

Network Systems
Science & Advanced
Computing

Biocomplexity Institute
& Initiative

University of Virginia

Estimation of COVID-19 Impact in Virginia

March 17th, 2021

(data current to March 15th – 16th)

Biocomplexity Institute Technical report: TR 2021-028



BIOCOMPLEXITY INSTITUTE

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



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 and show signs of flattening out**
- VA mean weekly incidence slightly down to 15/100K from 16/100K, US also down (to 16 from 19 per 100K)
- Significant progress made in last month, however 82% of VA counties above mean rate of Summer 2020
- Projections continue to be down but are flattening out across Commonwealth
- Recent updates:
 - Adjusted Seasonal Effects scenarios to account for spring and summer weather
 - Accelerated vaccine schedule with Johnson & Johnson added as base case in anticipation of boost in vaccine supplies
 - Adjustment to death outcome modeling rescaled based on date of death from VDH data, higher resolution hospital data incorporated for hospital calibration
- The situation is changing rapidly. Models continue to be updated regularly.



Situation Assessment



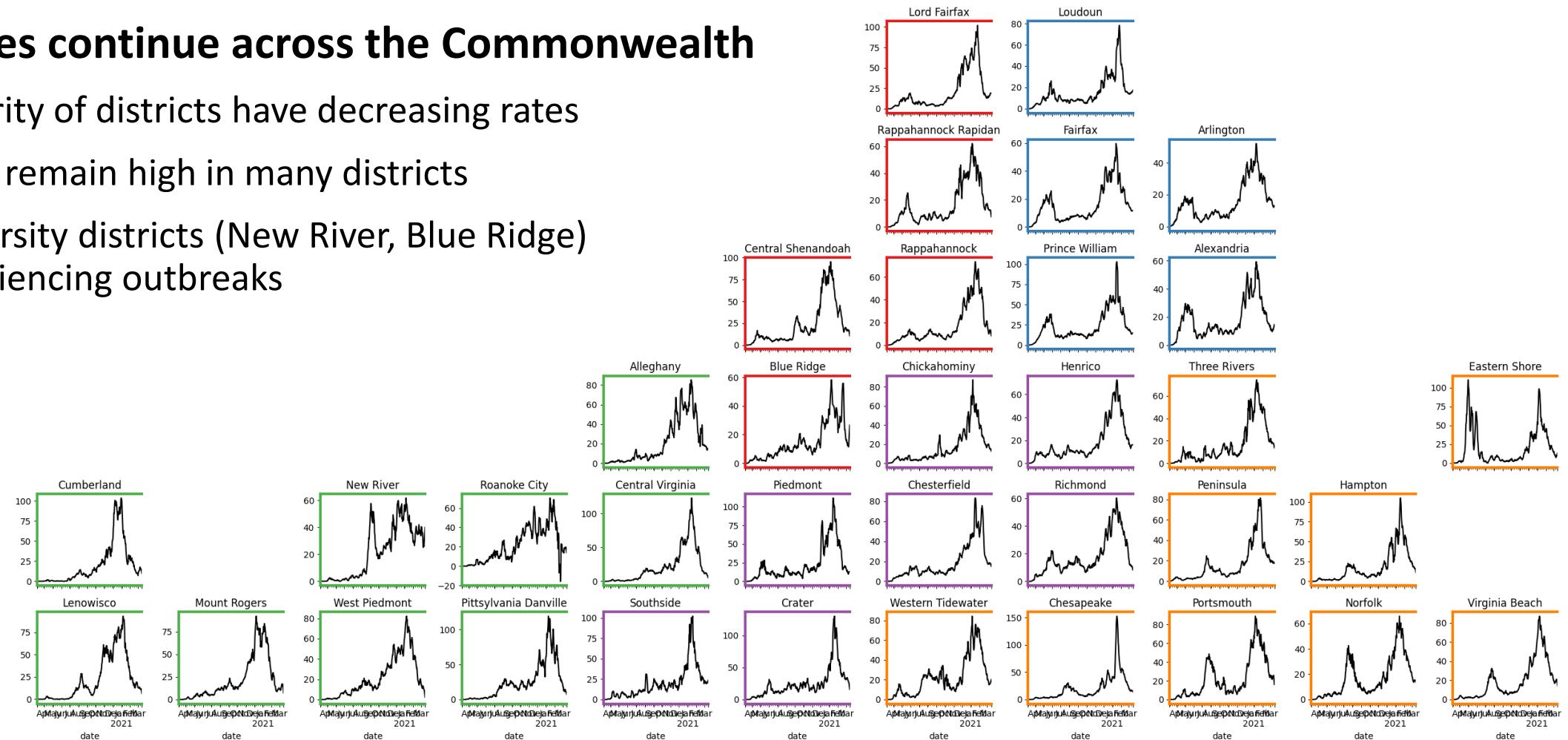
UNIVERSITY OF VIRGINIA

BIOCOMPLEXITY INSTITUTE

Case Rate (per 100k) by VDH District

Declines continue across the Commonwealth

- Majority of districts have decreasing rates
- Rates remain high in many districts
- University districts (New River, Blue Ridge) experiencing outbreaks

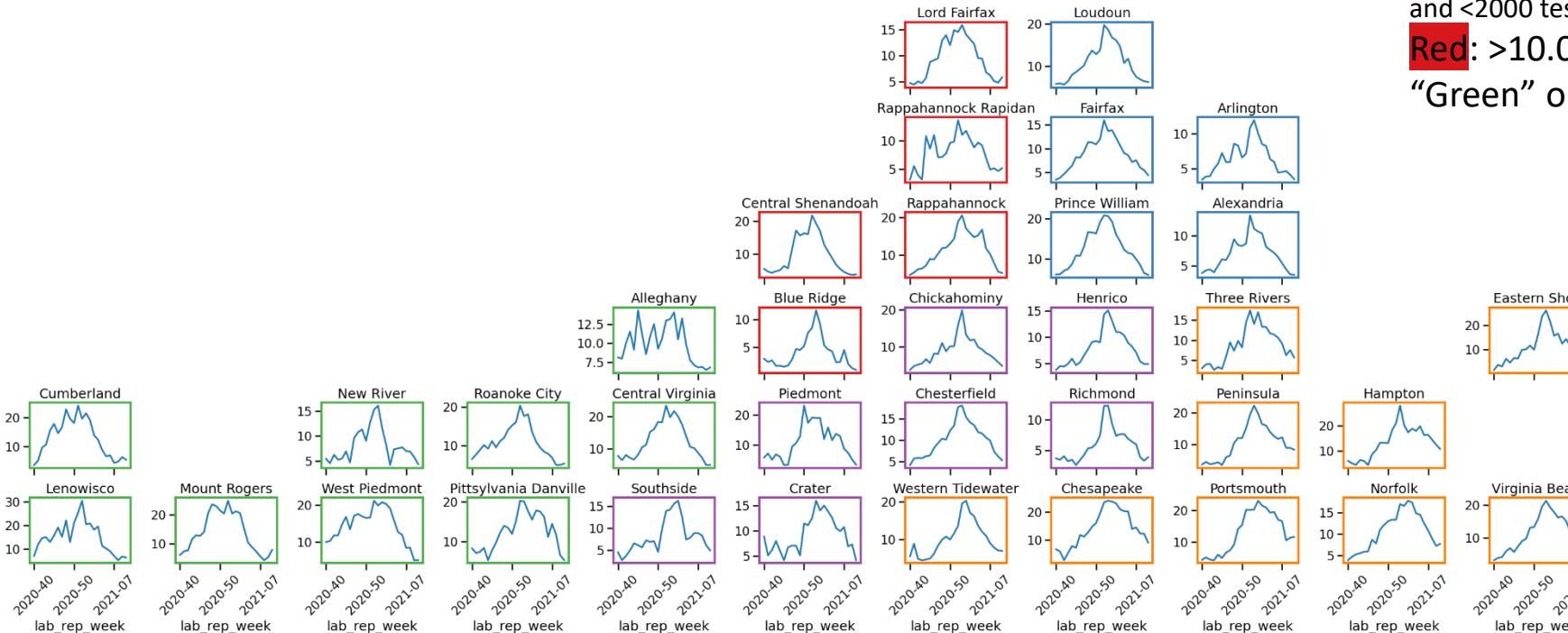


UNIVERSITY of VIRGINIA

Test Positivity by VDH District

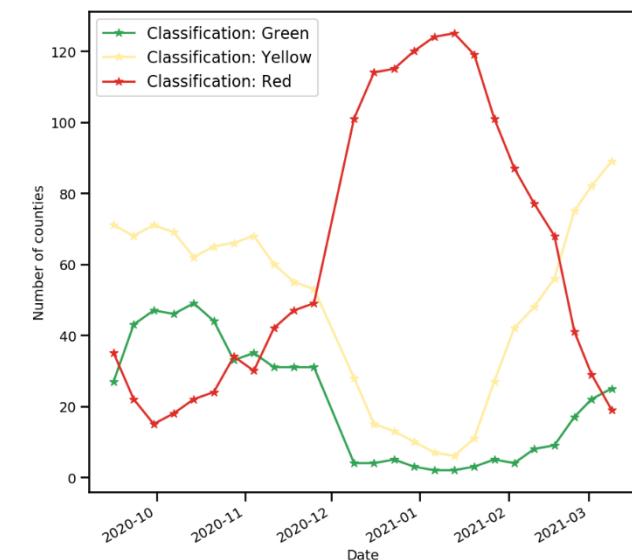
Weekly changes in test positivity by district

- Rates continue to decline
- More counties are below 5% than over 10% for first time since October



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"

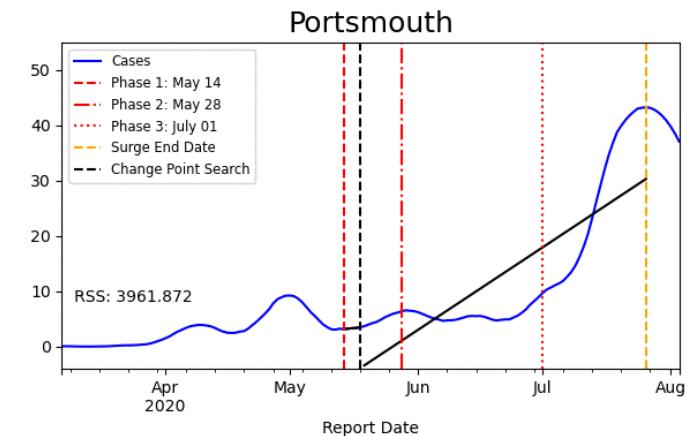


District Trajectories

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



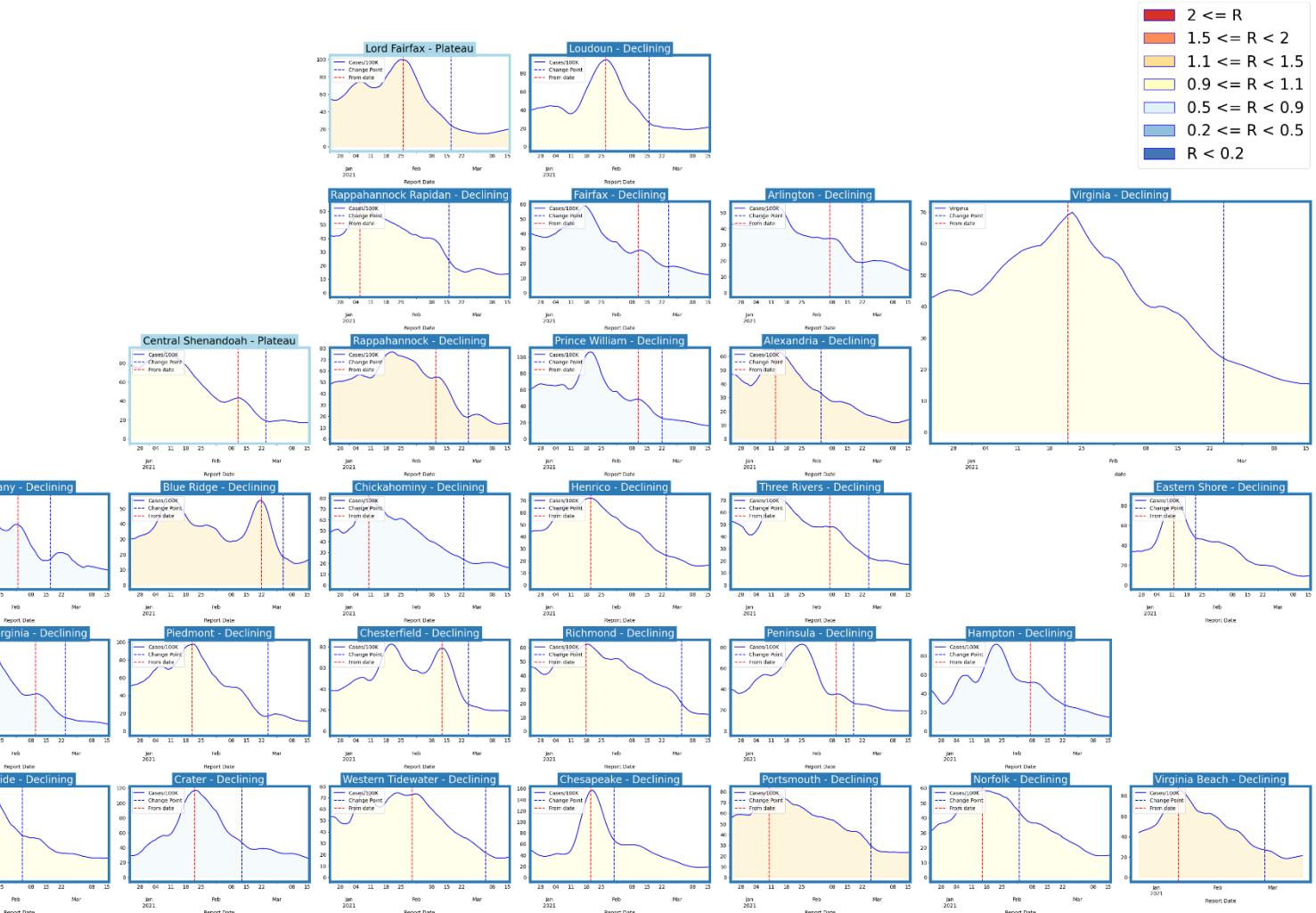
Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	32 (29)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	1 (4)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	2 (2)
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	31 (29)
Plateau	2 (4)
Slow Growth	2 (2)
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

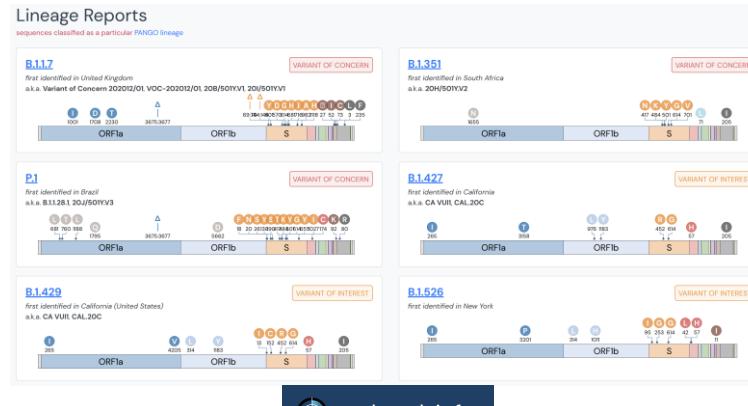
- Current evidence supports that new variants can:
 - Increase transmissibility
 - Increase severity (more hospitalizations and/or deaths)
 - Limit immunity from prior infection and vaccination
- Genomic surveillance remains very limited
 - Challenges ability to estimate impact in US to date and estimation of arrival and potential impact in future
 - B.1.1.7 is most frequent and well studied

Lineages Of Concern

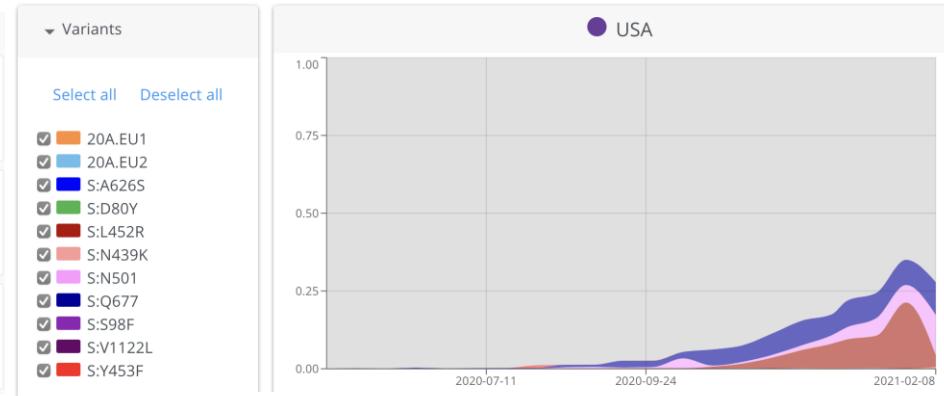
LoC name	PANGO lineage	NextStrain lineage	Other synonyms	Emergence date	Emergence location	Key AA substitutions in spike protein	Impact
B.1.1.7	B.1.1.7	20I/501Y.V1	VOC 202012/01, UK variant	September 2020	Southeast England	H69-, V70-, N501Y, D614G, P681H	Increased transmissibility; S gene target failure (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

Variant	Reported Cases in US	Number of Jurisdictions Reporting
B.1.1.7	4,690	50
B.1.351	143	25
P.1	25	10



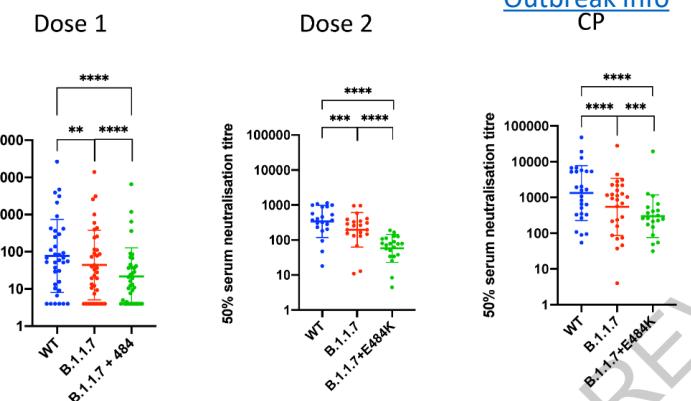
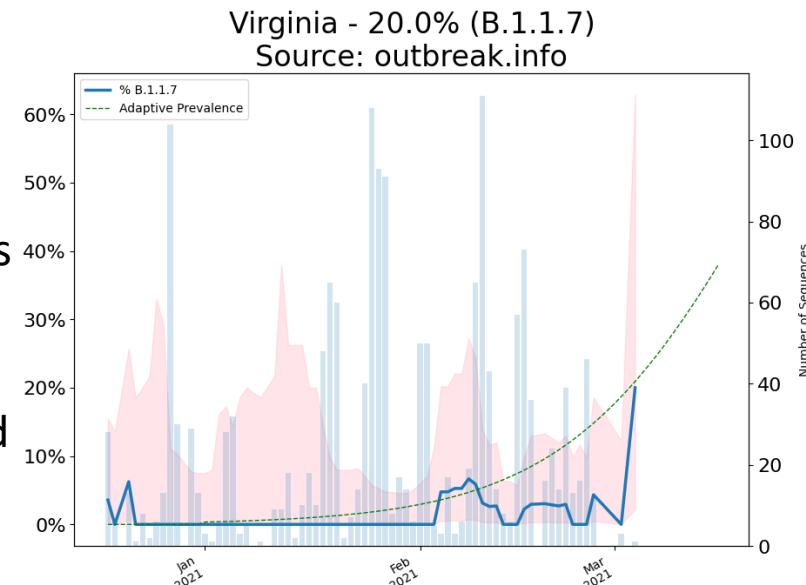
[Outbreak Info](#)



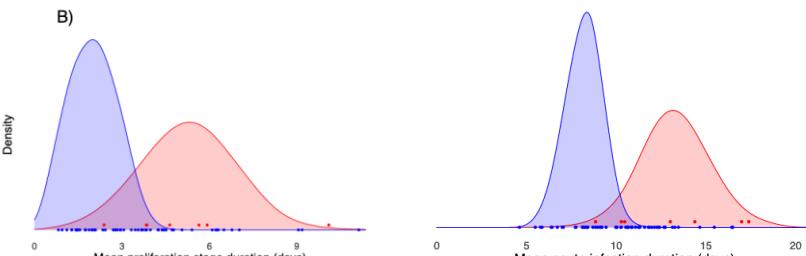
SARS-CoV2 Variants of Concern

Lineage B.1.1.7

- B.1.1.7 has been detected in Virginia and all other states as of Mar 14th (10-20 day delay for genotyping), and has continued to rapidly grow. Current estimates place national frequency at ~10% and Virginia at 20%
- Virginia is a little below but still within bounds of estimates based on growth rates indicating it will predominate (eg reach 50% frequency) by late March and is 35%-45% more transmissible
- A cluster with the E484K mutation has been described indicating multiple independent acquisitions in UK, potential for aiding immune escape
- 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
- Update to Rasmussen et al. study estimates B.1.1.7 to have the highest “fitness” advantage of all observed variants and mutations of note



Serum from 37 vaccinated individuals showed fair neutralization response to B.1.1.7 with additional E484K mutation Nature

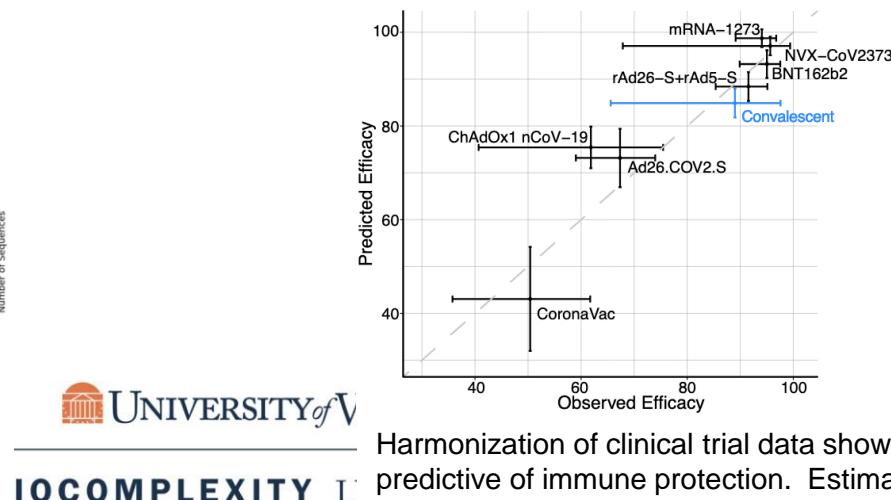
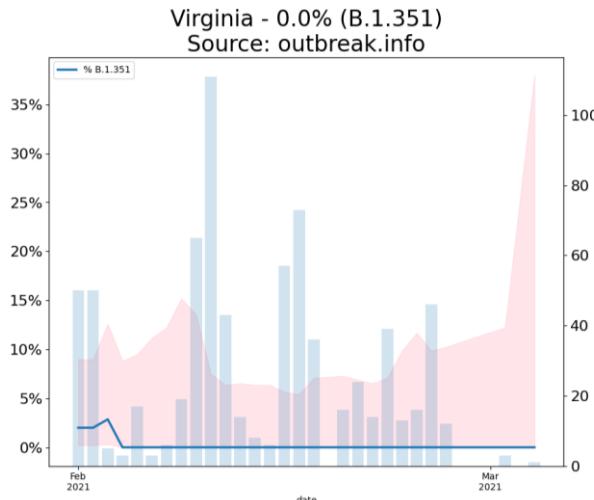


Variant B.1.1.7 may cause longer infections with similar peak viral concentration compared to non-B.1.1.7. May contribute to B.1.1.7's increased transmissibility.
<https://dash.harvard.edu/handle/1/37366884>

SARS-CoV2 Variants of Concern

Lineage B.1.351

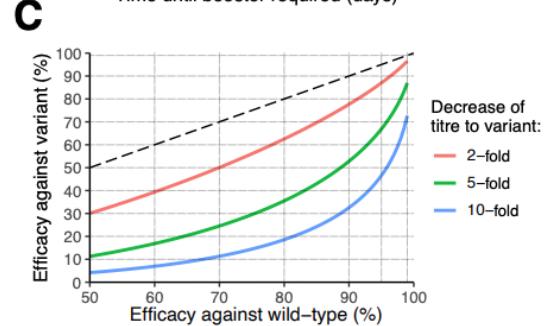
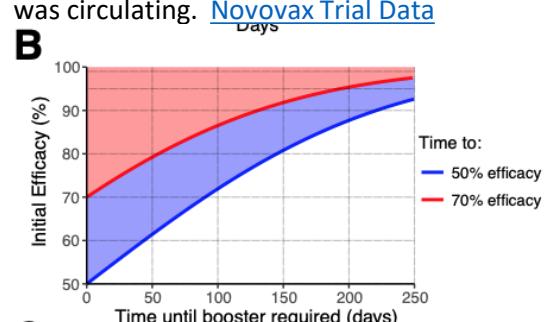
- Emerging strain initially identified in South Africa shows signs of vaccine escape, currently 143 reported cases in 25 states (including 20 now in Virginia) as of Mar 14th
- Recent study based on clinical trial data shows that convalescent serum neutralization is highly predictive of actual immune protection for infection, thus B.1.351 may require booster vaccinations, and provides estimates for timing.
- New study in NEJM demonstrates serum neutralization across the strains from different vaccine recipients (Pfizer)
- New study in Nature suggests this variant could be up to 50% more transmissible as well, and that other mutations associated with transmissibility can be acquired rapidly
- A study has demonstrated that T cell response from mRNA vaccinated individuals are not significantly degraded across these “immune escaping” variants



	Vaccine n=7,020	Placebo n=7,020
Total	10	96
Mild	1	28
Moderate	9	63
Severe	0	5
Vaccine Efficacy	96.4%	
Original COVID-19	95% CI: 73.8, 99.5	
Vaccine Efficacy	86.3%	
B.1.1.7 variant	95% CI: 71.3, 93.5	

Table 1. Final analysis of United Kingdom Phase 3 Trial.

New vaccine candidate from Novavax concluding trials and shows diminished but significant efficacy in arm conducted in South Africa while B1.1.351 was circulating. [Novavax Trial Data](#)

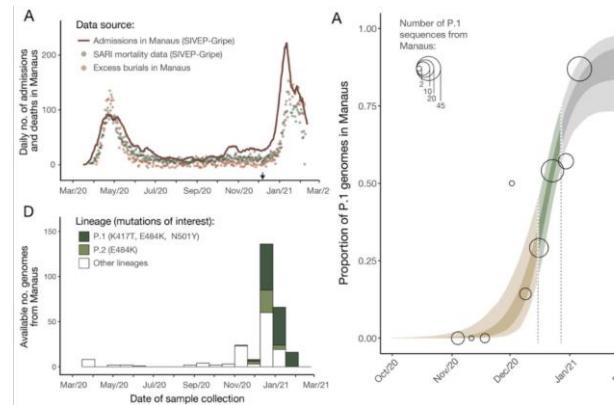


Harmonization of clinical trial data shows neutralisation level is highly predictive of immune protection. Estimates on fold reduction and protection as well as proposed timing of boosters are provided. [MedArxiv](#)

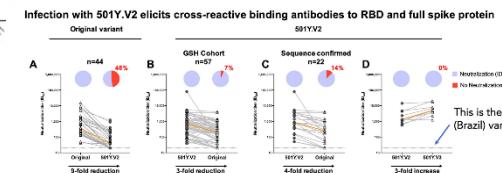
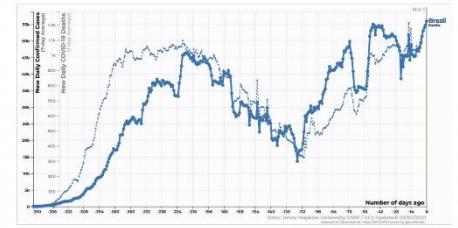
SARS-CoV2 Variants of Concern

Lineage P.1

- Present in at least 15 cases in 9 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 2 months than all of 2020
- [Recent study](#) estimates it to be 1.4-2.2 times more transmissible and able to partially evade protective immunity



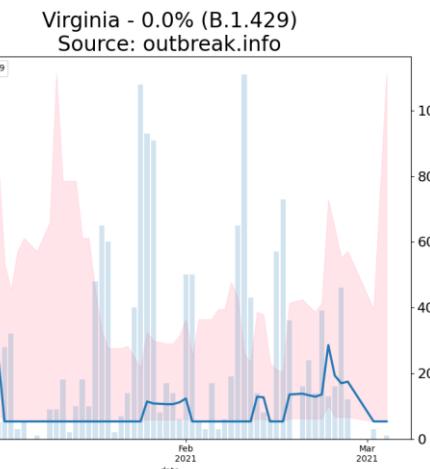
The tragedy in Brazil <https://t.co/GCCxhrlf04> by @terrence_mccoy "The variant known as P.1, which was discovered earlier this year, has stamped the Amazonian city of Manaus, leading to more deaths in January and February than in all of 2020."



Limited neutralization from COVID-19 patient sera. [BioRxiv](#)

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](#)
- With very limited sampling, this variant has been identified in sequences from Virginia, though has a recent estimated frequency of 0% (down from 10% last week)



Estimating Daily Reproductive Number

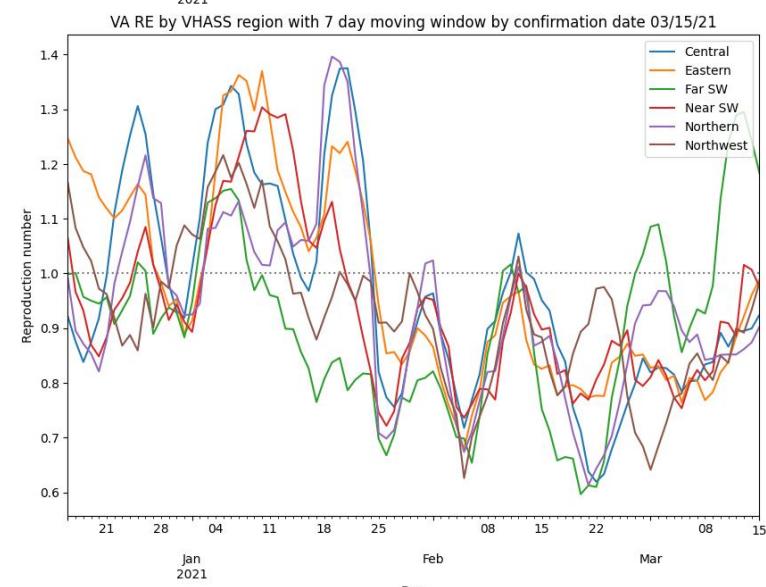
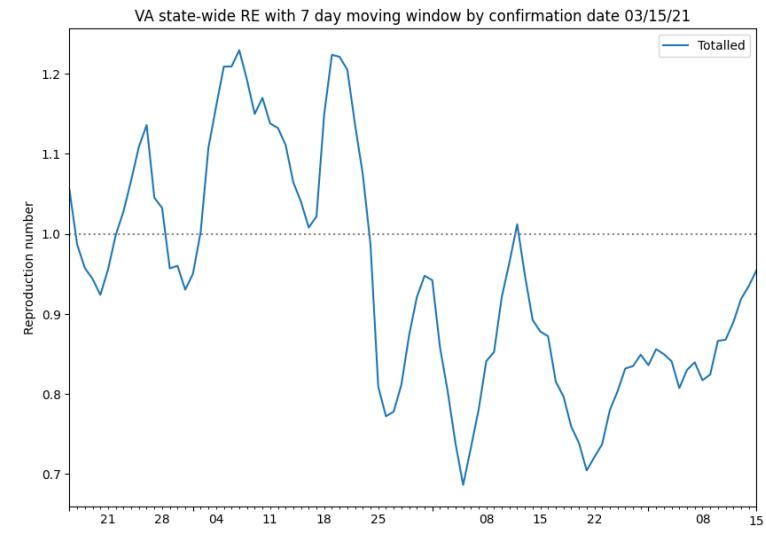
March 15th Estimates

Region	Date Confirmed	R _e	Date Confirmed Diff Last Week
State-wide	0.955		0.137
Central	0.924		0.091
Eastern	0.989		0.220
Far SW	1.184		0.257
Near SW	0.976		0.171
Northern	0.902		0.060
Northwest	0.983		0.158

Methodology

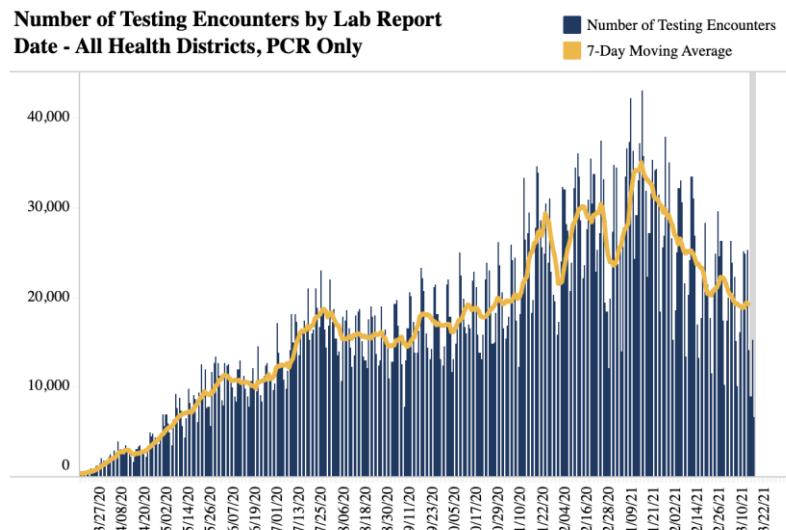
- Wallinga-Teunis method (EpiEstim¹) for cases by confirmation date
- Serial interval: 6 days (2 day std dev)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

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

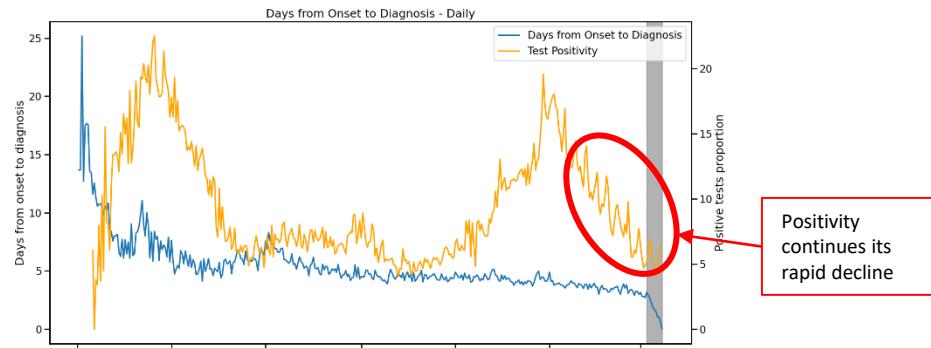
Timeframe (weeks)	Mean days	% difference from overall mean
July (26-30)	6.2	-7%
Aug (31-34)	4.9	-26%
Sept (35-38)	4.5	-32%
Oct (39-43)	4.5	-33%
Nov (44-47)	4.5	-33%
Dec (48-49)	4.2	-37%
Jan (00-04)	3.9	-41%
Feb (05-08)	3.4	-49%
Overall (13-05)	6.7	--



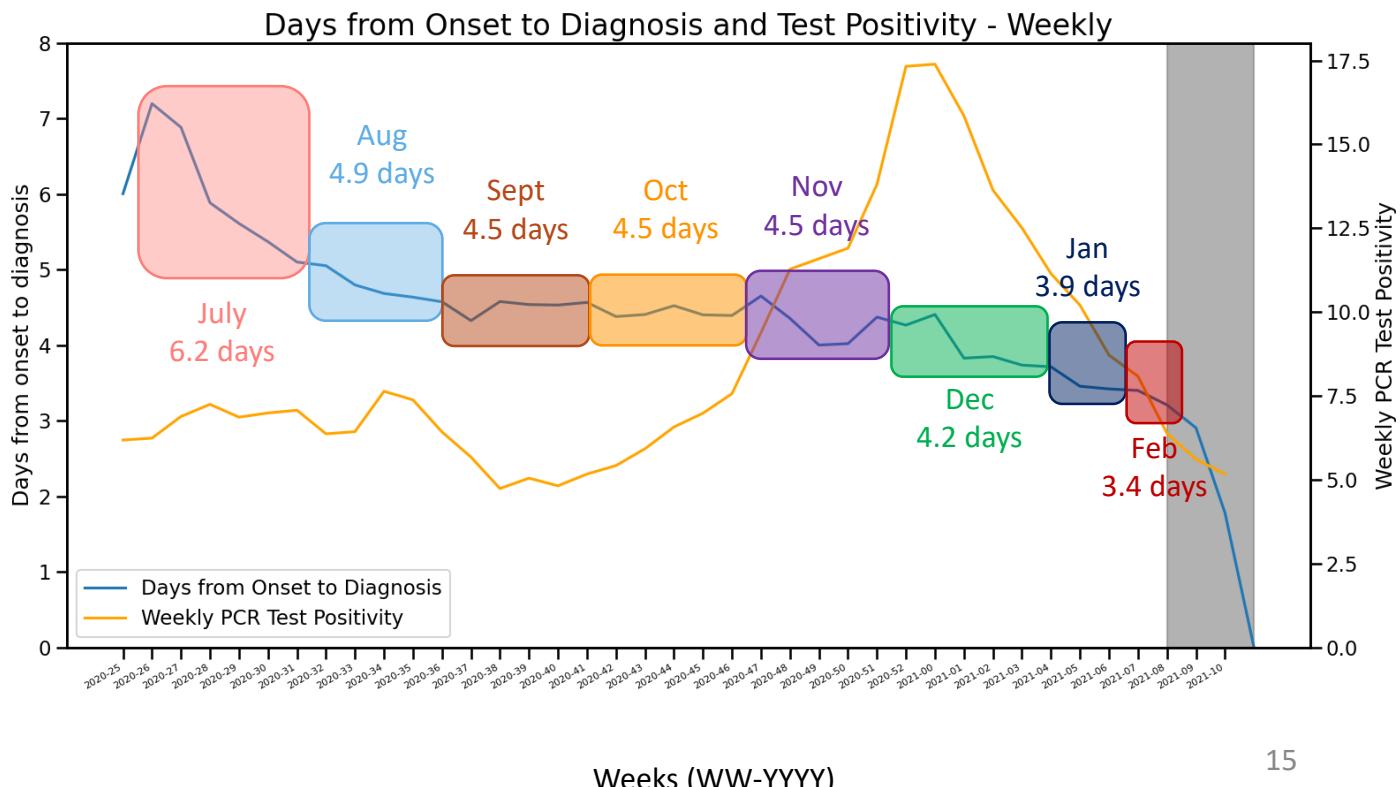
17-Mar-21

Accessed 9:15am March 17, 2021
<https://www.vdh.virginia.gov/coronavirus/>

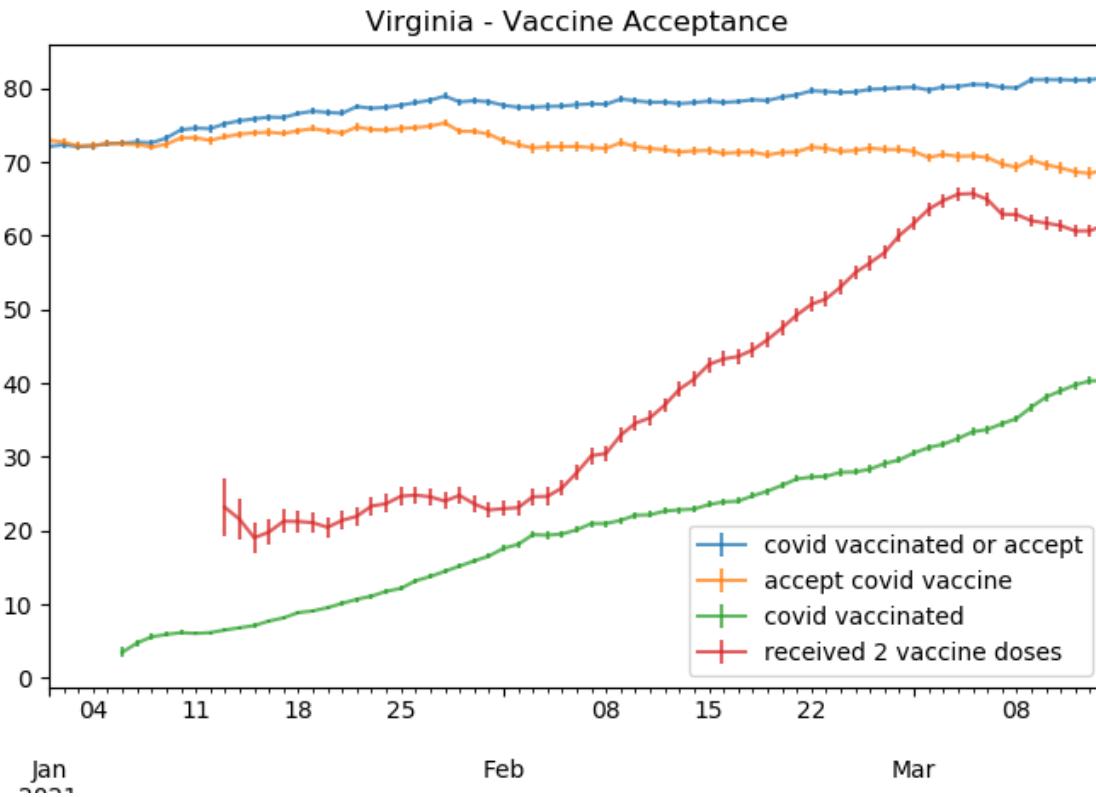
Test positivity vs. Onset to Diagnosis



Positivity continues its rapid decline

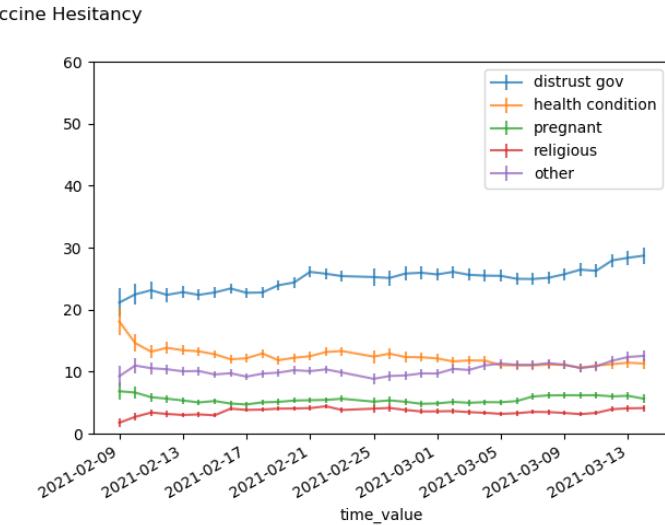
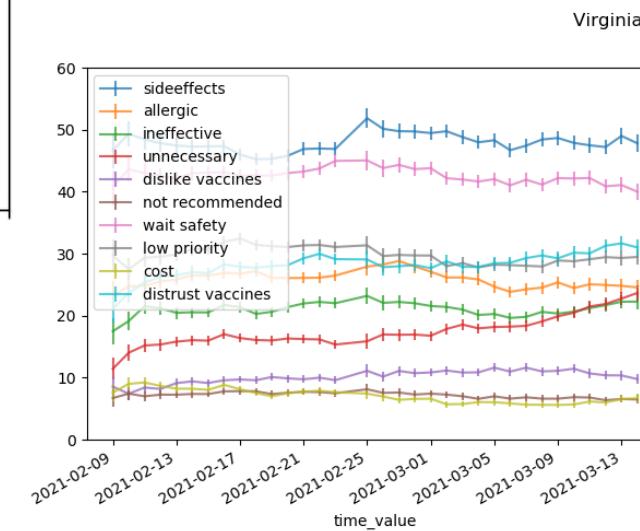


Vaccine Acceptance in Virginia



Acceptance remains high:

- Proportion of Virginians that would definitely or probably accept vaccination if offered today
- Nearly 80% Virginians have already or will choose to be vaccinated
- Down very slightly from high at end of January, but has been stable for several weeks
- Top reasons for hesitancy: side effects, safety, distrust



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



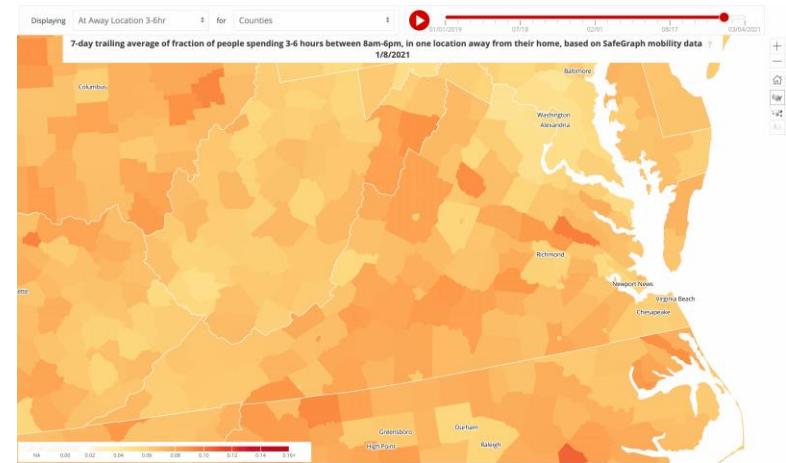
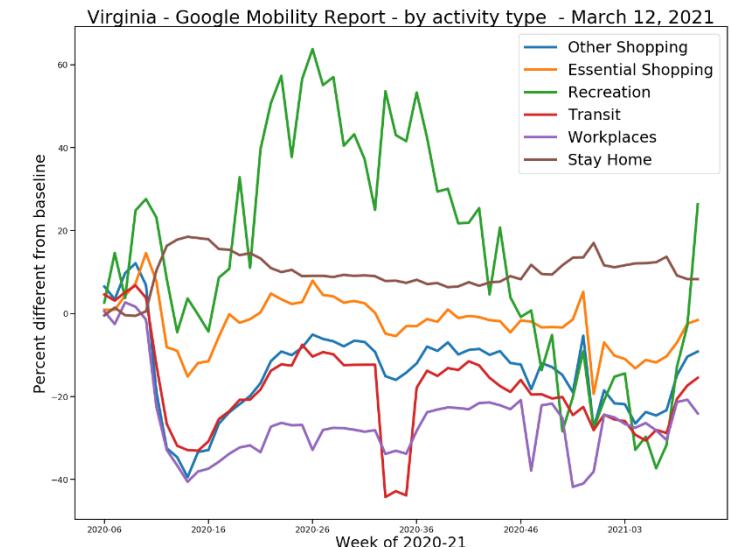
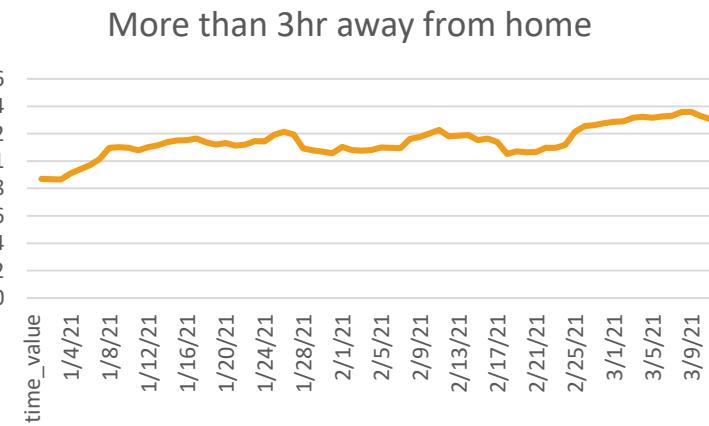
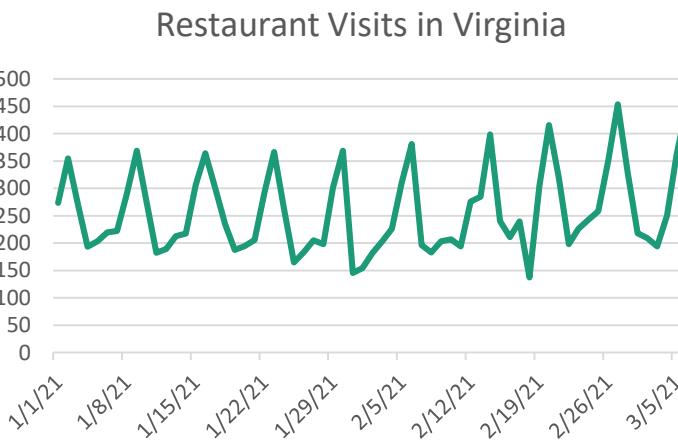
UNIVERSITY OF VIRGINIA

BIOCOMPLEXITY INSTITUTE

Shifting Behaviors in Virginia

Trend upward in Mobility and Leaving Home in last couple weeks:

- Google Mobility has increased mobility to Workplaces, Transit, Other Shopping
 - SafeGraph shows uptick in restaurant visits over last 3 weeks
 - SafeGraph shows slight rise in percent of individuals spending more than 3 hours away from home
 - Geographic distribution shows shifts more strong in central and southwest



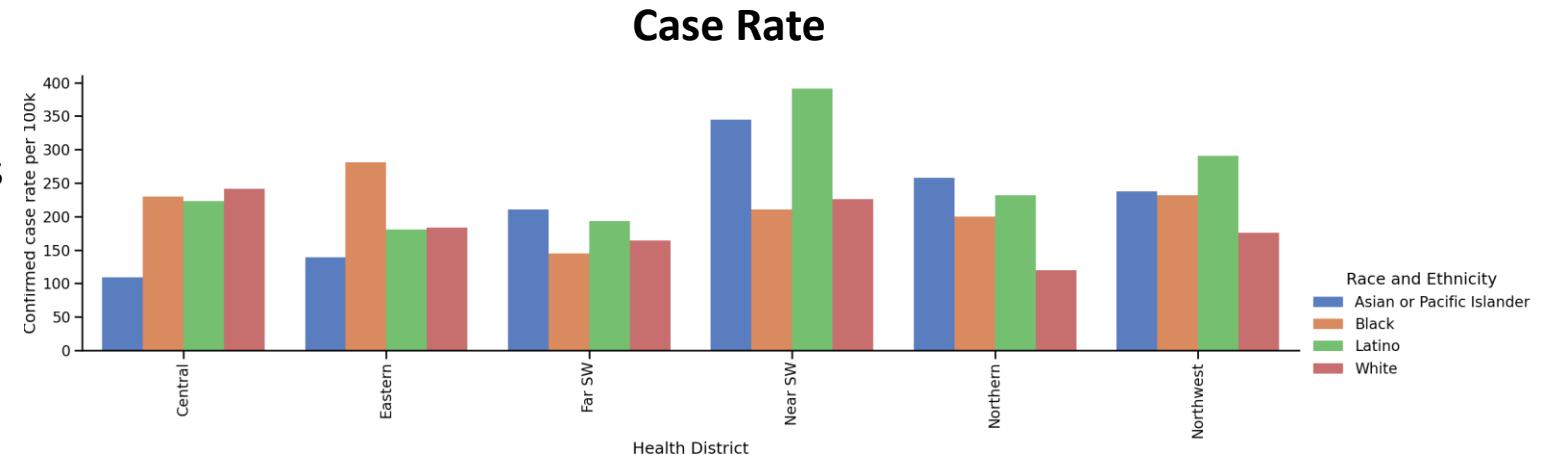
Data Source: <https://covidcast.cmu.edu>



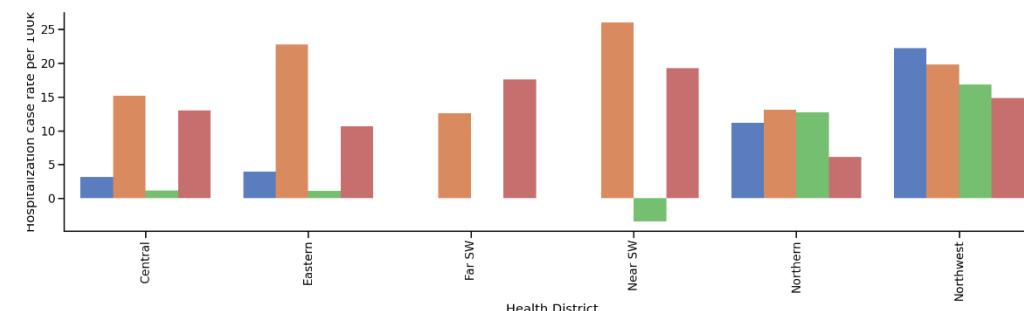
Race and Ethnicity – Recent Rate Changes (per 100K)

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

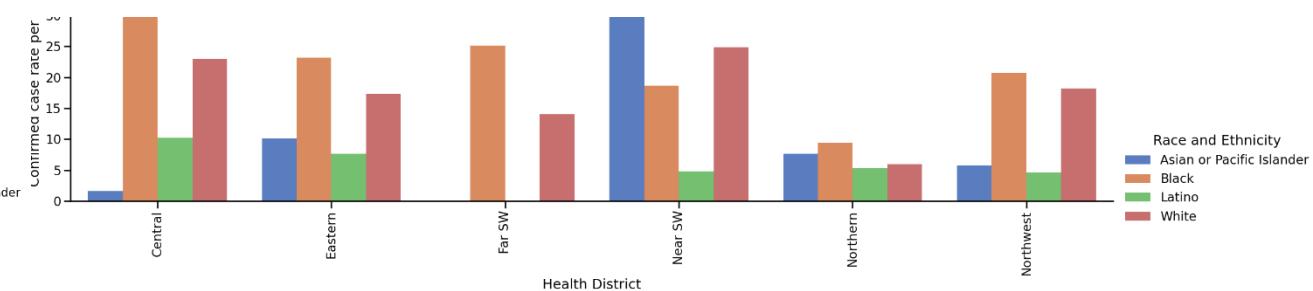
- Two week change in population level rates
- Black, Latinx and 2 or more races populations have much higher changes in rates; disparity is more pronounced in some regions than others
- Based on 2019 census race-ethnicity data by county



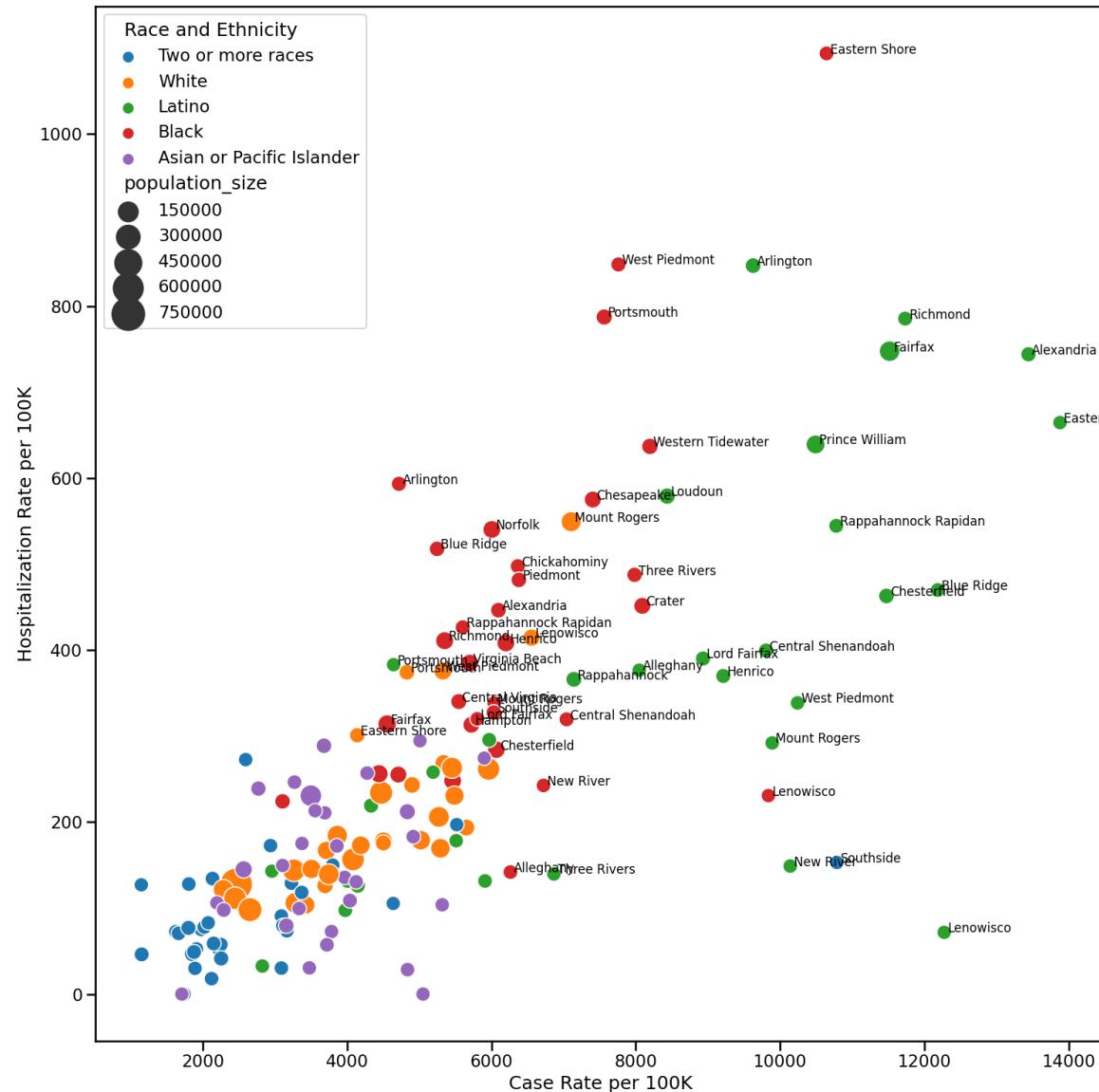
Hospitalization Rate



Death Rate



Race and Ethnicity cases per 100K

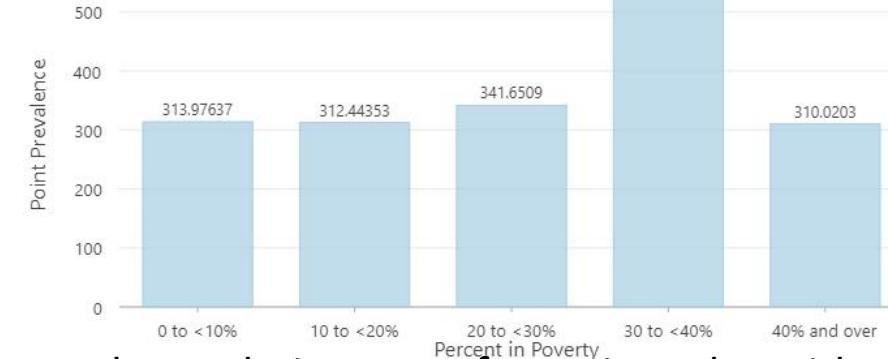


Rates per 100K of each Racial-Ethnic population by Health District

- 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)

Case Rates are associate with Poverty levels

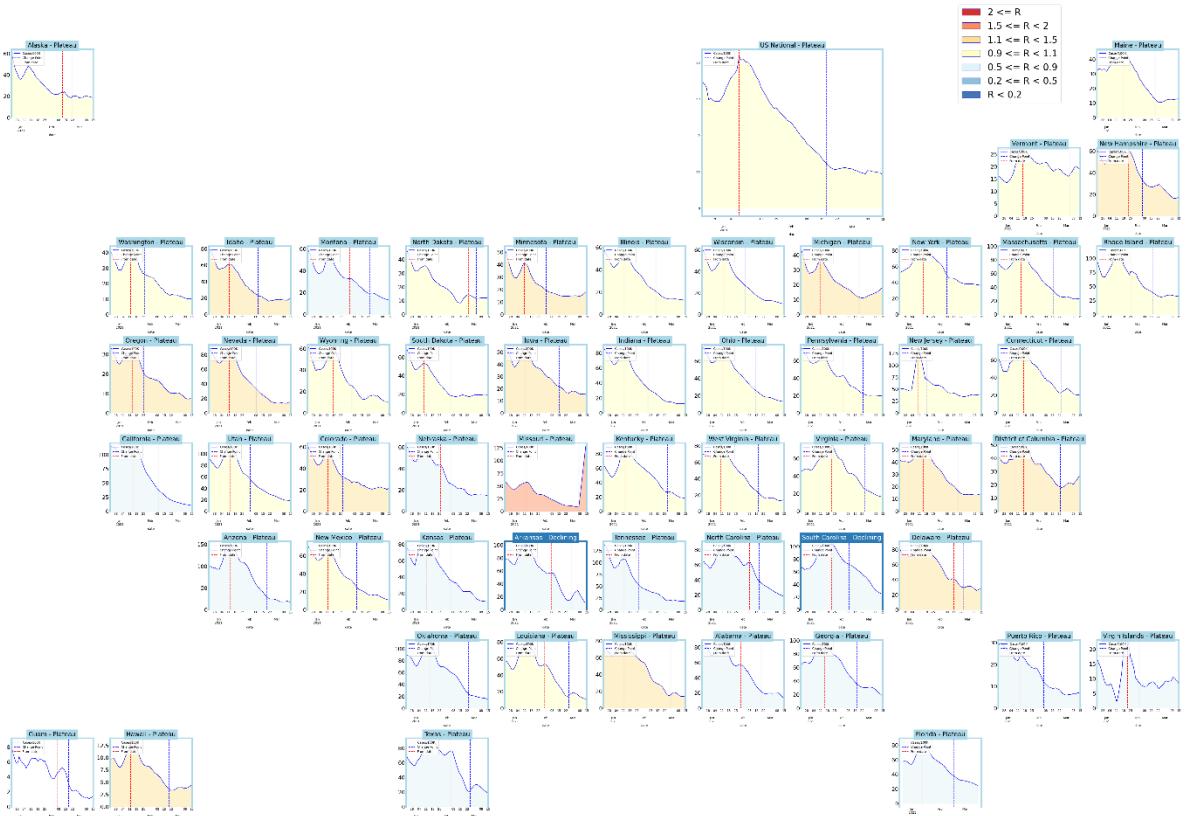
Weekly Point Prevalence vs Poverty Rate (Weighted)



Total cumulative cases from Zip codes with different levels of poverty by population. This association may be stronger at the census tract level

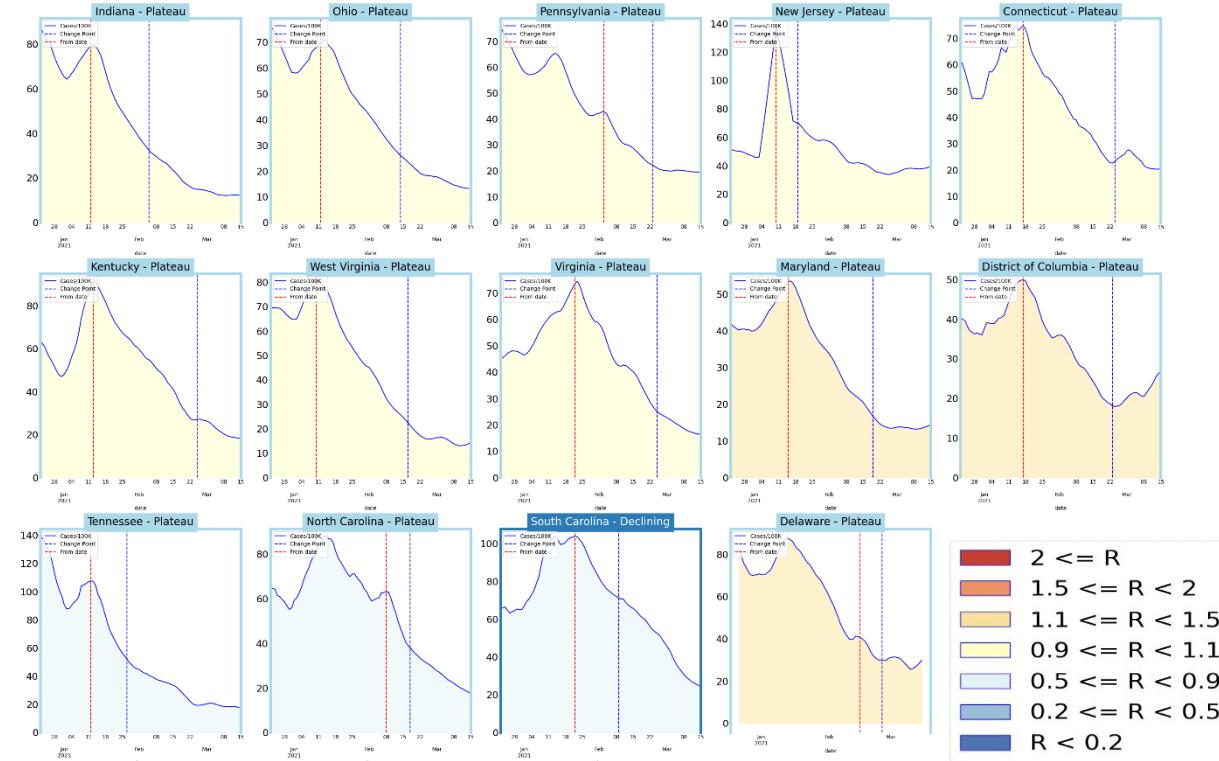
Other State Comparisons

Trajectories of States



- Nearly all states are plateaued (51) with a few declining (2)

Virginia and her neighbors



- VA shifted to plateau along with all but South Carolina
- Rates remain elevated and several show trends toward very slow growth

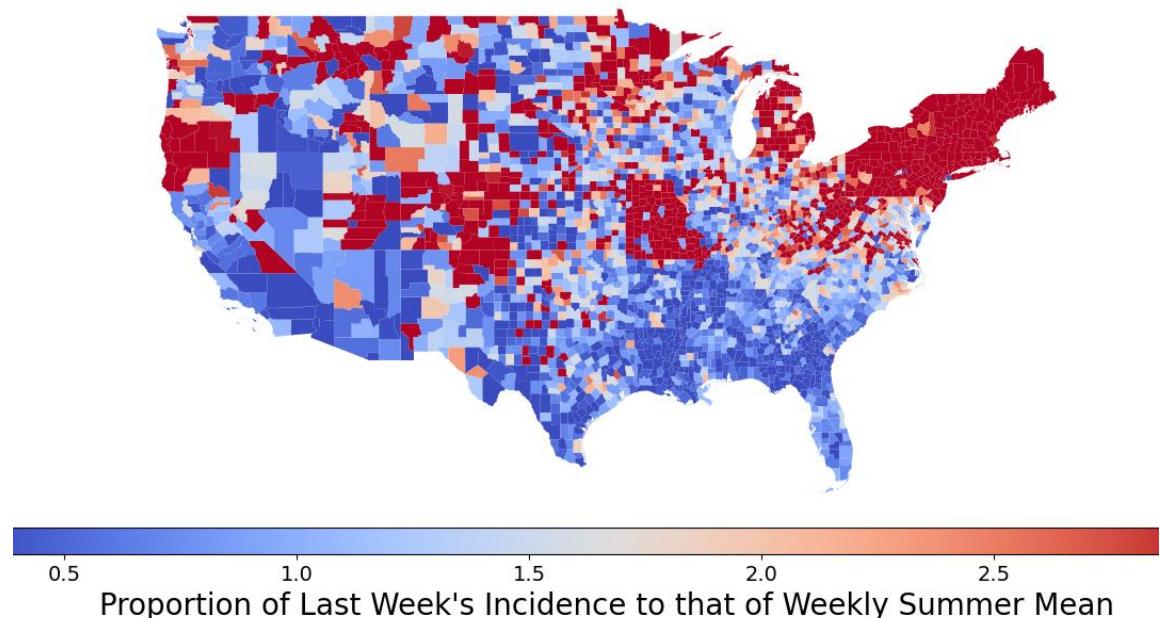


UNIVERSITY OF VIRGINIA

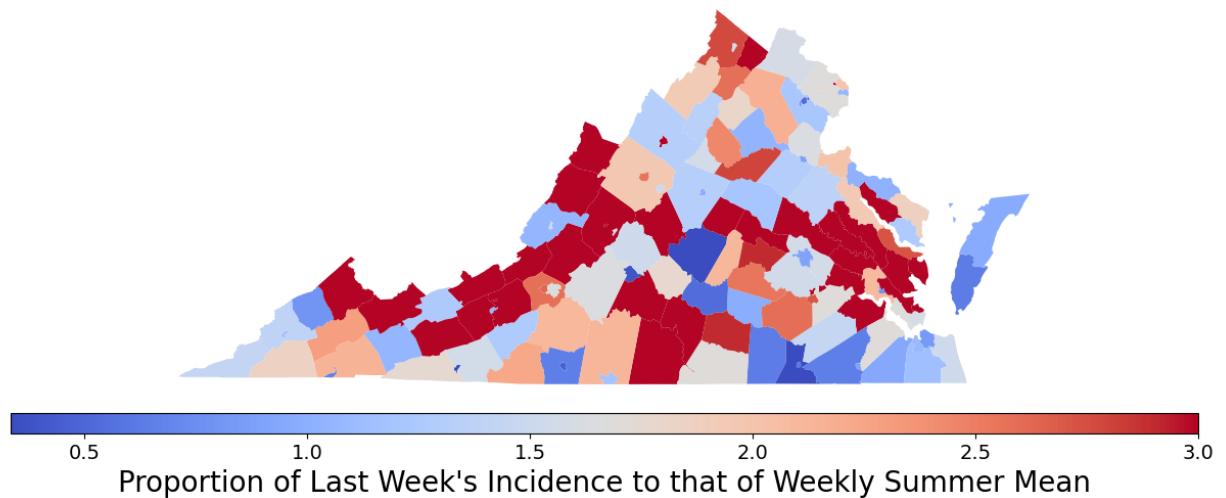
Current Week vs. Summer Mean (June-Aug 2020)

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

Recent Incidence Compared to Weekly Summer Mean by County
Mean: 10.94; Median: 1.28; IQR: 0.6-2.84



Recent Incidence Compared to Weekly Summer Mean by County
Mean: 2.37; Median: 1.7; IQR: 1.18-2.98



- 59% of US counties are above the summer mean case rate compared to 63% last week
- 82% of VA counties are above the average rate for the summer compared to 88% last week

Zip code level weekly Case Rate (per 100K)

Case Rates in the last week by zip code

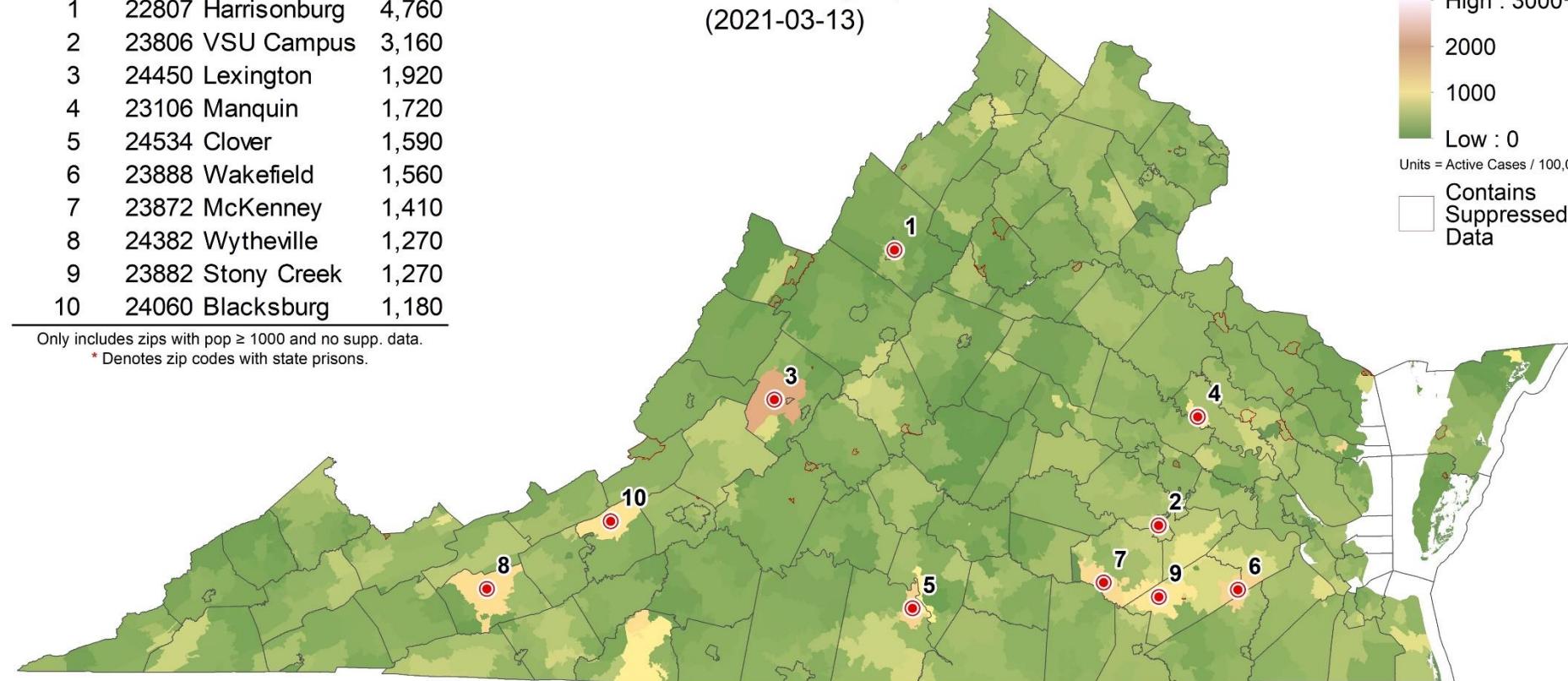
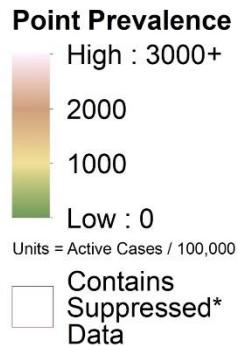
- Universities still dominate the top 10 list
- Concentrations of high rates scattered across the Commonwealth
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code	Name	Prev
1	22807	Harrisonburg	4,760
2	23806	VSU Campus	3,160
3	24450	Lexington	1,920
4	23106	Manquin	1,720
5	24534	Clover	1,590
6	23888	Wakefield	1,560
7	23872	McKenney	1,410
8	24382	Wytheville	1,270
9	23882	Stony Creek	1,270
10	24060	Blacksburg	1,180

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

* Denotes zip codes with state prisons.

Point Prevalence by Zip Code
(2021-03-13)



Based on Spatial Empirical Bayes smoothed point prevalence for week ending 2021-03-13



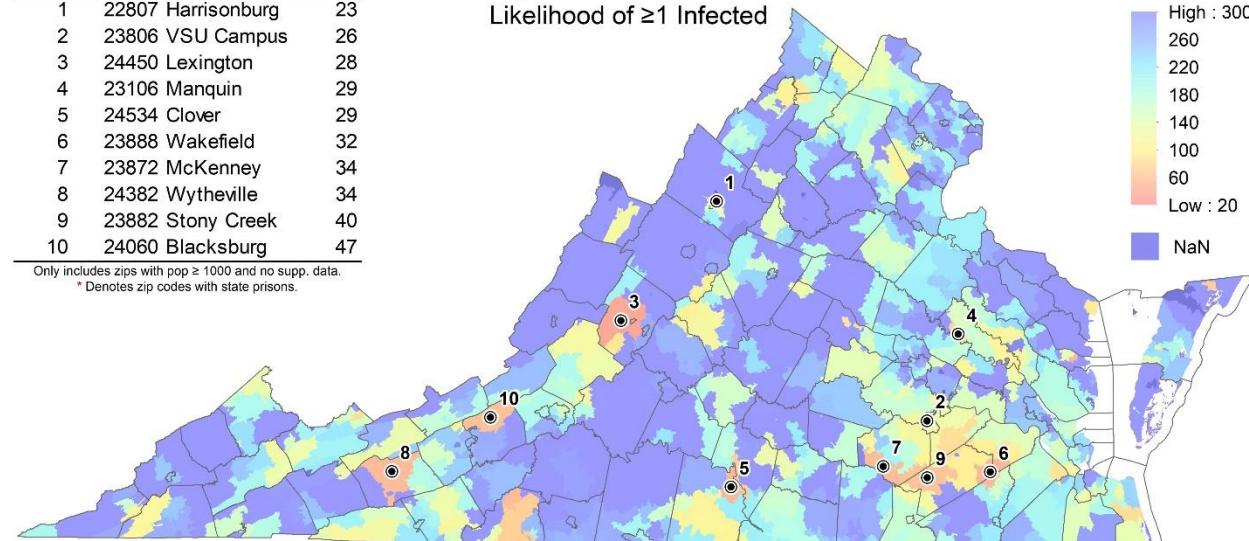
Risk of Exposure by Group Size

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)

- Assumes 3 undetected infections per confirmed case (ascertainment rate from recent seroprevalence survey)
- On left, minimum size of a group with a 50% chance an individual is infected by zip code (eg in a group of 23 in Harrisonburg, there is a 50% chance someone will be infected)
- Some zip codes have high likelihood of exposure even in groups of 25

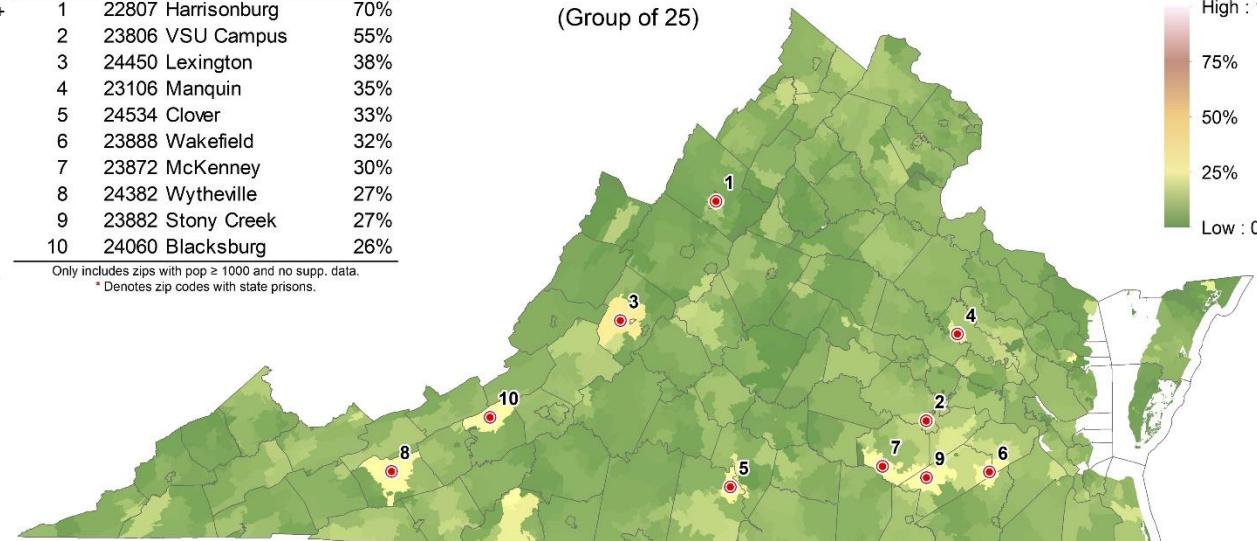
Rank	Zip Code Name	Size
1	22807 Harrisonburg	23
2	23806 VSU Campus	26
3	24450 Lexington	28
4	23106 Manquin	29
5	24534 Clover	29
6	23888 Wakefield	32
7	23872 McKenney	34
8	24382 Wytheville	34
9	23882 Stony Creek	40
10	24060 Blacksburg	47

Group Size Needed for 50% Likelihood of ≥ 1 Infected



Group Size	Rank	Zip Code Name	Likelihood
High : 300+	1	22807 Harrisonburg	70%
260	2	23806 VSU Campus	55%
220	3	24450 Lexington	38%
180	4	23106 Manquin	35%
140	5	24534 Clover	33%
100	6	23888 Wakefield	32%
60	7	23872 McKenney	30%
Low : 20	8	24382 Wytheville	27%
NaN	9	23882 Stony Creek	27%
NaN	10	24060 Blacksburg	26%

Likelihood of ≥ 1 Infected Members (Group of 25)



Current Spatial Hot Spots

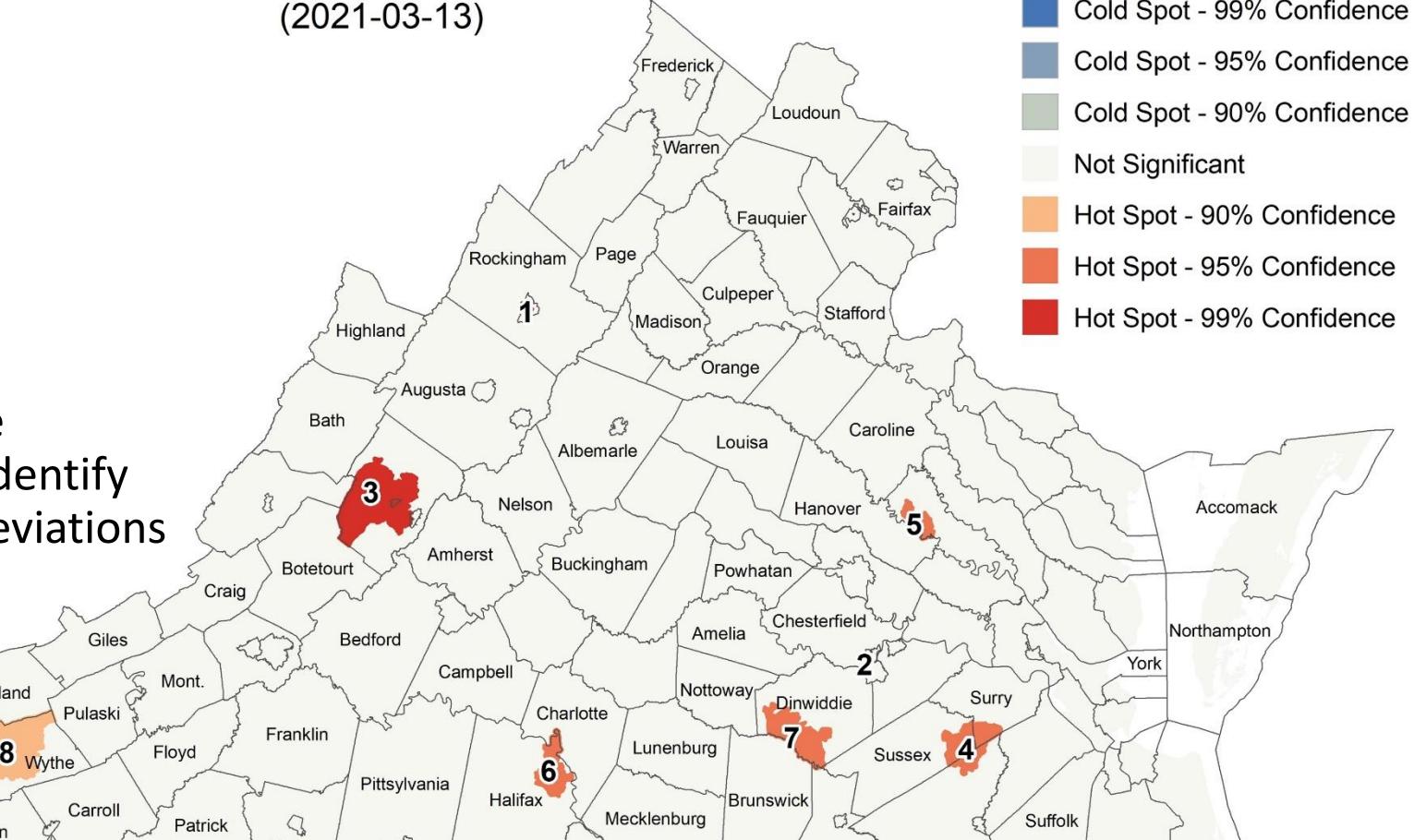
Spot	Zip Code	Name	Conf.
1	22807	Harrisonburg	99%
2	23806	VSU Campus	99%
3	24450	Lexington	99%
4	23888	Wakefield	95%
5	23106	Manquin	95%
6	24534	Clover	95%
7	23872	McKenney	95%
8	24382	Wytheville	90%

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

* Denotes zip codes with state prisons.

Hot Spots compare the weekly case prevalence to nearby zip codes to identify areas with statistically significant deviations

Point Prevalence Hot Spots by Zip Code
(2021-03-13)



Based on Global Empirical Bayes smoothed point prevalence for week ending 2021-03-13



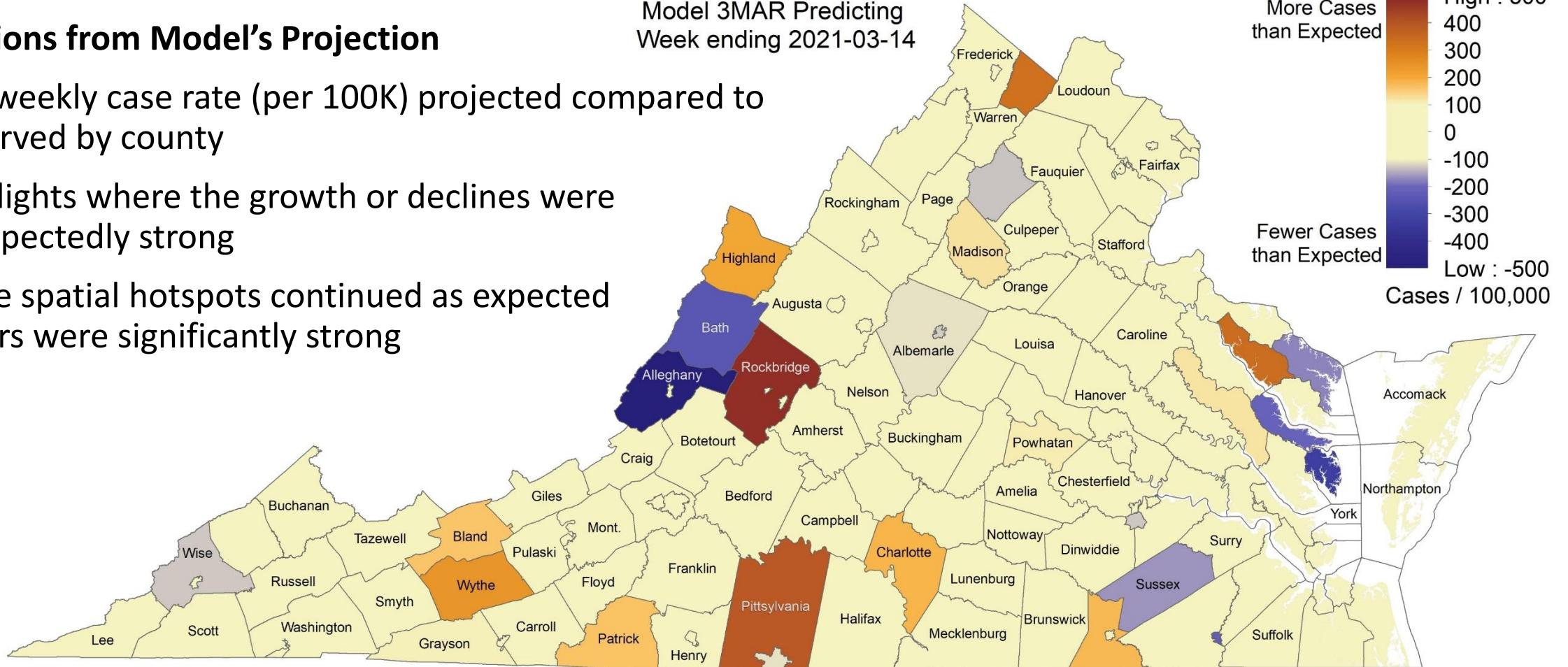
Temporal Hot Spots – Model Deviations

Deviations from Model's Projection

- The weekly case rate (per 100K) projected compared to observed by county
- Highlights where the growth or declines were unexpectedly strong
- Some spatial hotspots continued as expected others were significantly strong

Weekly Point Prevalence Model Residuals

Model 3MAR Predicting
Week ending 2021-03-14



Model Update – Adaptive Fitting



Adaptive Fitting Approach

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

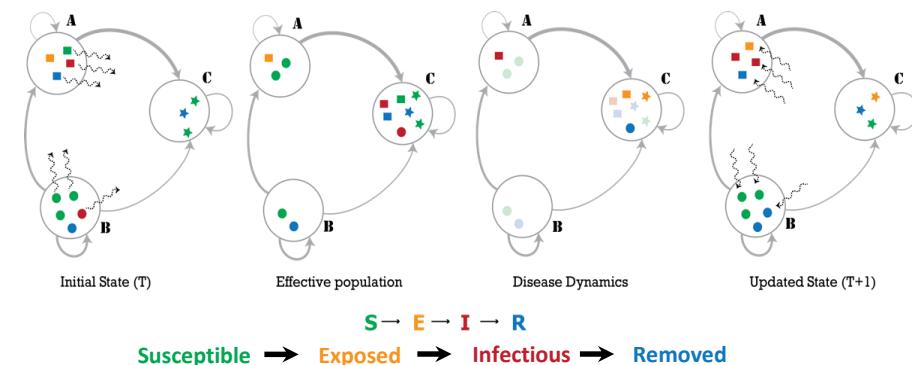
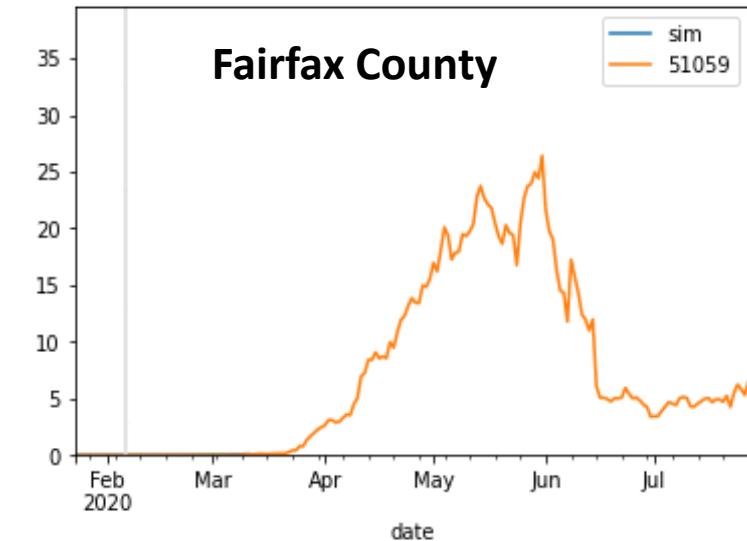
- Allows history to be precisely captured, and used to guide bounds on projections

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



Using Ensemble Model to Guide Projections

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

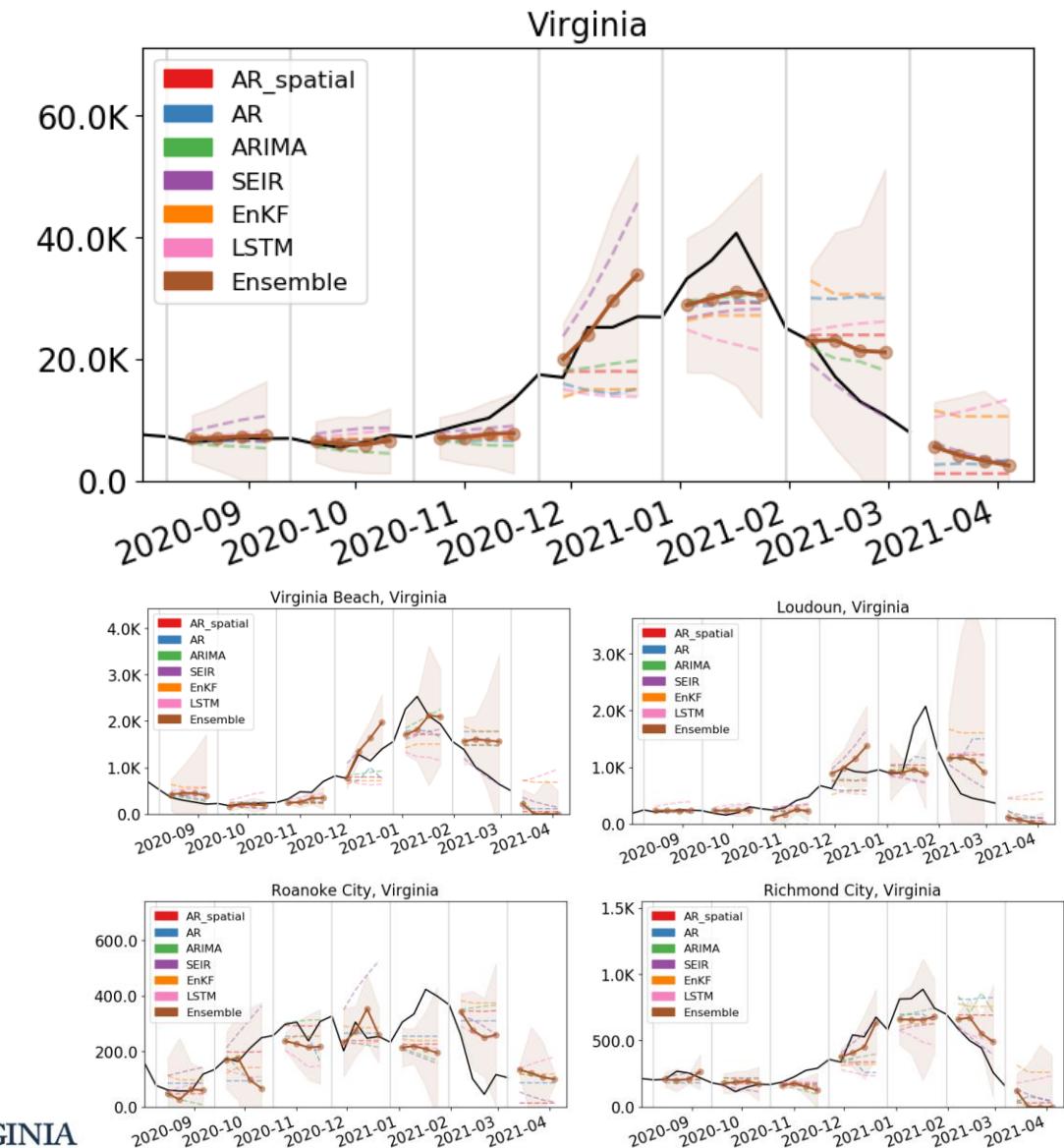
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

Weekly forecasts 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.



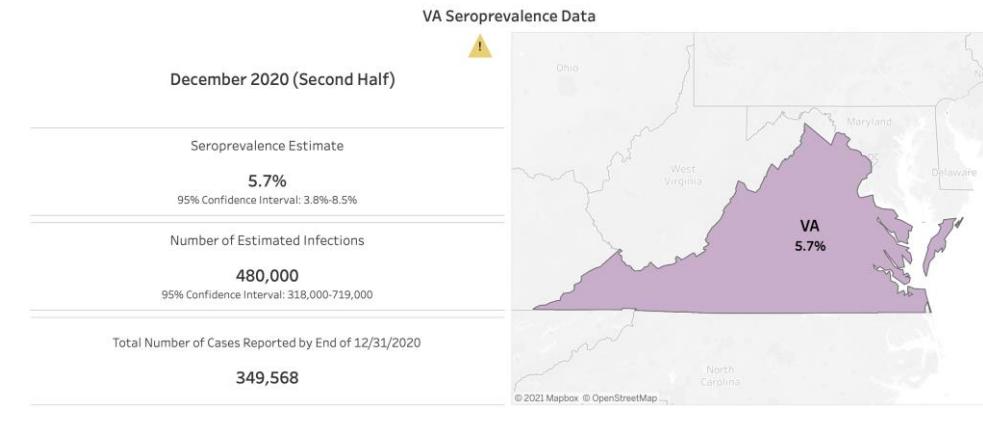
Seroprevalence updates to model design

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 ascensions 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:

Cases, Hospitalizations and Deaths					
Total Cases*			Total Hospitalizations**	Total Deaths	
598,468			25,517	10,154	
(New Cases: 1,327) [†]	Confirmed†	Probable†	Confirmed†	Probable†	Confirmed†
	470,403	128,065	24,233	1,284	8,470
					Probable†
					1,684

* 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://www.cdc.gov/nndss/conditions/coronavirus-disease-2019-covid-19/case-definition/2020/08/05/>

Outbreaks	
Total Outbreaks*	Outbreak Associated Cases
2,750	67,414

* 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**
6,220,455	5.4%

* 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
44	0

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

Accessed 9:15am March 17, 2021

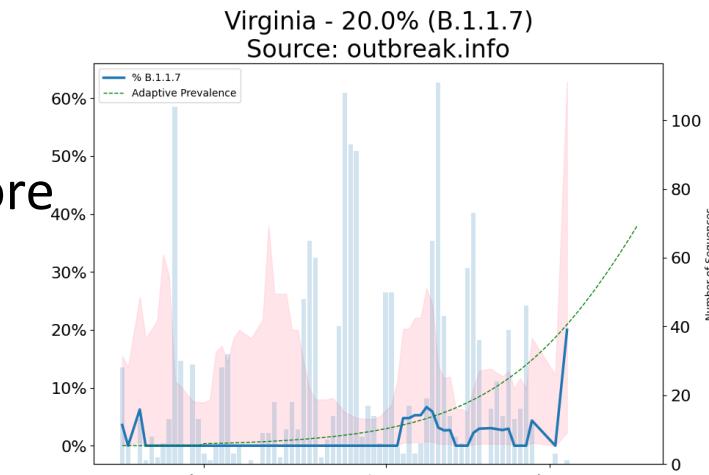
<https://www.vdh.virginia.gov/coronavirus/>

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 – Novel Variants

- Several novel variants of SARS-CoV2 are being tracked
 - Some are more transmissible, some may escape immunity from previous natural infection and/or vaccination, others may be more severe
- 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
 - **Emergence timing:** Gradually assumes predominance over the next 2 weeks, reaching 50% frequency in late March as estimated in a recent [MMWR report from CDC](#) and refined by [Andersen et al.](#).
- Variant planning Scenario:
 - **VariantB117:** Current projected transmissibility continues to increase gradually over 2 months to level 50% more transmissible



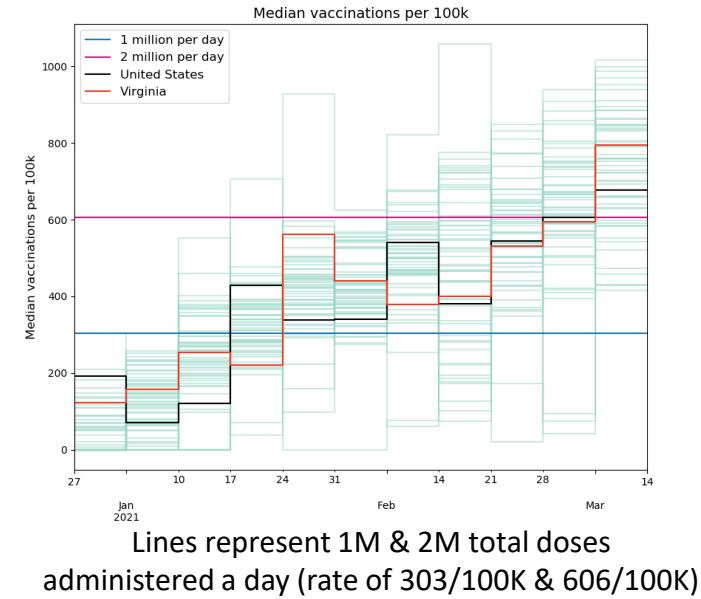
Estimated frequency from public genome repository with added analysis: 20%
Current frequency used in model: 35%



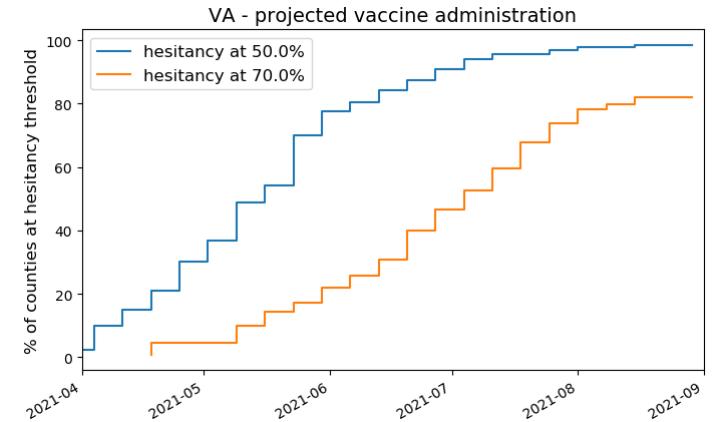
Scenarios – Vaccines

- Vaccination is well underway and accelerating its pace
- Vaccine efficacy varies over course of vaccine
 - FDA EUAs show 50% efficacy achieved 2 weeks after 1st dose, and 95% 2 weeks after 2nd dose
 - Assuming 3.5 week (average of Pfizer and Moderna) gap between doses
 - Johnson & Johnson included with 70% efficacy 2 weeks after 1st (and only) dose
- Accelerated administration pace will reach vaccine hesitancy thresholds more quickly
 - Demand still outpaces supply
 - Estimate based on current rates that some counties may reach thresholds as soon as late April, with potentially half by mid July

VA Vaccination Rates



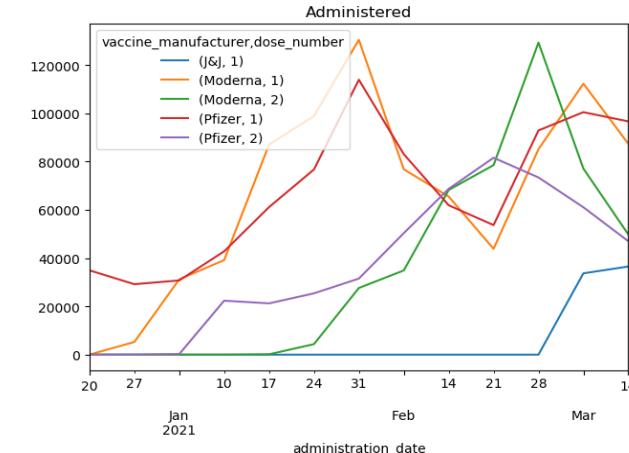
Anticipated Vax Hesitancy Impact



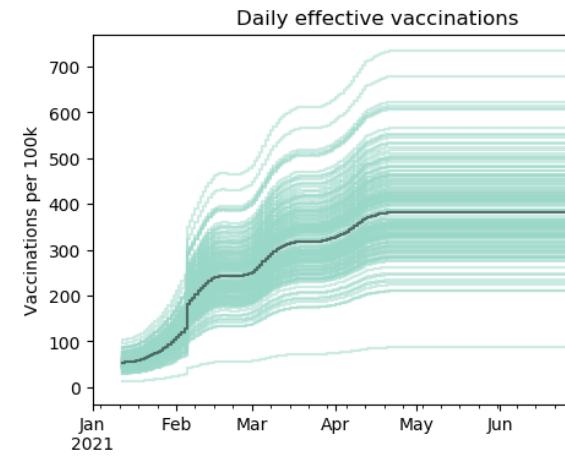
Scenarios – Vaccines

- Administration schedule uses reported administrations and anticipated supplies to generate vaccine schedule (past and future)
 - Data from [VDH](#) used to assess county level variations and dosage (these data are in data package)
- Current administration rate used as baseline courses with **future supplies estimated to have a 30% increase**
 - **Rate:** 400 FIRST DOSES per 100K per day
 - Total of ~40K 1st doses / day, ~30% increase over current rate
 - **Total Administrations:** This pace leads to eventually reaching 64K administered a day, implying 32K fully vaccinated a day
 - **Location:** Per capita distribution across all counties

Weekly dose administrations



Modeled Vaccine Induced Immunity



All VA counties, state in black

Current rollouts and scenarios inspired by MIDAS Network COVID-19 Scenario Hub: <https://github.com/midas-network/covid19-scenario-modeling-hub>

Scenarios – Seasonal Effects and Vaccines

Three scenarios combine these seasonal effects and use the accelerated 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



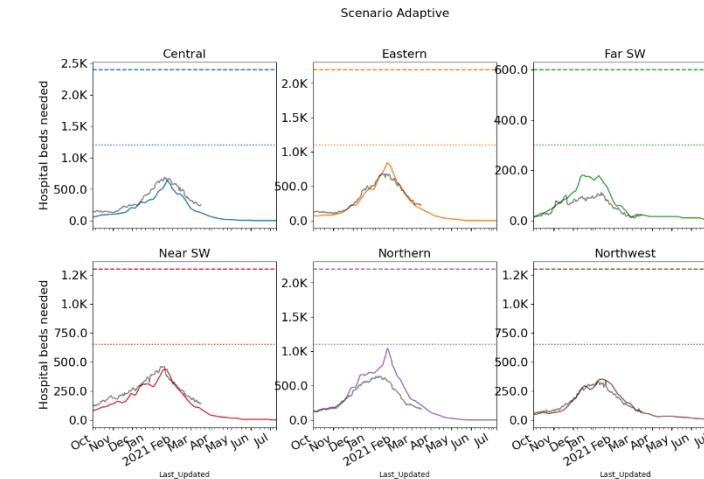
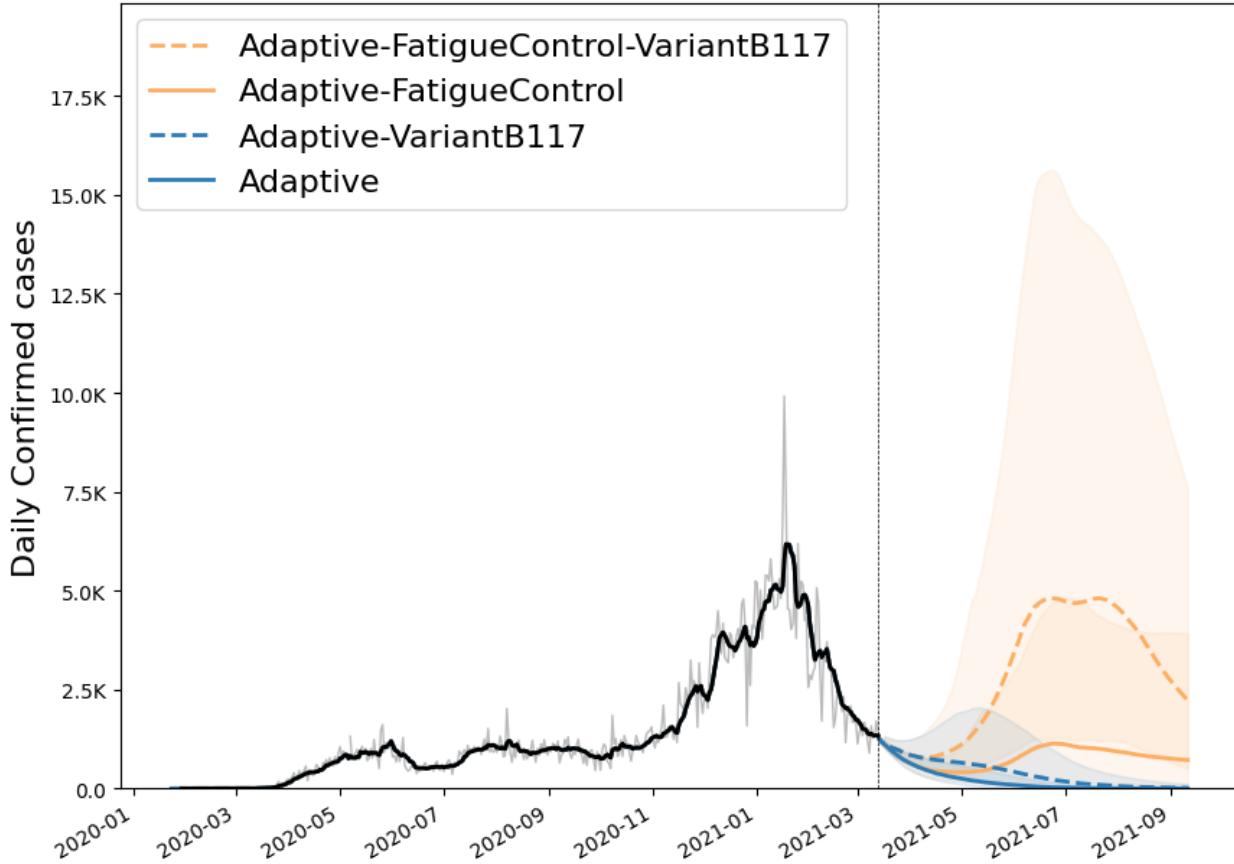
BIOCOMPLEXITY INSTITUTE

Outcome Projections

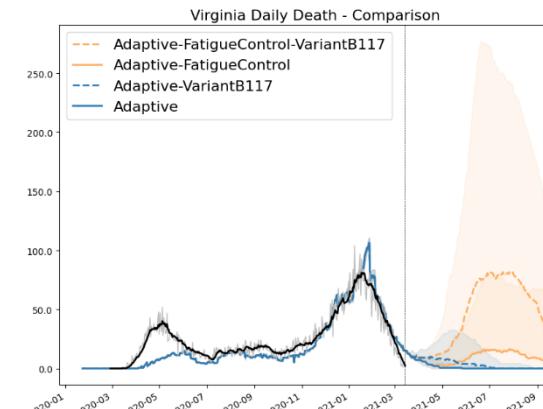
Estimated Hospital Occupancy

Confirmed cases

Virginia Daily Confirmed - Comparison

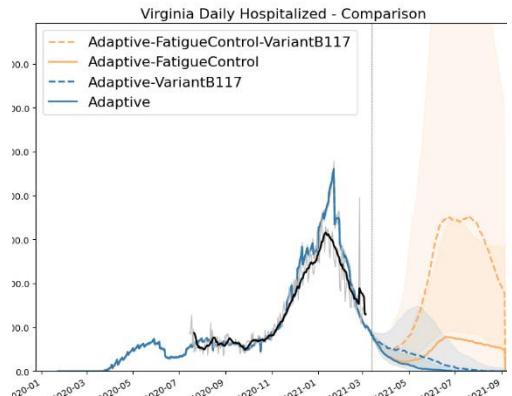


Daily Deaths



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

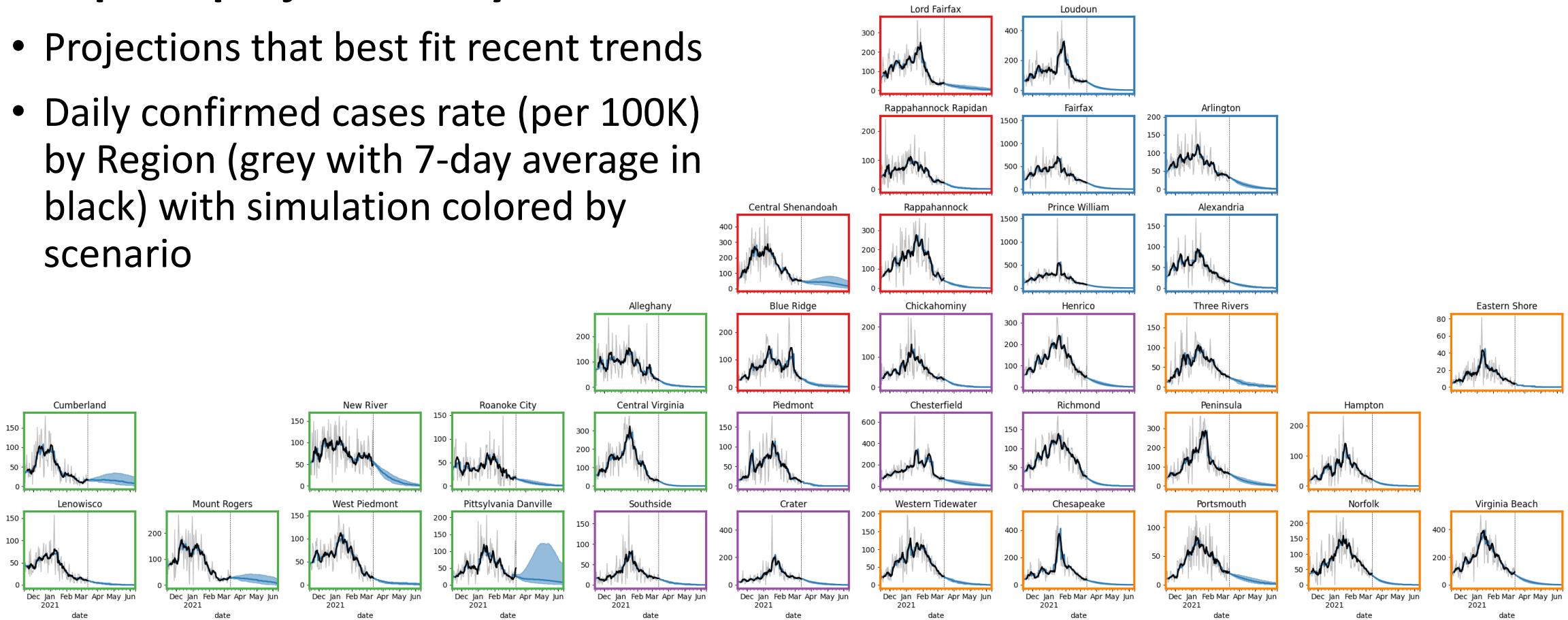
Daily Hospitalized



District Level Projections: Adaptive

Adaptive projections by District

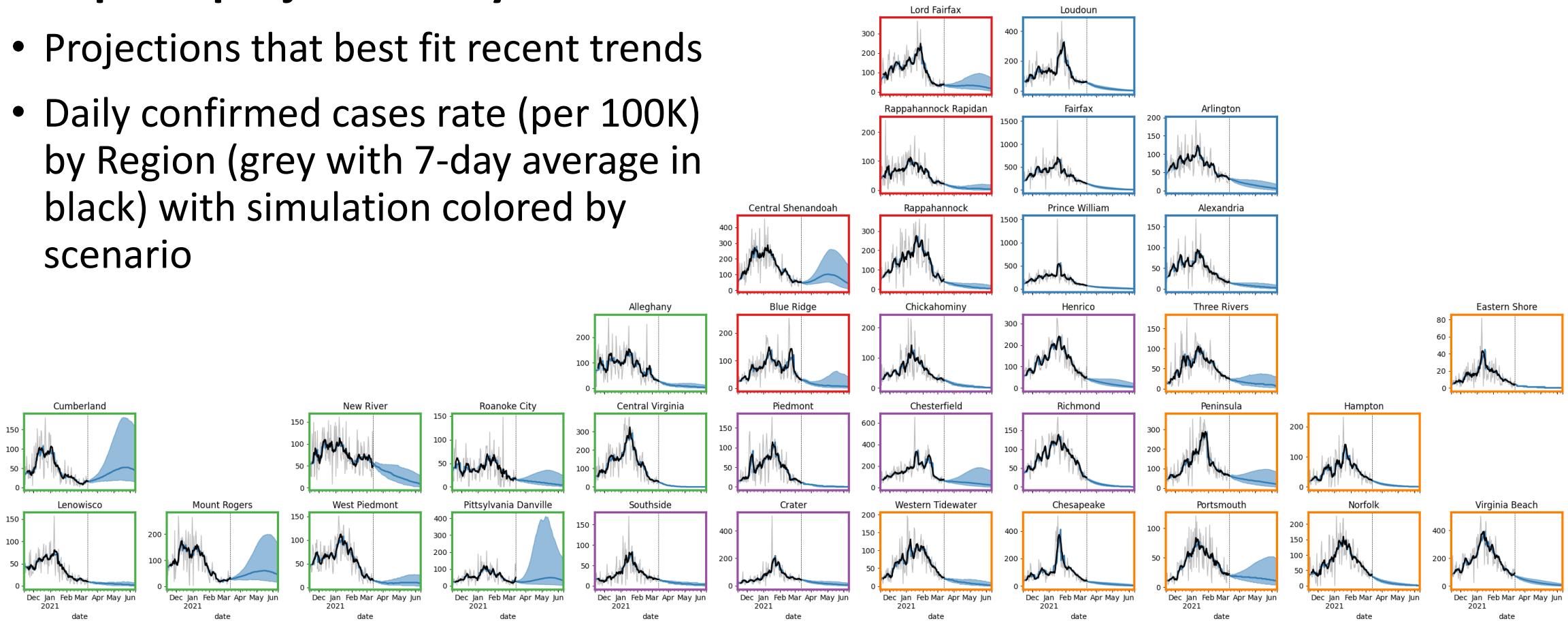
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-VariantB117

Adaptive projections by District

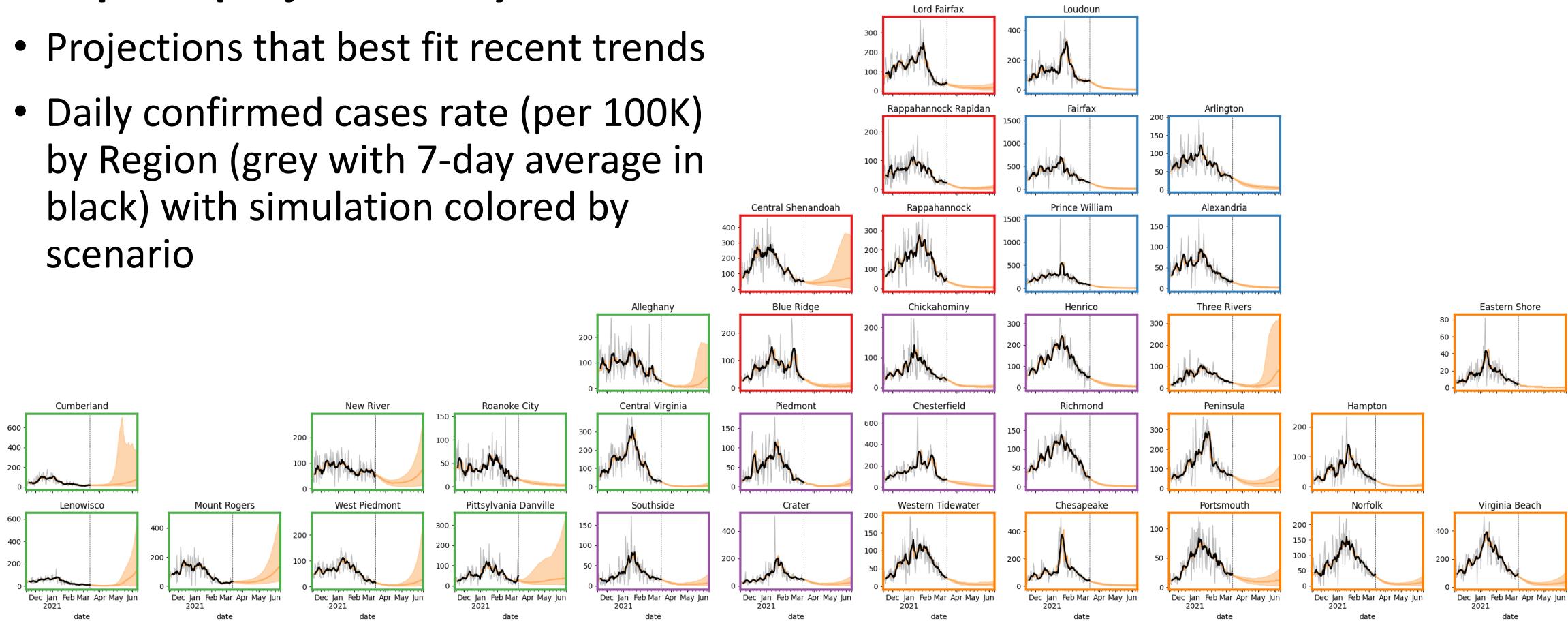
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-FatigueControl

Adaptive projections by District

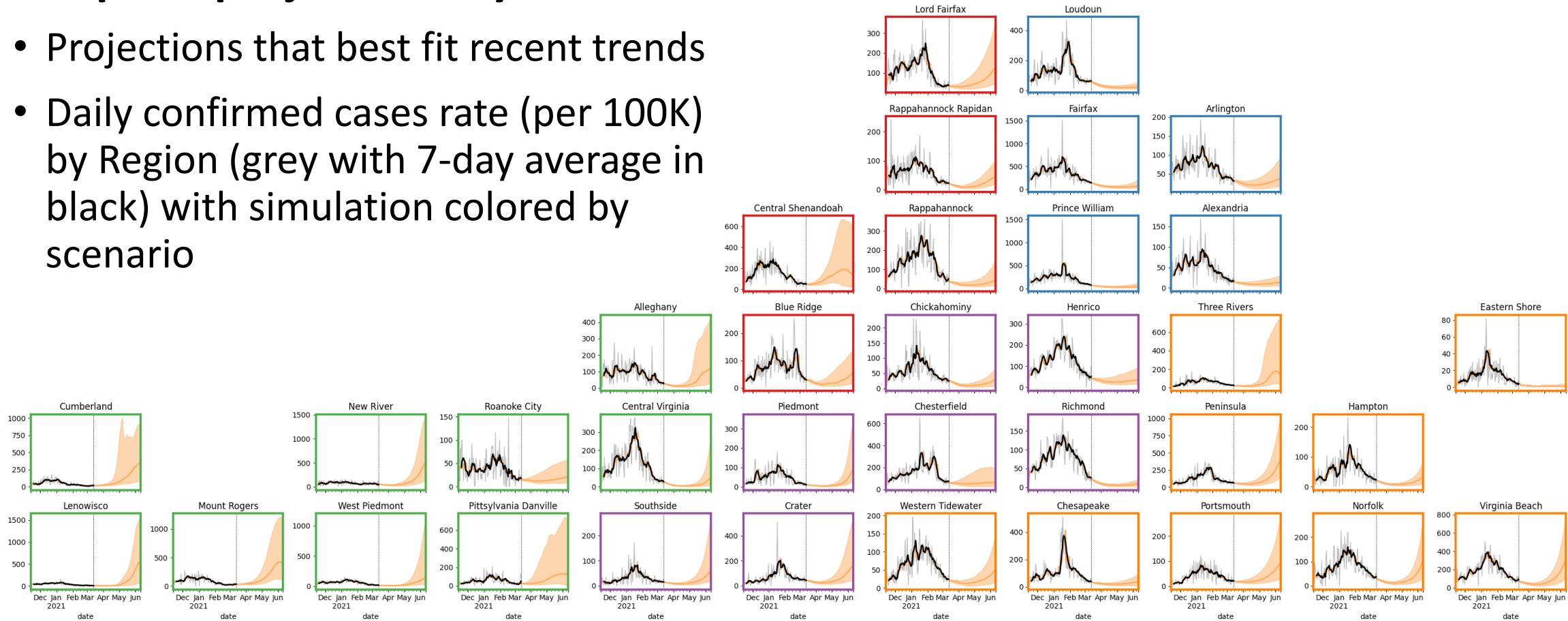
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-FatigueControl-VariantB117

Adaptive projections by District

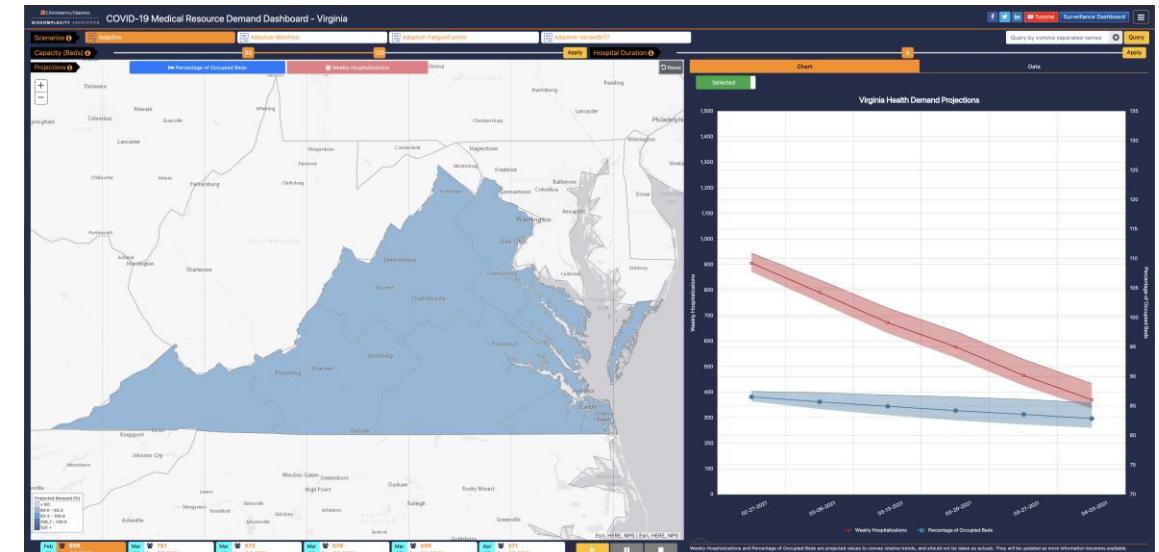
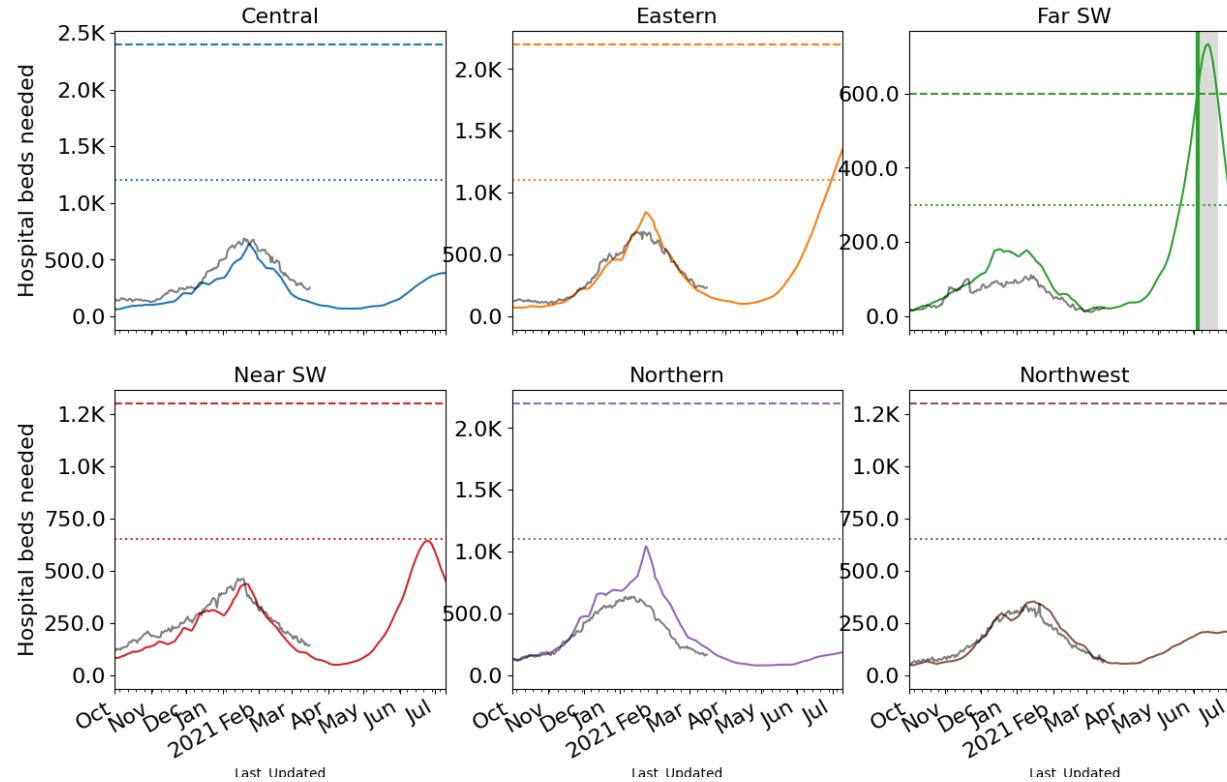
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



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:

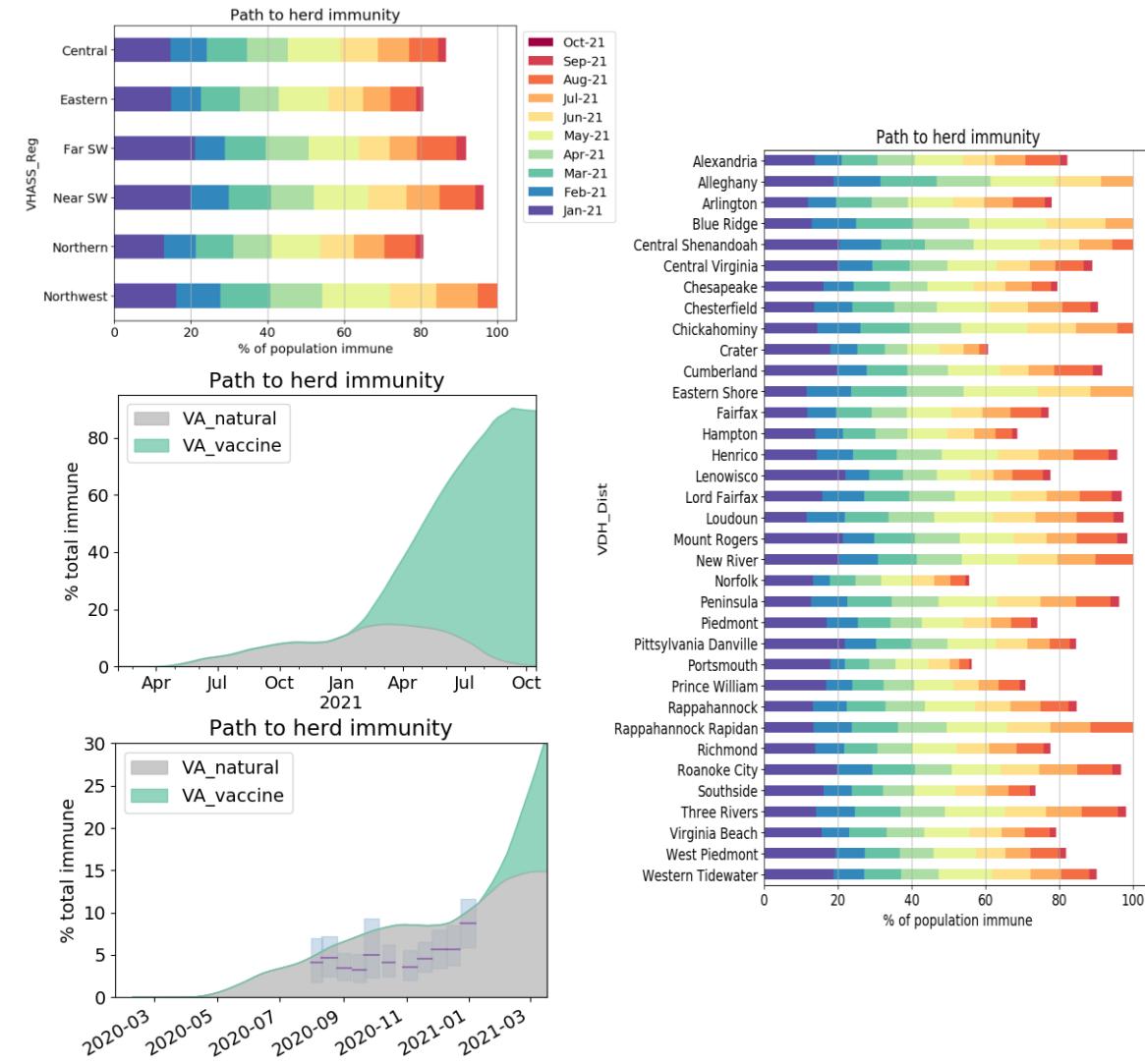
- Far SW may reach surge bed capacity in June
- Eastern, Near SW approach initial bed capacity in June as well

* 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

- Population level immunities above 75% (assuming even distribution in the population) will be effective for preventing significant outbreaks of COVID-19
- 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



Weekly Cases and Hospitalizations

Weekly confirmed cases

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-VariantB117	Adaptive-Fatigued Control -VariantB117
3/14/21	9,372	9,373	9,373	9,373
3/21/21	7,477	7,474	7,702	7,706
3/28/21	5,741	5,748	6,758	6,772
4/4/21	4,462	4,473	5,938	5,950
4/11/21	3,540	3,600	5,422	5,501
4/18/21	2,818	3,152	5,106	5,654
4/25/21	2,266	2,956	4,875	6,343
5/2/21	1,836	2,875	4,617	7,410
5/9/21	1,470	2,934	4,358	9,130
5/16/21	1,178	3,174	4,058	11,718
5/23/21	940	3,644	3,700	15,308
5/30/21	738	4,360	3,266	20,060

Weekly Hospitalizations

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-VariantB117	Adaptive-Fatigued Control -VariantB117
3/14/21	650	650	650	650
3/21/21	503	503	517	517
3/28/21	375	375	452	452
4/4/21	269	268	402	404
4/11/21	210	217	361	364
4/18/21	160	181	344	376
4/25/21	125	159	338	425
5/2/21	113	157	306	513
5/9/21	87	169	278	628
5/16/21	58	187	256	825
5/23/21	40	223	232	1,090
5/30/21	34	283	208	1,429



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 and show signs of flattening out**
- VA mean weekly incidence slightly down to 15/100K from 16/100K, US also down (to 16 from 19 per 100K)
- Significant progress made in last month, however 82% of VA counties above mean rate of Summer 2020
- Projections continue to be down but are flattening out across Commonwealth
- Recent updates:
 - Adjusted Seasonal Effects scenarios to account for spring and summer weather
 - Accelerated vaccine schedule with Johnson & Johnson added as base case in anticipation of boost in vaccine supplies
 - Adjustment to death outcome modeling rescaled based on date of death from VDH data, higher resolution hospital data incorporated for hospital calibration
- The situation is changing rapidly. 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> (Accessed on 04/10/2020).

Virginia Department of Health. COVID-19 in Virginia. <http://www.vdh.virginia.gov/coronavirus/> (Accessed on 04/10/2020)

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?

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



UNIVERSITY OF VIRGINIA

BIOCOMPLEXITY INSTITUTE

Supplemental Slides



BIOCOMPLEXITY INSTITUTE

Date of Onset Reproductive Number

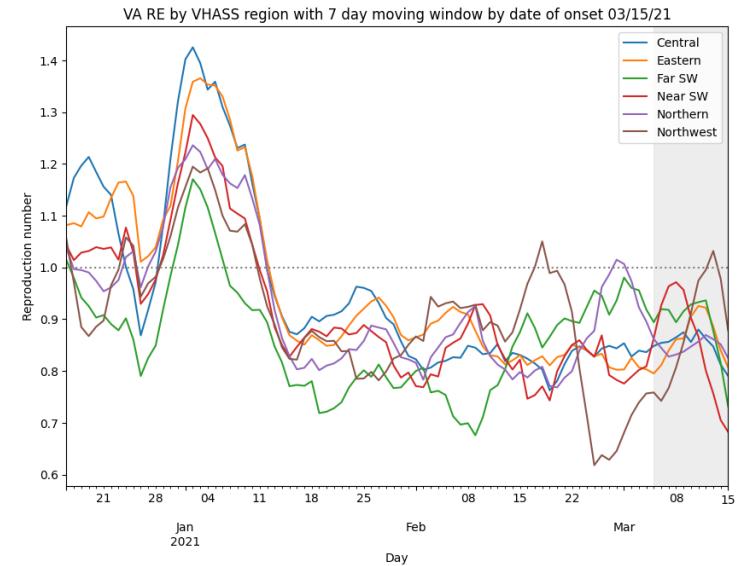
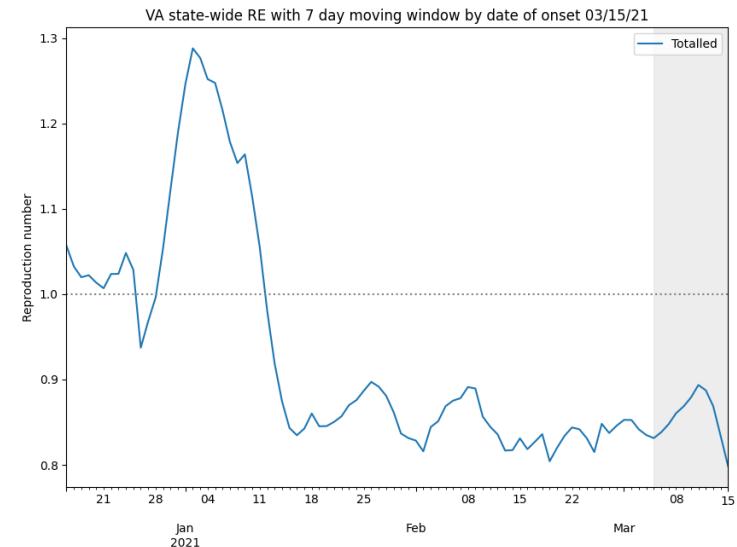
Mar 6th Estimates

Region	Date of Onset	Date Onset Diff
	R _e	Last Week
State-wide	0.838	0.028
Central	0.854	0.016
Eastern	0.811	0.065
Far SW	0.919	0.042
Near SW	0.926	0.095
Northern	0.844	-0.100
Northwest	0.742	0.114

Methodology

- Wallinga-Teunis method (EpiEstim¹) for cases by date of onset
- Serial interval: 6 days (2 day std dev)
- Recent estimates may be unstable due to backfill

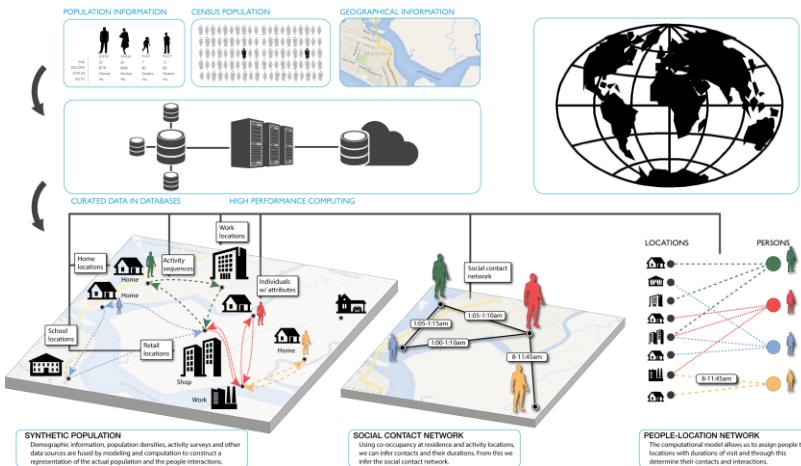
1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512,
<https://doi.org/10.1093/aje/kwt133>



Agent-based Model (ABM)

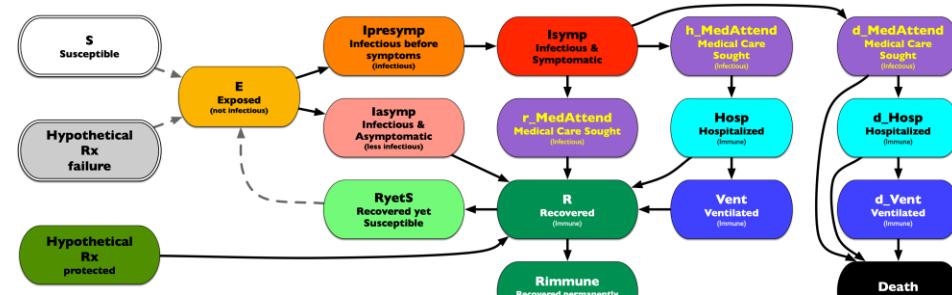
EpiHiper: Distributed network-based stochastic disease transmission simulations

- 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

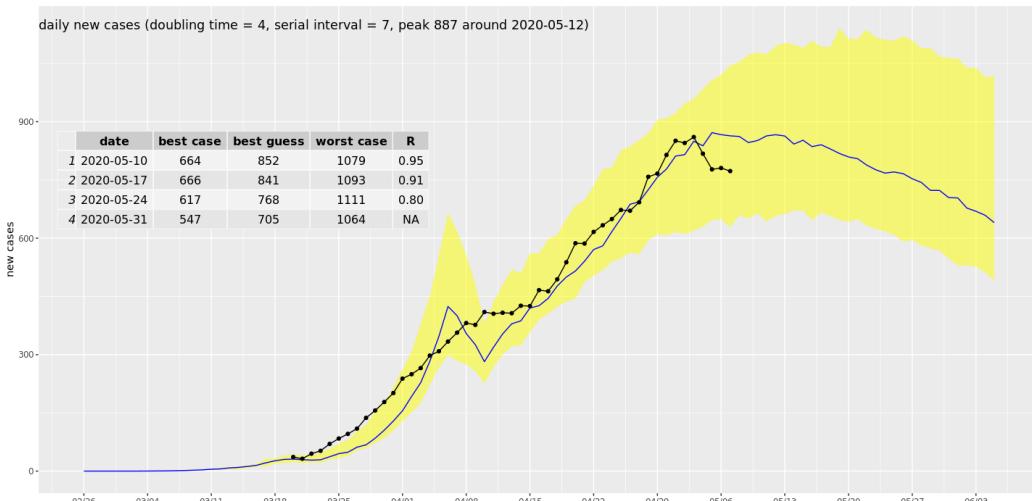


UNIVERSITY OF VIRGINIA

ABM Social Distancing Rebound Study Design

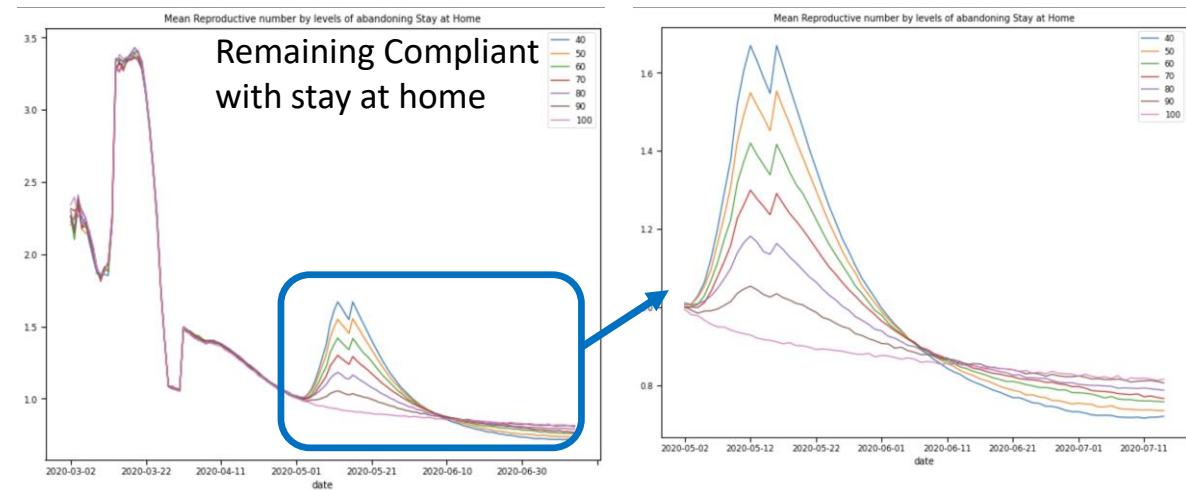
Study of "Stay Home" policy adherence

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



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