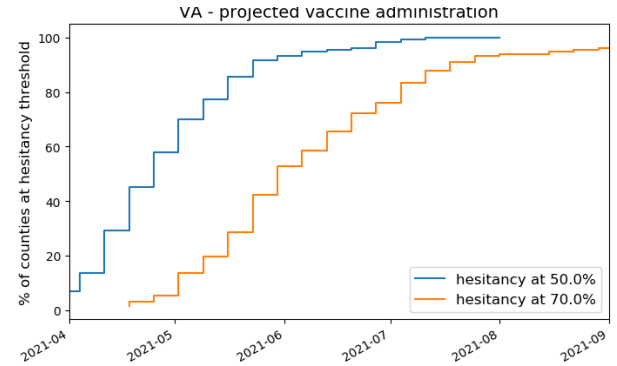
- Projected vaccine schedules constructed using current administrations rates by dose and manufacturer for VA counties.
- Assumed vaccine efficacies
  - Pfizer/Moderna: 50% after first dose, 95% after second dose
  - J &J : 67% efficacy after first (and only) dose
  - Average 3.5 week gap between Pfizer/Moderna doses
  - Delay to efficacy from dose assumed to be 14 days
- Accelerated administration pace will reach vaccine hesitancy thresholds more quickly
  - Currently assuming 70% acceptance threshold for all counties
  - Under current administration rates, 50% of counties could hit this threshold
  - Might be earlier for counties with lower acceptance rate



All doses (national)



Virginia doses administered by manufacturer



Anticipated Vax Hesitancy Impact

Scenarios – Seasonal Effects and Vaccines

Three scenarios combine these seasonal effects and use the current vaccine schedule

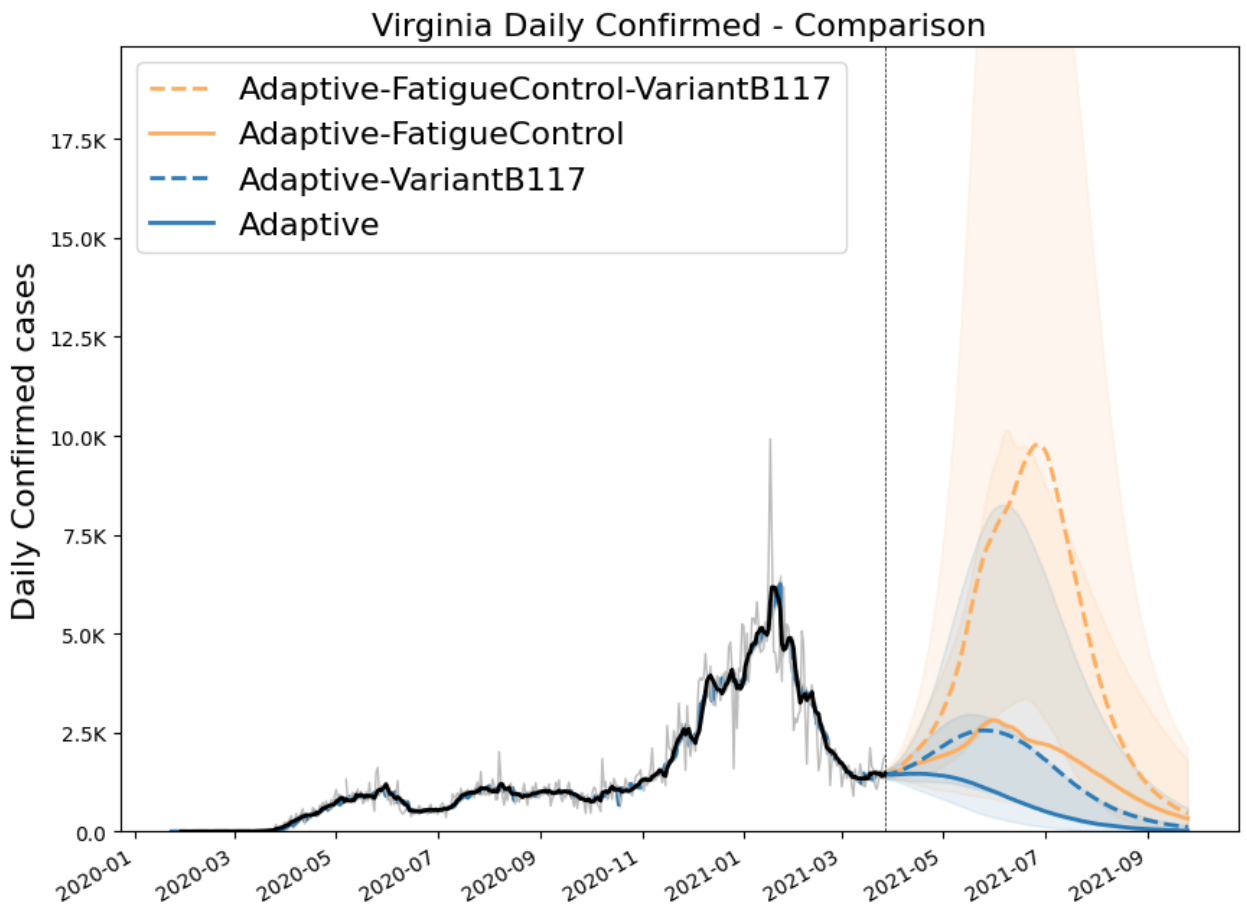
- **Adaptive**: No seasonal effects from base projection
  - If things continue as they are
- **Adaptive-FatigueControl**: Fatigued control seasonal effects
  - If we revert to slightly worst transmission experienced in last 6 months
- **Adaptive-VariantB117**: Boosting of transmissibility from the emergence of B.1.1.7
  - If new variants begin to predominate and boost transmission, this assumes current seasonal affects remain the same (eg like Adaptive)
- **Adaptive-FatigueControl-VariantB117:** Fatigued control and txm boost from B.1.1.7

Counterfactuals with no vaccine ("NoVax") are provided for comparison purposes

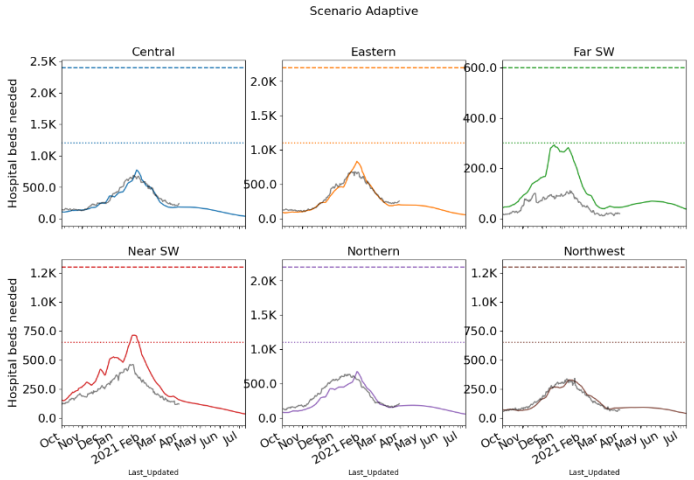
Model Results

Outcome Projections

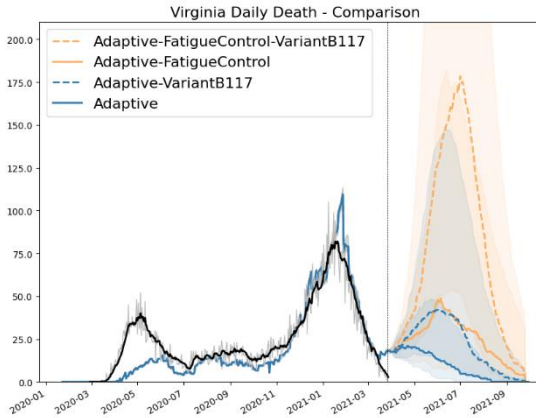
Confirmed cases



Estimated Hospital Occupancy

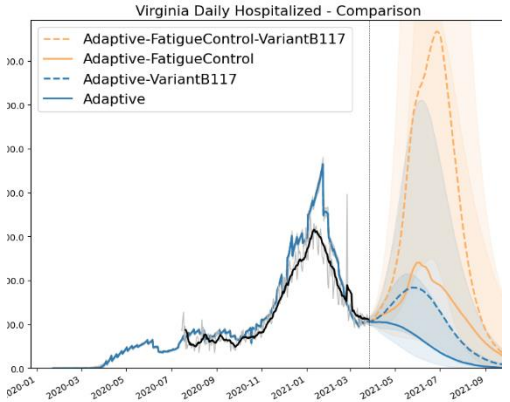


Daily Deaths



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

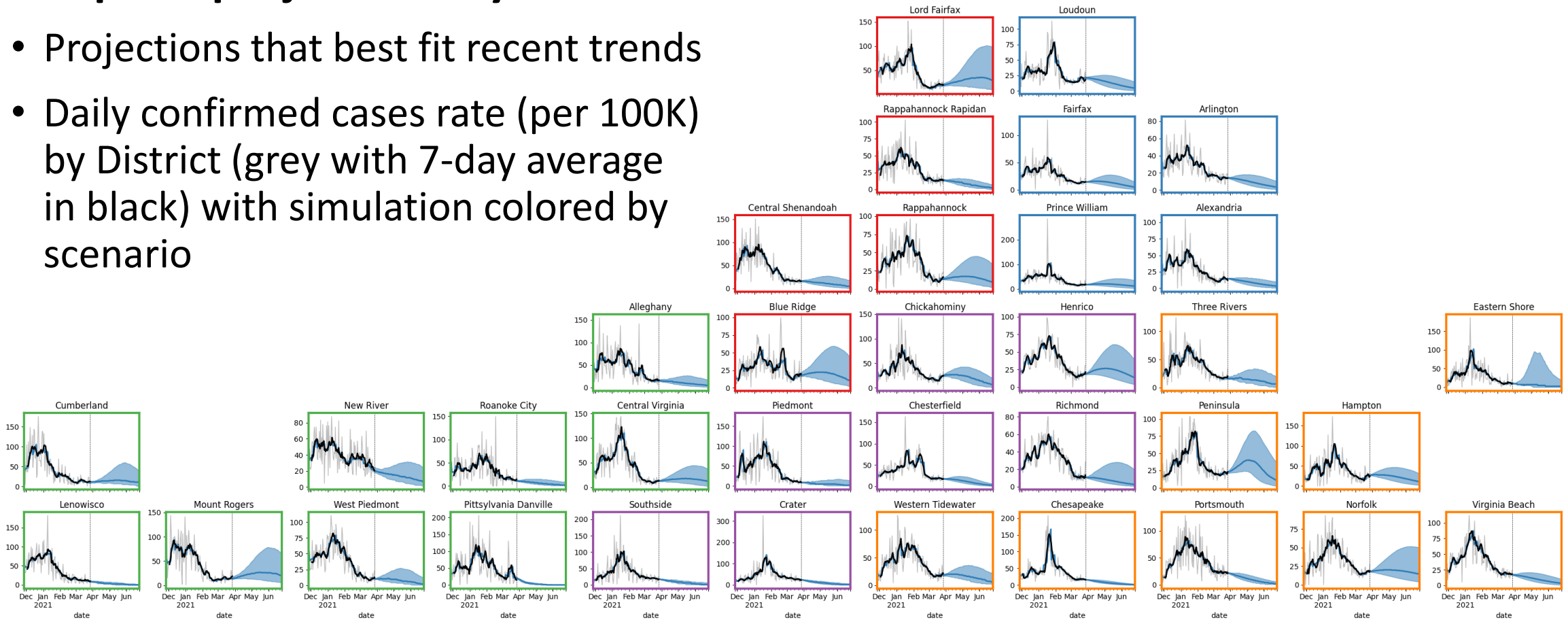
Daily Hospitalized



District Level Projections: Adaptive

Adaptive projections by District

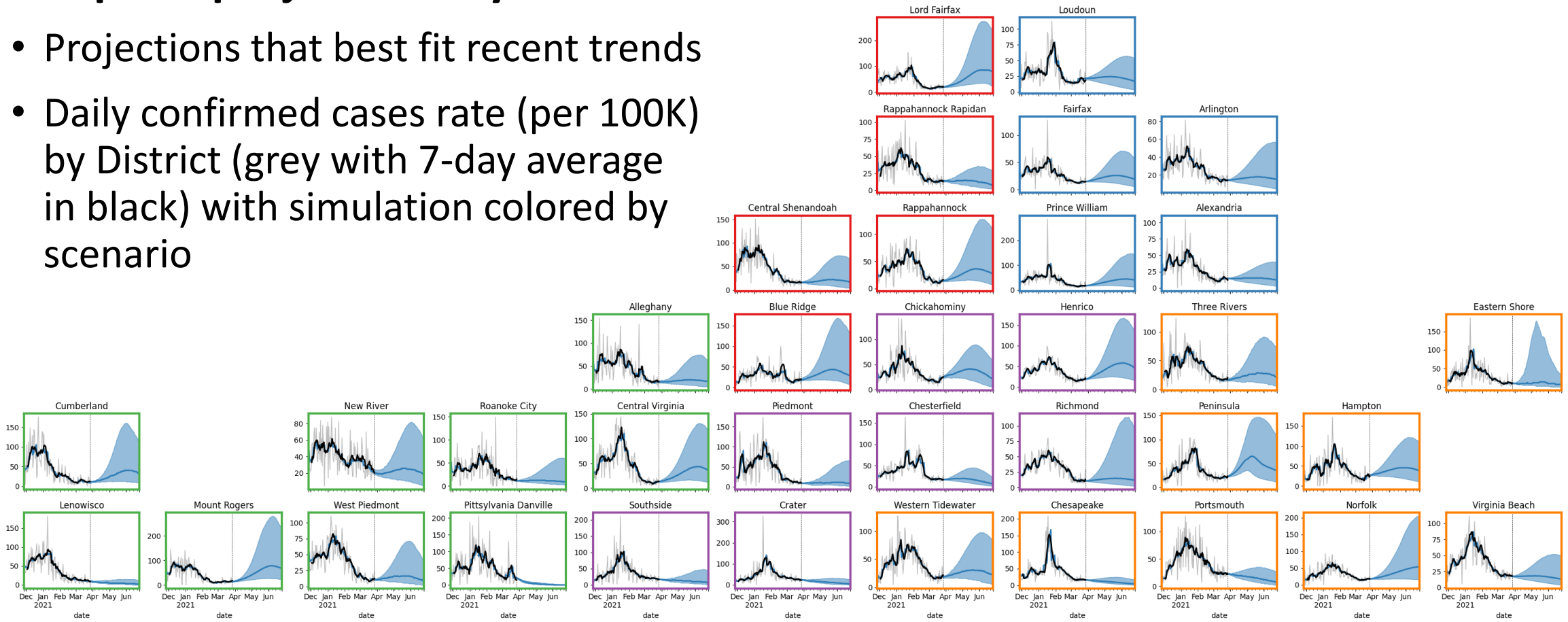
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by District (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-VariantB117

Adaptive projections by District

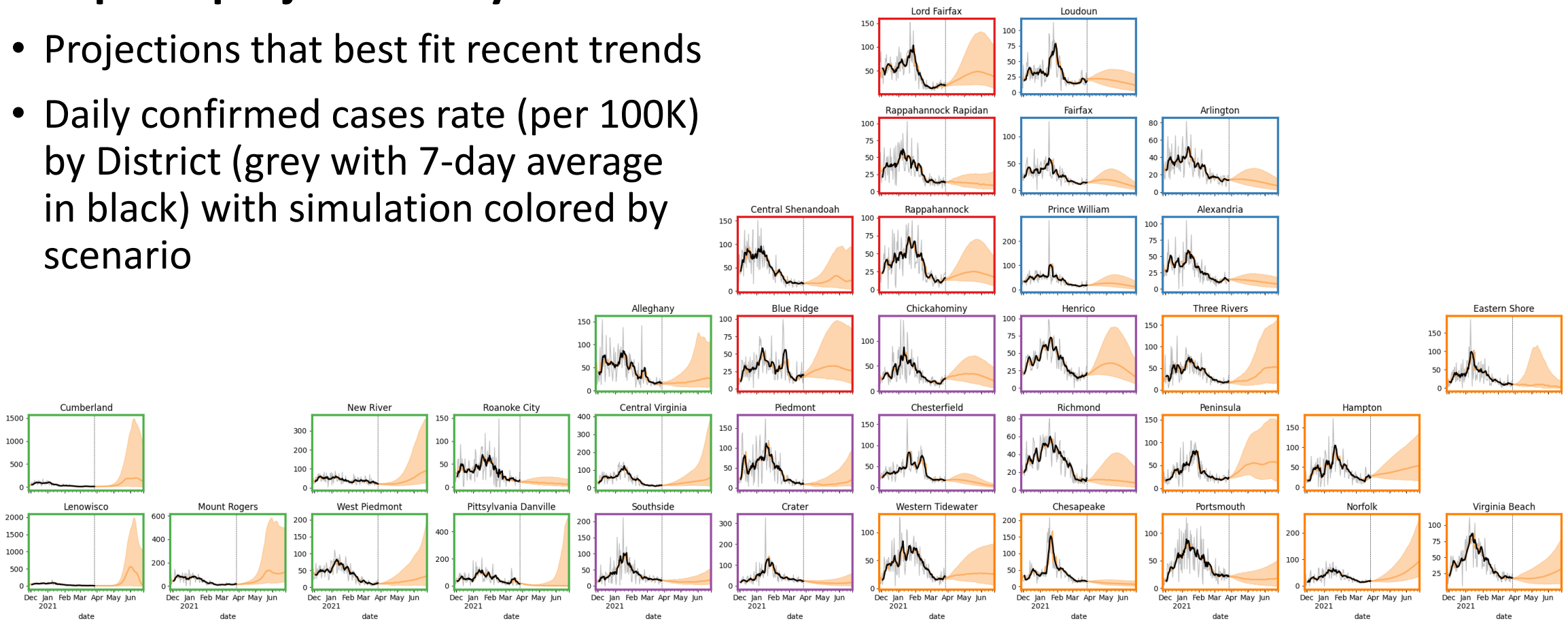
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by District (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-FatigueControl

Adaptive projections by District

- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by District (grey with 7-day average in black) with simulation colored by scenario



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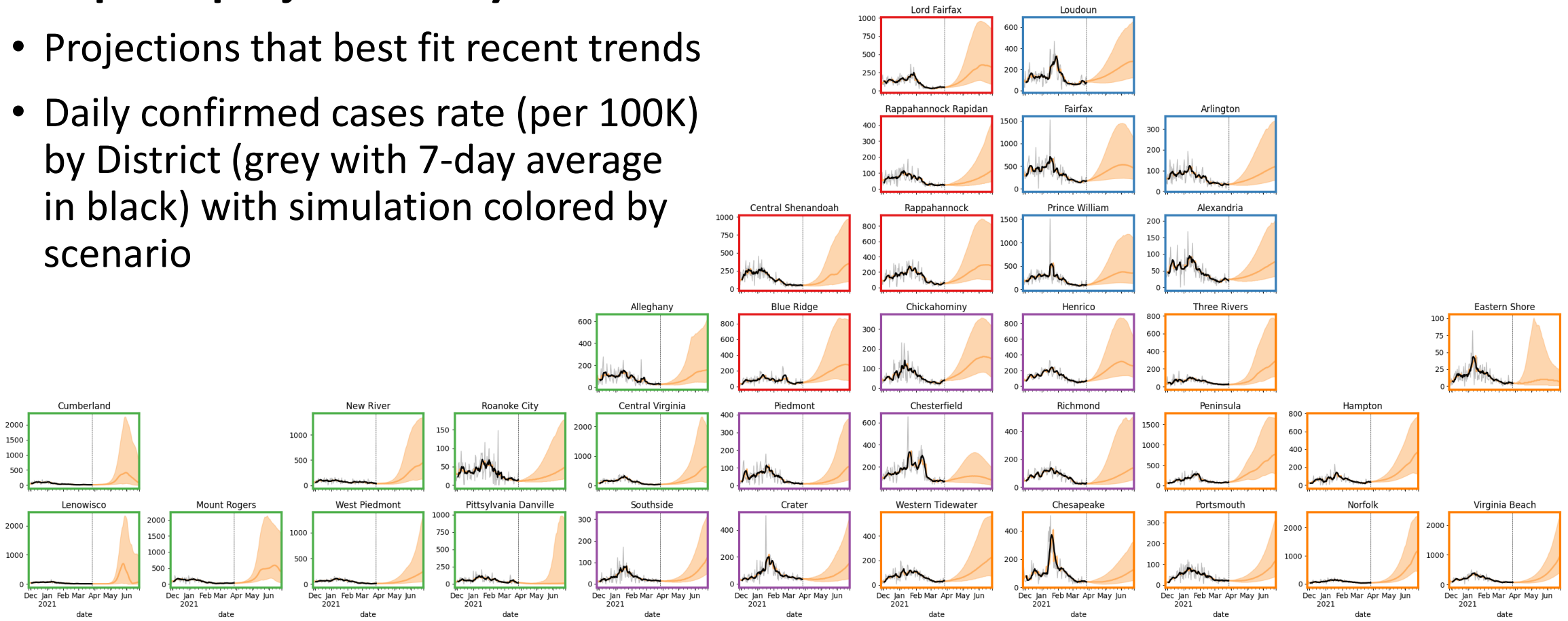
District Level Projections: Adaptive-FatigueControl-VariantB117

Adaptive projections by District

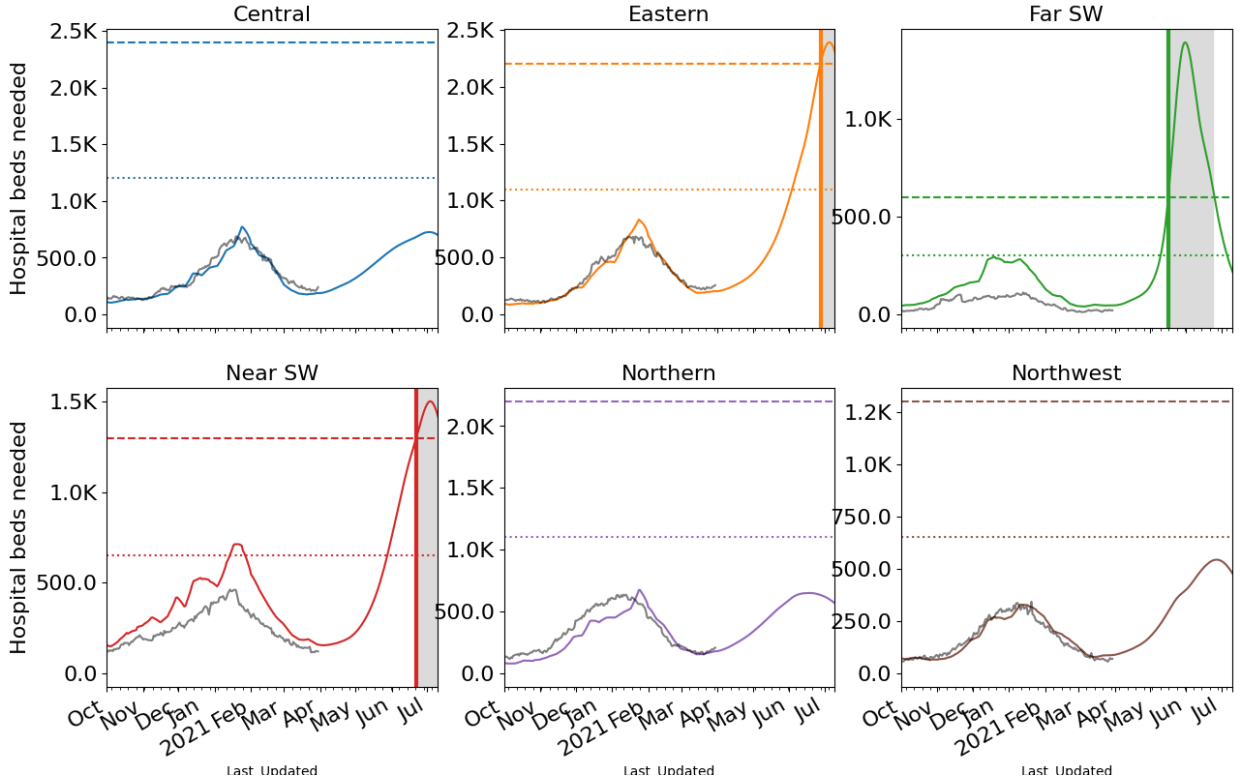
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by District (grey with 7-day average in black) with simulation colored by scenario

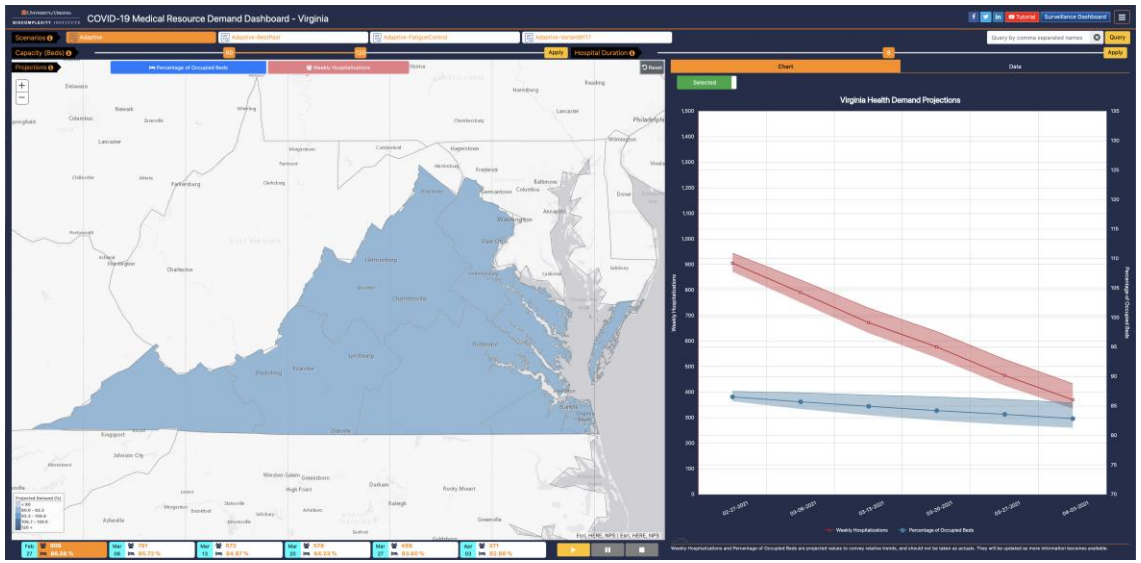


Hospital Demand and Bed Capacity by Region

Capacities* by Region – Adaptive-FatigueControl-VariantB117

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





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

If Adaptive-FatigueControl-VariantB117 scenario:

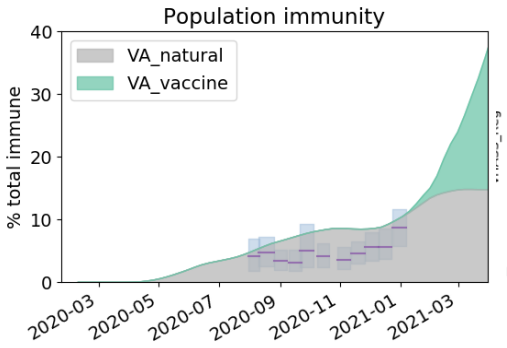
- Southwest & Eastern regions may reach surge bed capacity in late May to late June
- Eastern, Near SW approach initial bed capacity in June as well

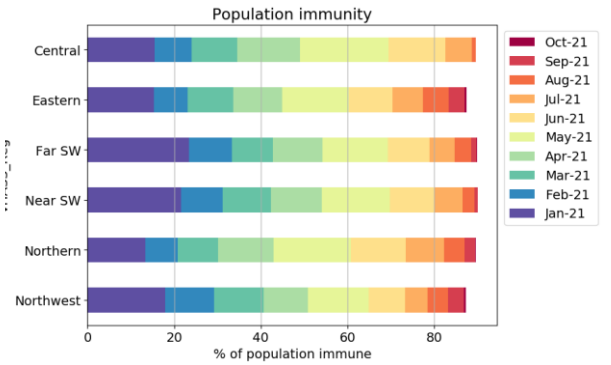
* Assumes average length of stay of 8 days

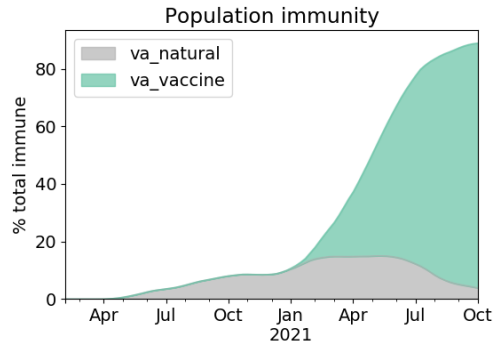
Virginia's Progress on Population Immunity

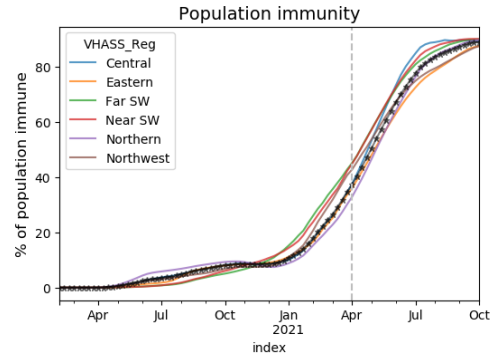
Natural Immunity and Vaccines combine to produce a population level of immunity

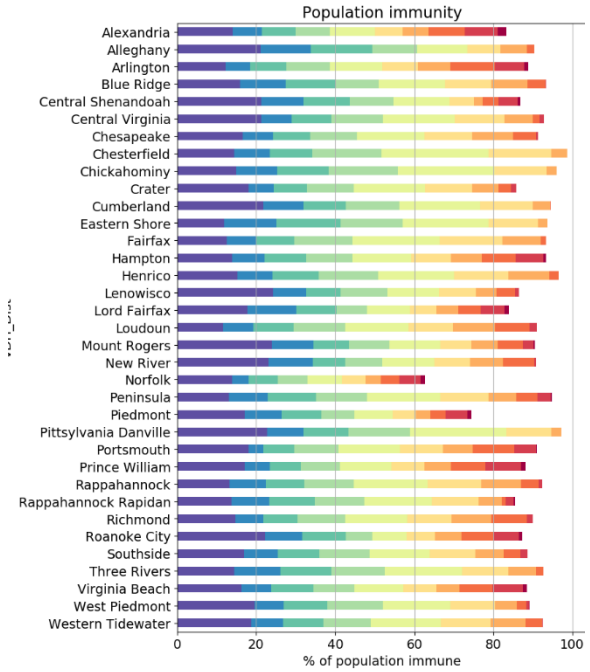
- How long immunity from infection with SARS-CoV2 lasts is not well understood but may vary based on severity of symptoms
  - We assume a conservative 6 month period of protection for these calculations
- Vaccine induced immunity is likely to last longer, we assume indefinite protection
  - This also 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
  - We assume 90% of adults will ultimately get vaccinated in these calculations but slow rates may prevent this from happening before October 2021











Key Takeaways

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

- **Case rates in Virginia have flattened and now have some growth**
- VA mean weekly incidence flat at 17.5/100K from 17/100K, US up (to 18.5 from 16.5 per 100K)
- Progress is stalling, 84% of VA counties above mean rate of Summer 2020
- Projections shifting to growth across Commonwealth, boosted by B.1.1.7
- Recent updates:
  - Currently challenged to estimate the impact on hospitalizations and deaths, as increased rates from Variant B.1.1.7 interact with decreases from vaccination of the most susceptible to these outcomes
  - Johnson & Johnson included in vaccine schedule and Seasonal Effects adjusted for spring and summer
- The situation continues to change. Models continue to be updated regularly.

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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?

Points of Contact

Bryan Lewis
brylew@virginia.edu

Srini Venkatramanan
srini@virginia.edu

Madhav Marathe
marathe@virginia.edu

Chris Barrett
ChrisBarrett@virginia.edu

Biocomplexity COVID-19 Response Team

Aniruddha Adiga, Abhijin Adiga, Hannah Baek, Chris Barrett, Golda Barrow, Richard Beckman, Parantapa Bhattacharya, Andrei Bura, Jiangzhuo Chen, Patrick Corbett, Clark Cucinell, Allan Dickerman, Stephen Eubank, Arindam Fadikar, Joshua Goldstein, Stefan Hoops, Ben Hurt, Sallie Keller, Ron Kenyon, Brian Klahn, Gizem Korkmaz, Vicki Lancaster, Bryan Lewis, Dustin Machi, Chunhong Mao, Achla Marathe, Madhav Marathe, Fanchao Meng, Henning Mortveit, Mark Orr, Joseph Outten, Akhil Peddireddy, Przemyslaw Porebski, SS Ravi, Erin Raymond, Jose Bayoan Santiago Calderon, James Schlitt, Aaron Schroeder, Stephanie Shipp, Samarth Swarup, Alex Telionis, Srinivasan Venkatramanan, Anil Vullikanti, James Walke, Amanda Wilson, Dawen Xie

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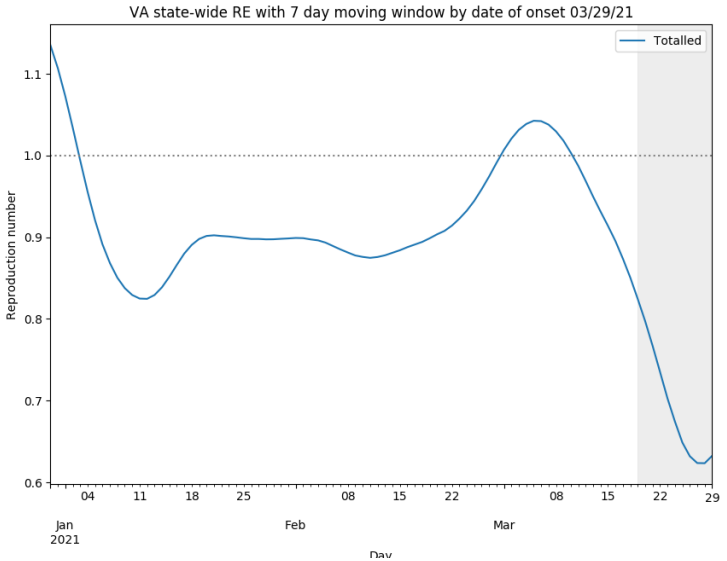
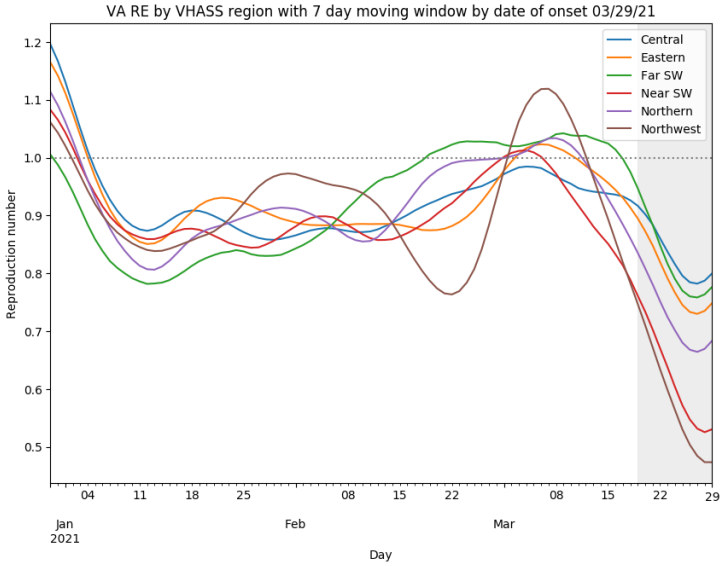
Supplemental Slides

Date of Onset Reproductive Number

Mar 20th Estimates

Region	Date of Onset R_e	Date Onset Diff Last Week
State-wide	0.797	0.045
Central	0.902	0.106
Eastern	0.873	0.022
Far SW	0.915	0.147
Near SW	0.734	-0.018
Northern	0.809	0.043
Northwest	0.710	-0.081





Methodology

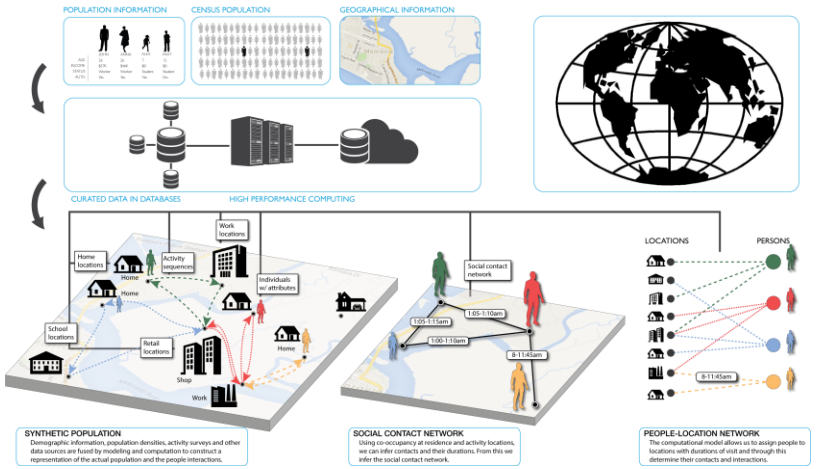
- Wallinga-Teunis method (EpiEstim[1]) for cases by **confirmation date**
- Serial interval: updated to discrete distribution from observations (mean=4.3, Flaxman et al, Nature 2020)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

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)

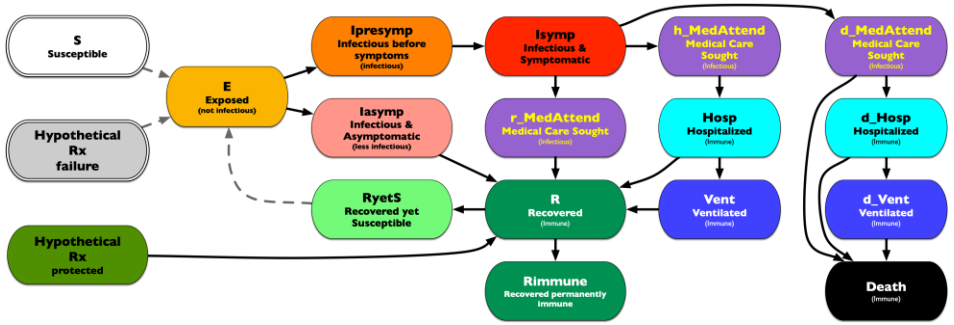
EpiHiper: Distributed network-based stochastic disease transmission simulations

- 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



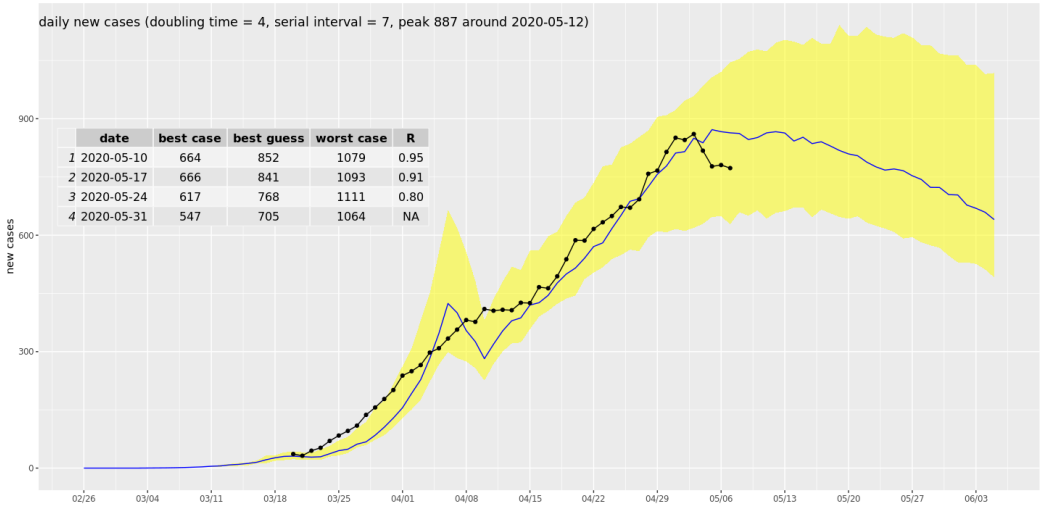
Detailed Disease Course of COVID-19

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

ABM Social Distancing Rebound Study Design

Study of ”Stay Home” policy adherence

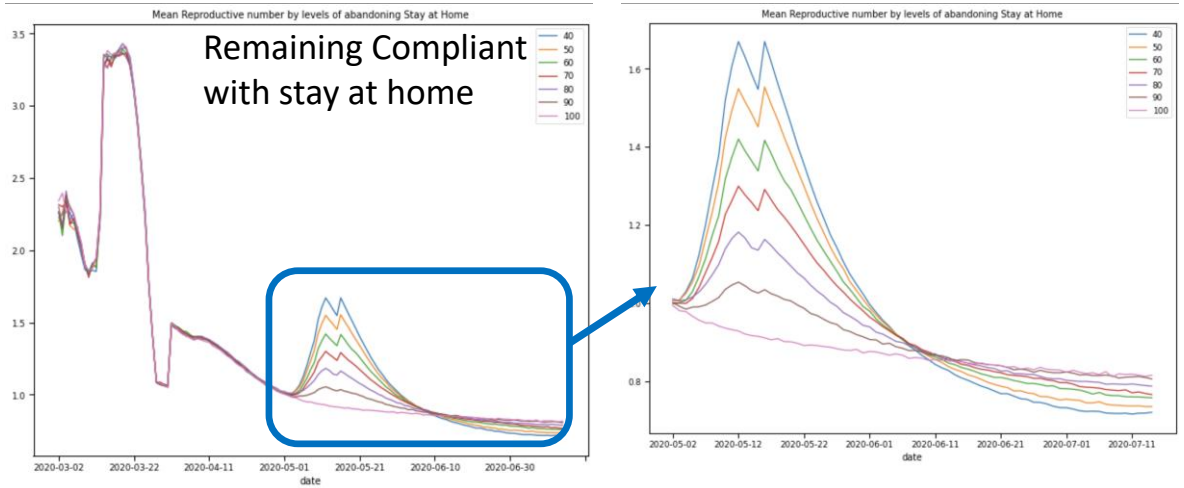
- Calibration to current state in epidemic
- Implement “release” of different proportions of people from ”staying at home”



	date	best case	best guess	worst case	R
1	2020-05-10	664	852	1079	0.95
2	2020-05-17	666	841	1093	0.91
3	2020-05-24	617	768	1111	0.80
4	2020-05-31	547	705	1064	NA

Calibration to Current State

- Adjust transmission and adherence to current policies to current observations
- For Virginia, with same seeding approach as PatchSim



Impacts on Reproductive number with release

- After release, spike in transmission driven by additional interactions at work, retail, and other
- At 25% release (70-80% remain compliant)
- Translates to 15% increase in transmission, which represents a 1/6th return to pre-pandemic levels