

Network Systems  
Science & Advanced  
Computing  
  
Biocomplexity Institute  
& Initiative  
  
University of Virginia

# Estimation of COVID-19 Impact in Virginia

February 17<sup>th</sup>, 2021

(data current to February 15<sup>th</sup> – 16<sup>th</sup>)

Biocomplexity Institute Technical report: TR 2021-020



---

**BIOCOMPLEXITY INSTITUTE**

[biocomplexity.virginia.edu](http://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](mailto:brylew@virginia.edu)

Srini Venkatramanan  
[srini@virginia.edu](mailto:srini@virginia.edu)

Madhav Marathe  
[marathe@virginia.edu](mailto:marathe@virginia.edu)

Chris Barrett  
[ChrisBarrett@virginia.edu](mailto: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 rate growth in Virginia continues to decline with a few hotspots emerging**
- VA mean weekly incidence down to 34/100K from 39/100K, US levels decline (to 23 from 29 per 100K)
- Case rates are still high, over a quarter of VA counties above half of their peak
- Projections are down across Commonwealth, though several districts are notably up
- Recent updates:
  - Variant B.1.1.7 scenarios included and added to control-based scenarios
  - Further updates to vaccination schedules, with fitting now including partially vaccinated population and future vaccinations based on current levels instead of goals
- The situation is changing rapidly. Models continue to be updated regularly.



# Situation Assessment

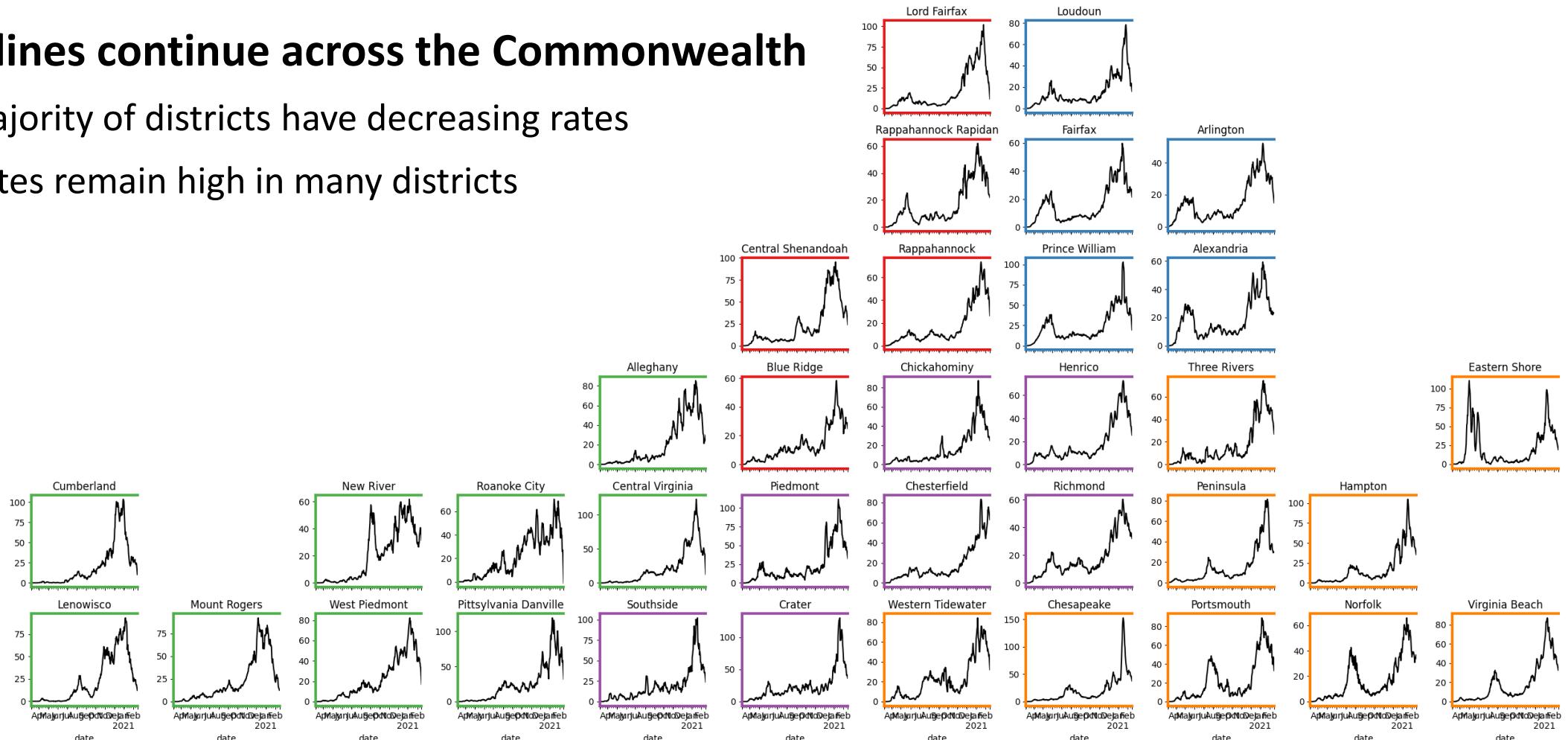
---



# Case Rate (per 100k) by VDH District

## Declines continue across the Commonwealth

- Majority of districts have decreasing rates
- Rates remain high in many districts

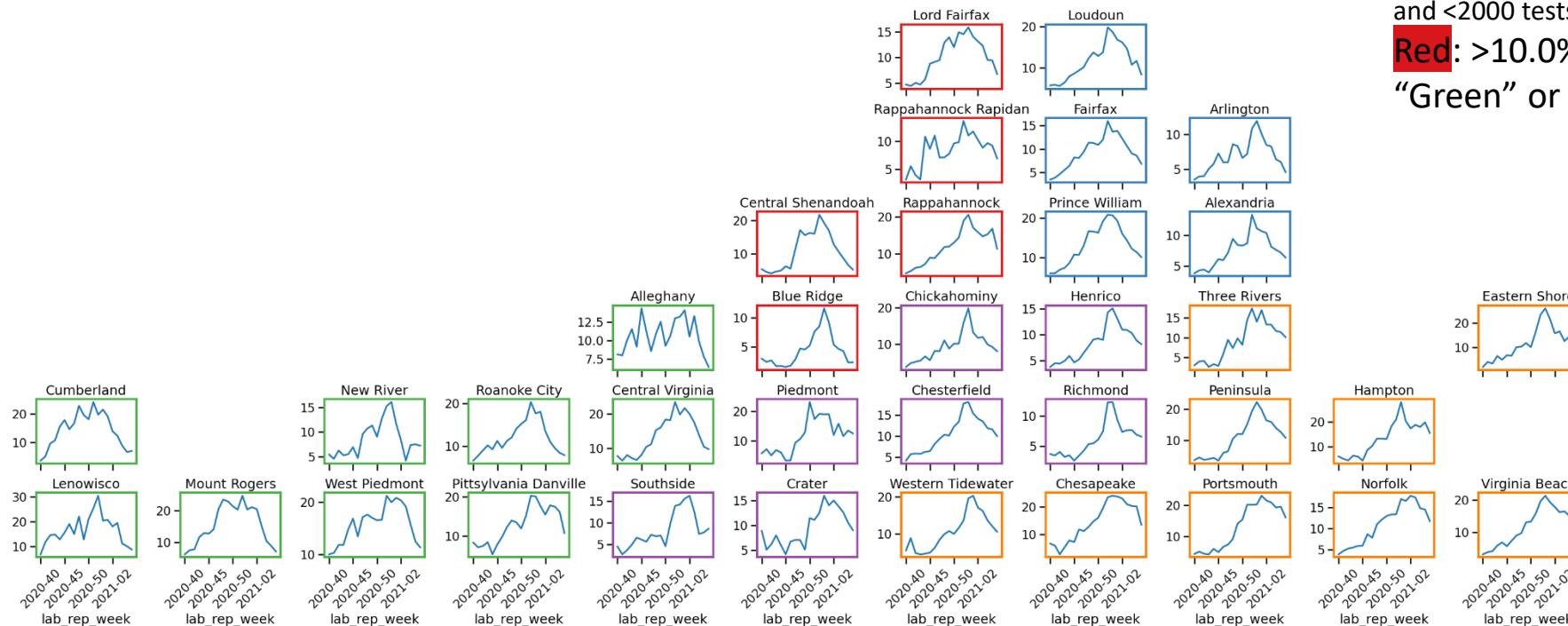


UNIVERSITY OF VIRGINIA

# Test Positivity by VDH District

## Weekly changes in test positivity by district

- Rates continue to decline
- Back to less than half of counties over 10% (as of Feb 10<sup>th</sup>)

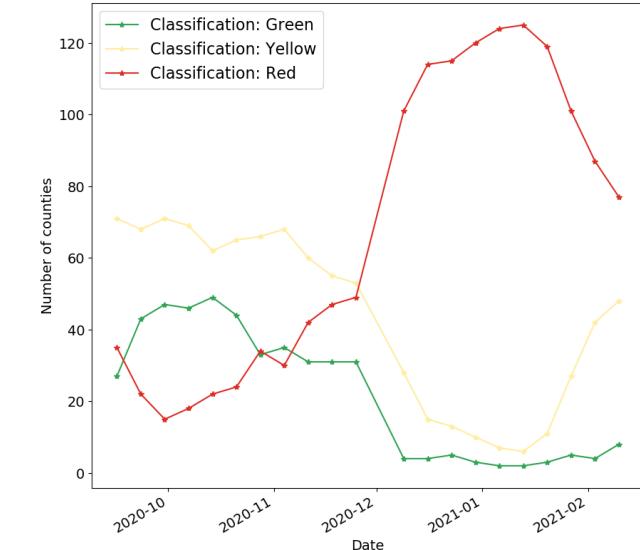


## County level test positivity rates for RT-PCR tests.

**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”

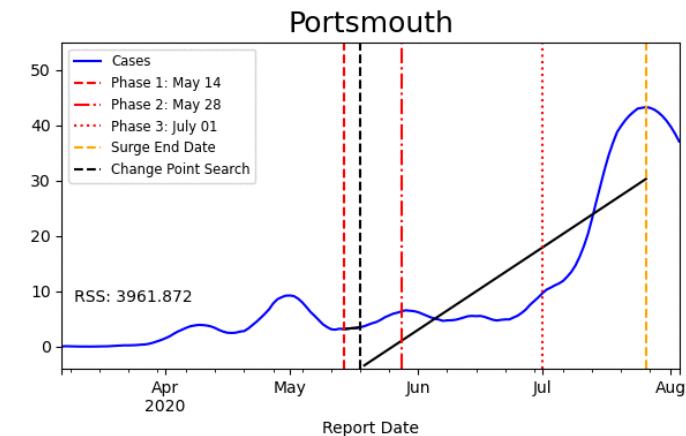


# District Trajectories

**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



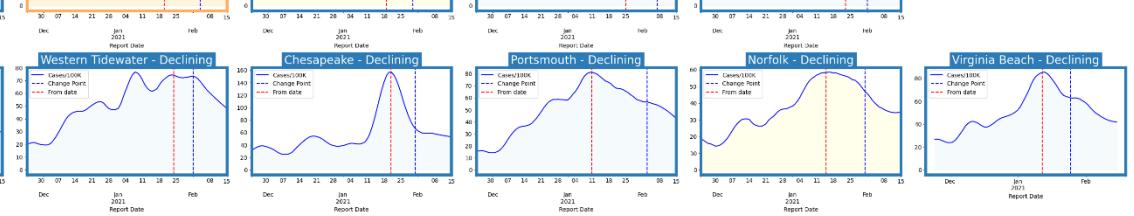
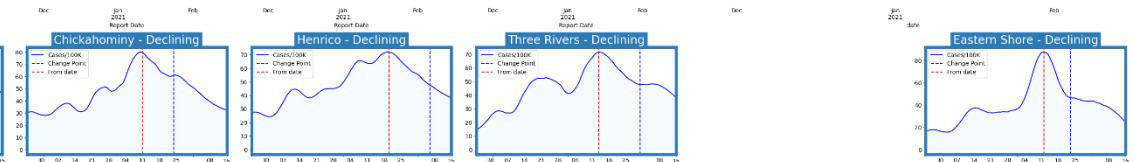
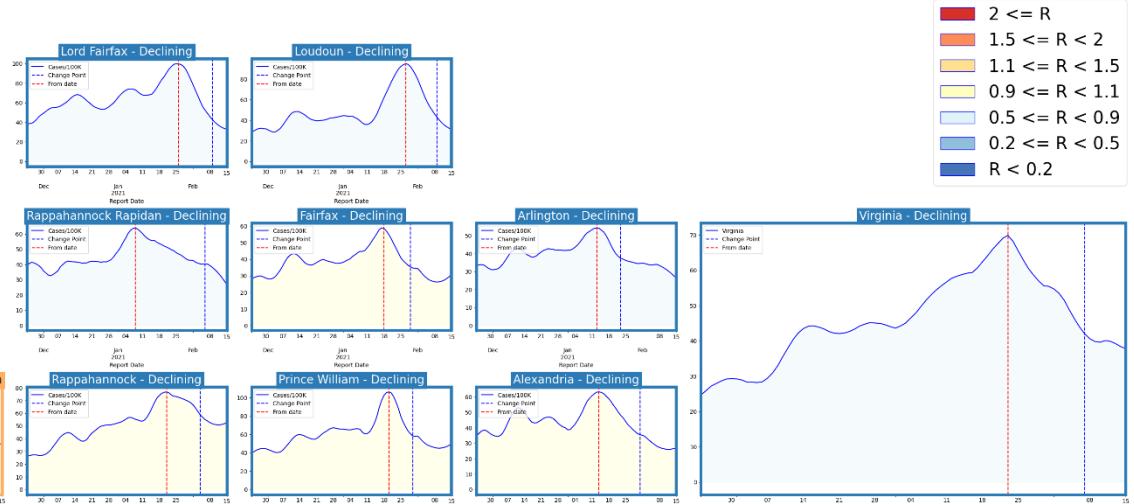
Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	30 (33)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	1 (0)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	4 (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	30 (33)
Plateau	1 (0)
Slow Growth	4 (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



# Estimating Daily Reproductive Number

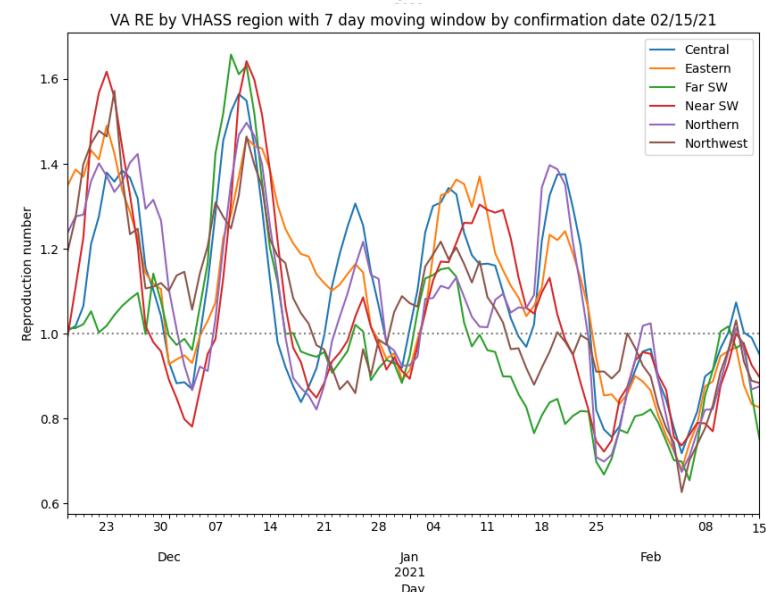
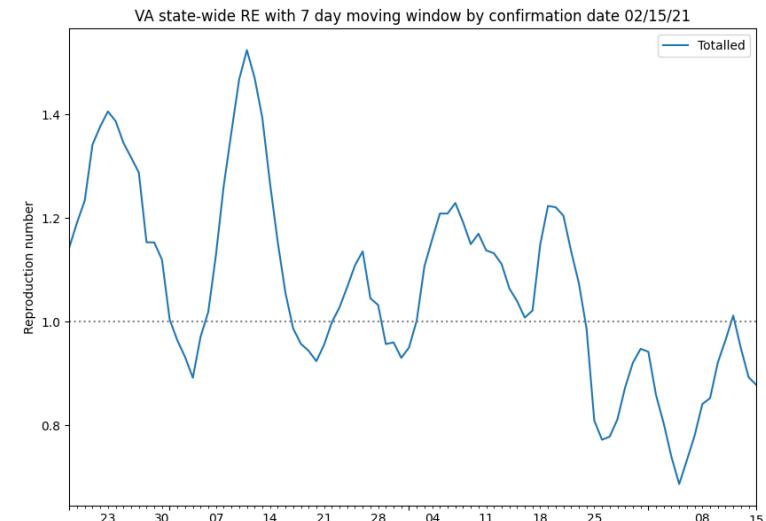
Feb 15<sup>th</sup> Estimates

Region	Date Confirmed	Date Confirmed R <sub>e</sub>	Diff Last Week
State-wide	0.878	0.098	
Central	0.951	0.135	
Eastern	0.826	0.039	
Far SW	0.752	0.013	
Near SW	0.897	0.108	
Northern	0.875	0.107	
Northwest	0.883	0.145	

## Methodology

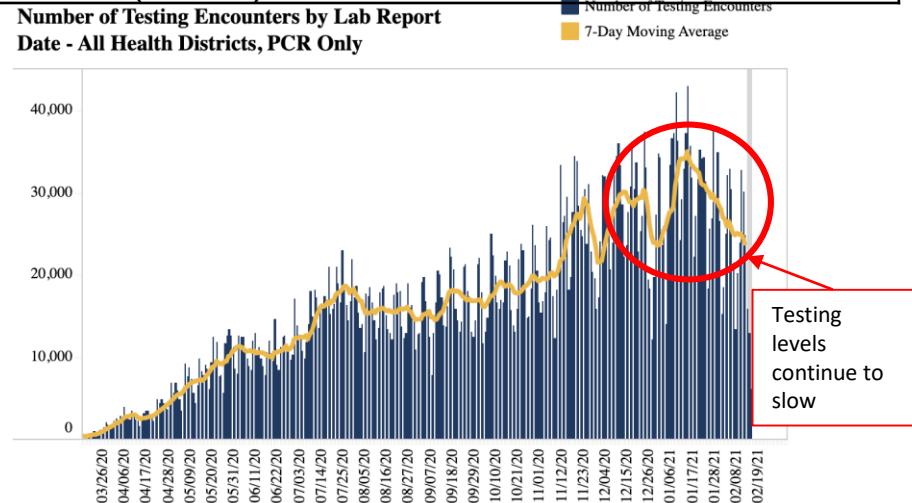
- Wallinga-Teunis method (EpiEstim<sup>1</sup>) for cases by confirmation date
- Serial interval: 6 days (2 day std dev)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

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>

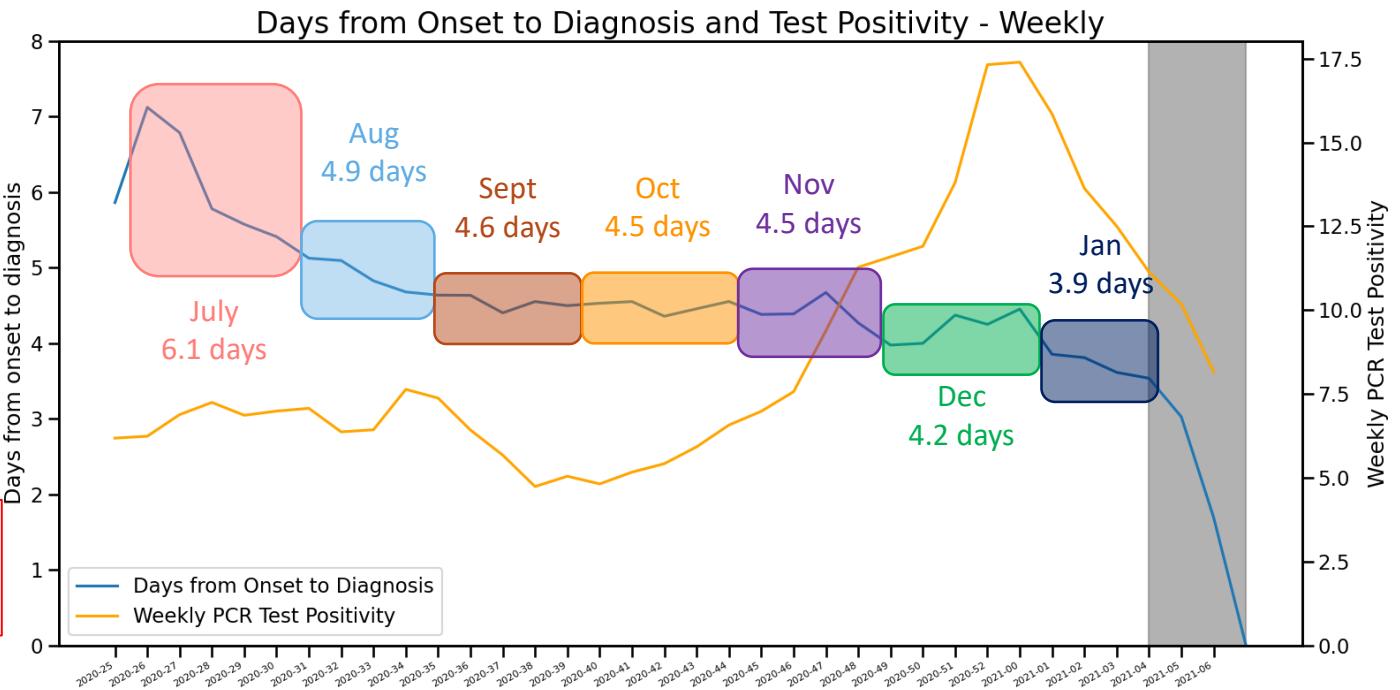
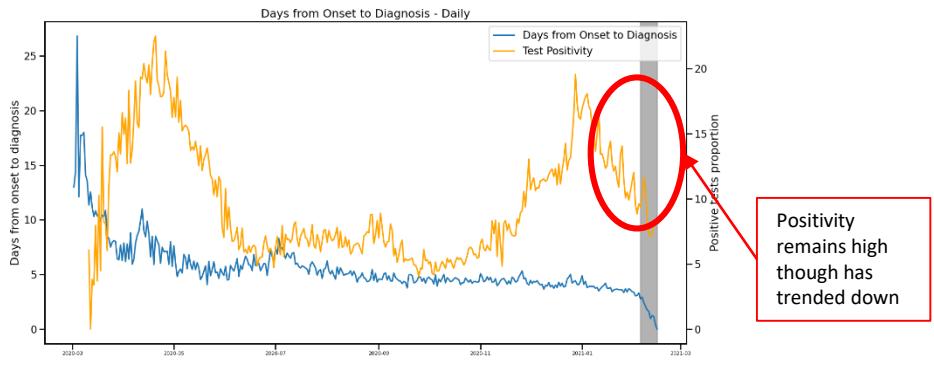


# Changes in Case Detection

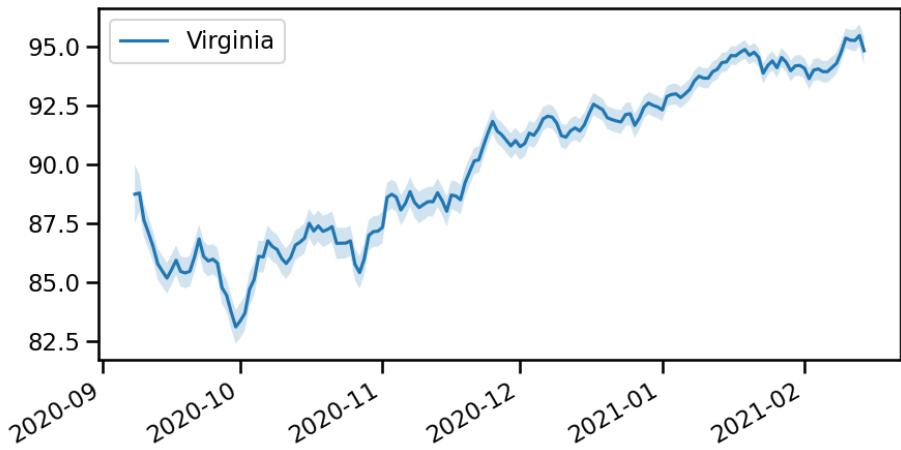
Timeframe (weeks)	Mean days	% difference from overall mean
May (17-21)	5.7	-21%
June (22-25)	5.8	-20%
July (26-30)	6.1	-15%
Aug (31-34)	4.9	-32%
Sept (35-38)	4.6	-37%
Oct (39-43)	4.5	-38%
Nov (44-47)	4.5	-38%
Dec (48-49)	4.2	-42%
Jan (00-04)	3.9	-47%
Overall (13-04)	7.2	--



## Test positivity vs. Onset to Diagnosis



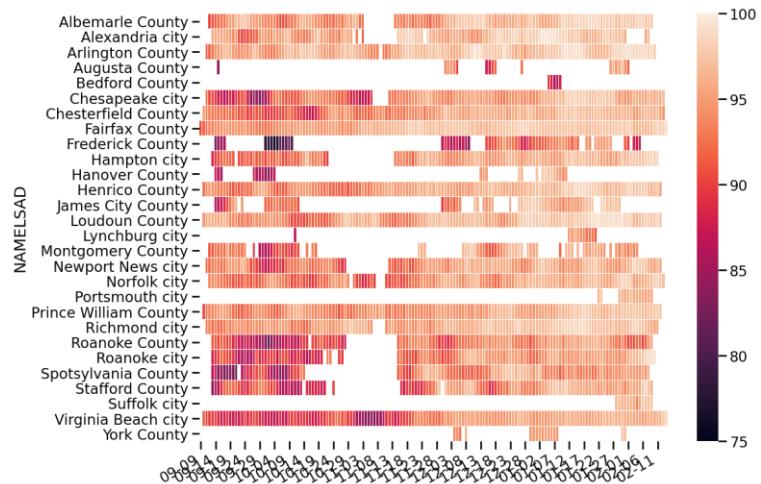
# Mask Usage in Virginia



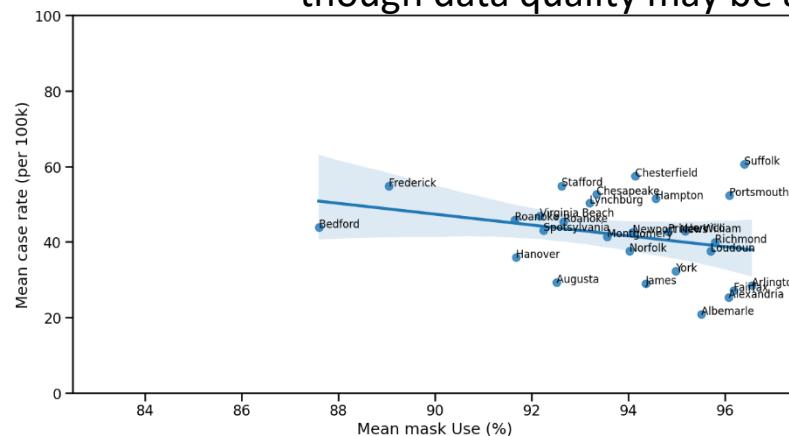
State level mask usage as reported via Facebook surveys has shown steady increase over past three months

- ~88% (early Nov) to ~94% (mid Feb)
- Some variance across the Commonwealth
- ~3000 daily responses from VA

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



Some county level fluctuations since beginning of Sept., though data quality may be affected by sample sizes



Lower correlation for VA counties between mask use and case rate due to rapid declines.  
Slope: - 1.4; for every % mask use we see a 1.4/100K case rate difference

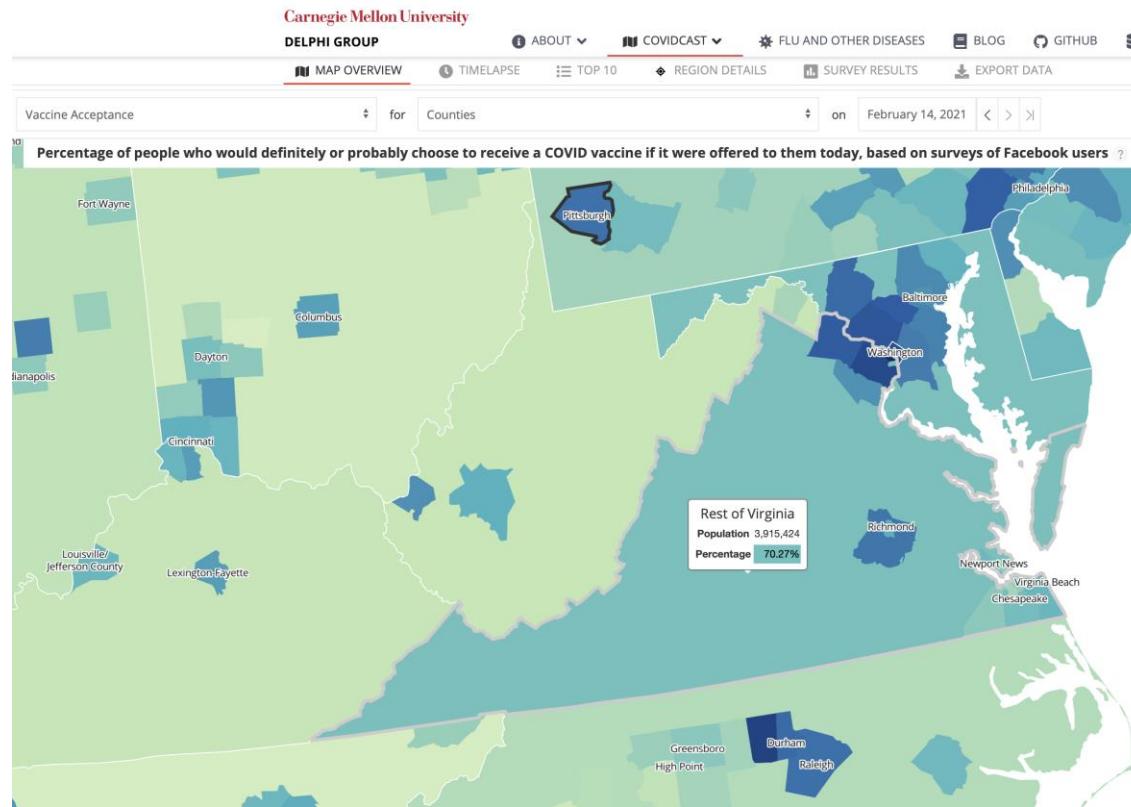


UNIVERSITY OF VIRGINIA

# Vaccine Acceptance

**Facebook administered survey:**  
Percent of people who would definitely or probably choose to receive a COVID vaccine if offered today

VA typically achieves 50-60% coverage with seasonal influenza vaccine (typically over the course of 3 months)



Vaccine Acceptance in Virginia



**Acceptance down since the end of January, but still relatively high: Nearly ¾ of Virginians are likely to choose to be vaccinated if offered today**

[COVIDcast Data Explorer](#)

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



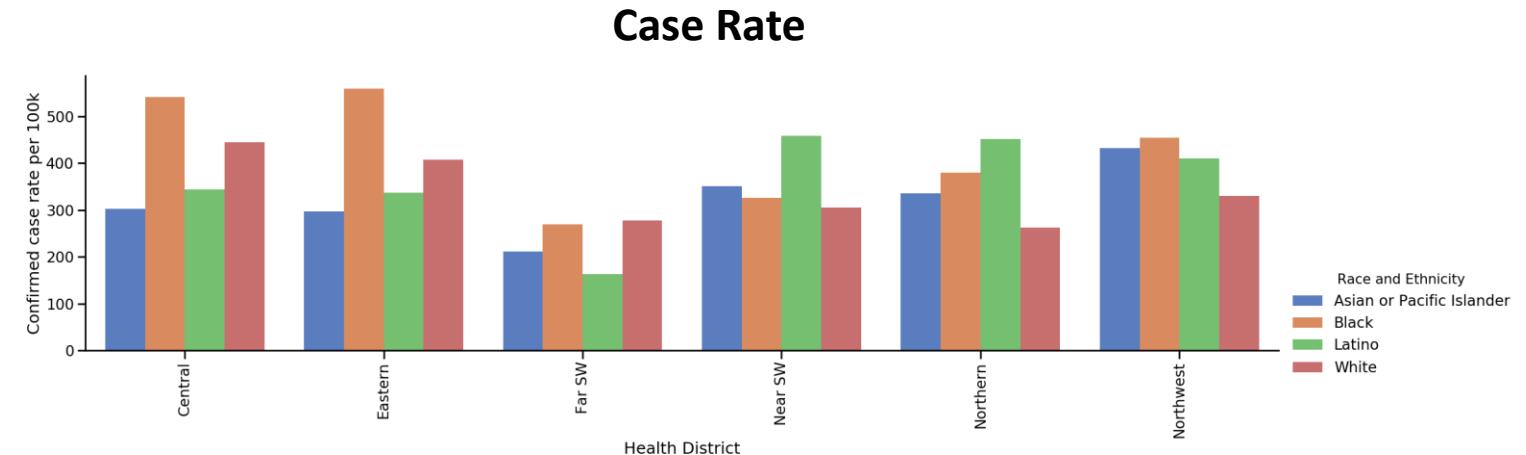
UNIVERSITY OF VIRGINIA

BIOCOMPLEXITY INSTITUTE

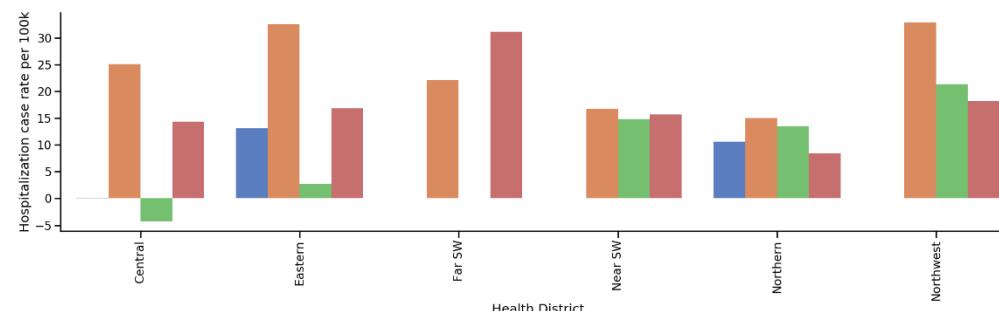
# Race and Ethnicity – Recent Rate Changes (per 100K)

## Recent Changes in Race and Ethnicity Rates (per 100k)

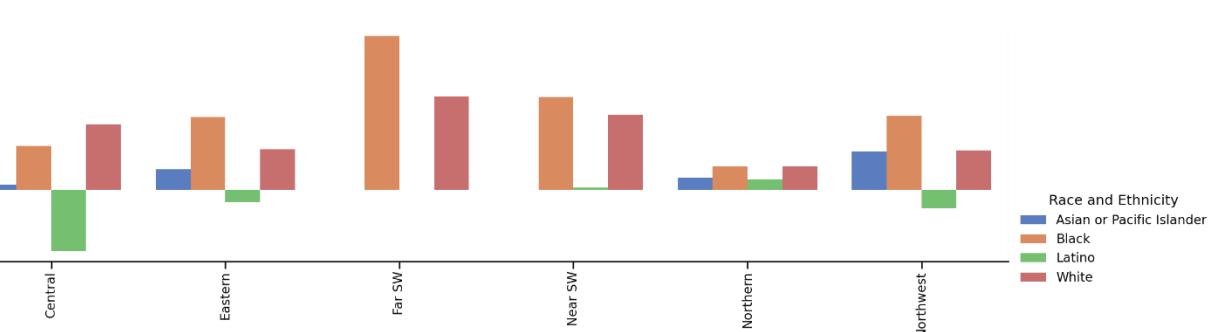
- Two week change in population level rates
- Black, Latinx and 2 or more races populations have much higher changes in rates; disparity is more pronounced in some districts than others
- Based on 2019 census race-ethnicity data by county



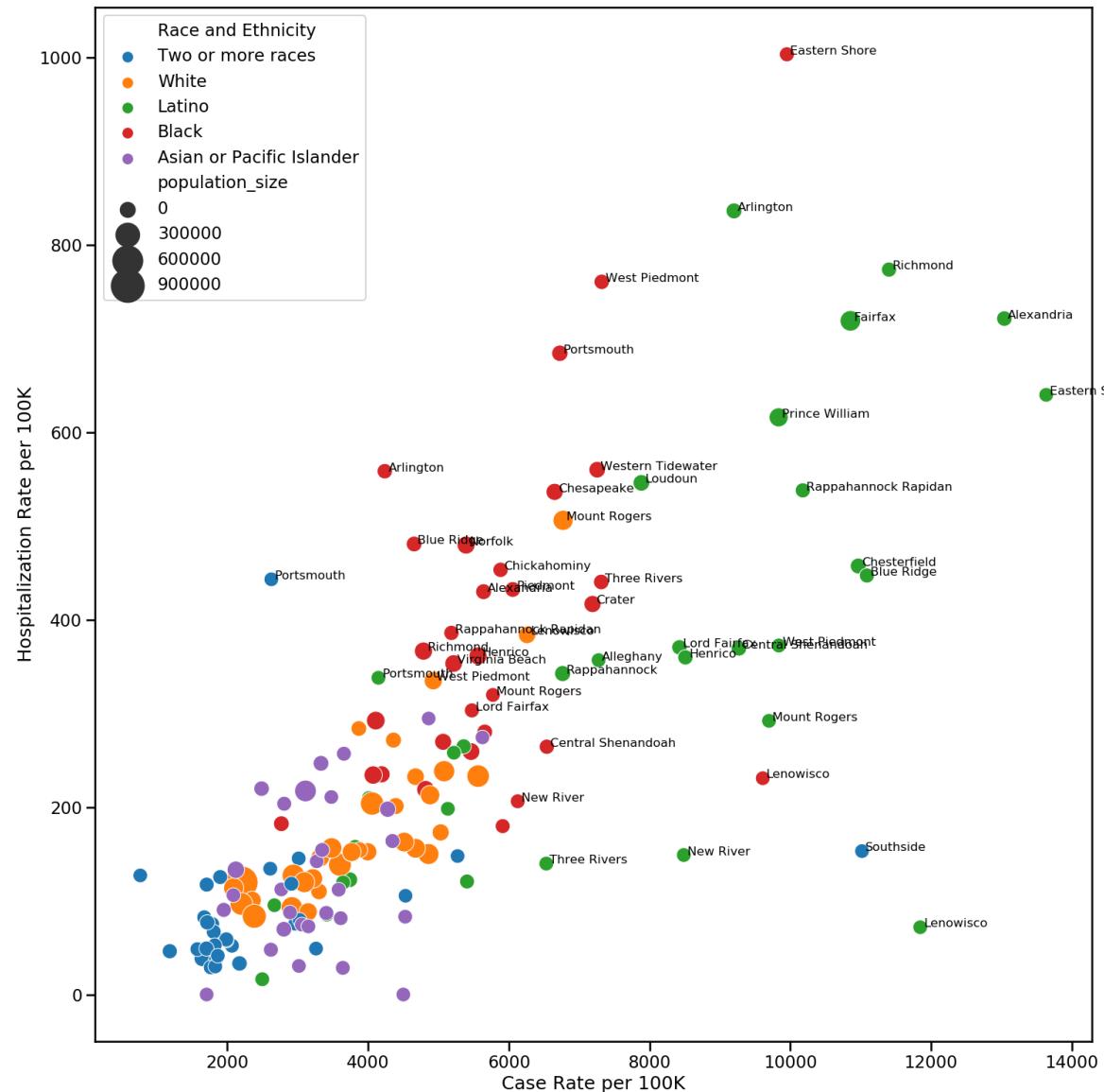
### Hospitalization Rate



### Death Rate



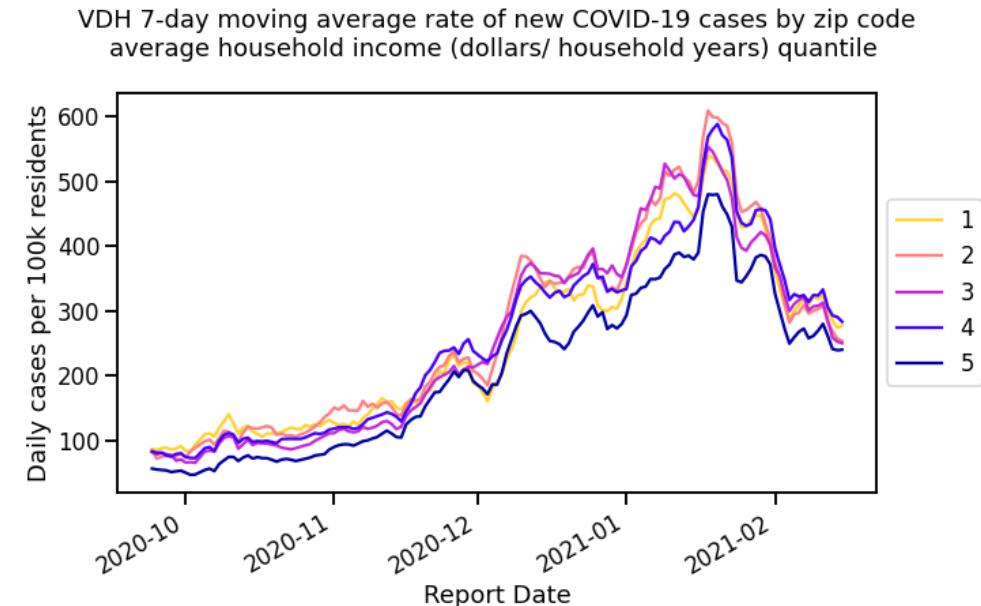
# Race and Ethnicity cases per 100K



## 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)

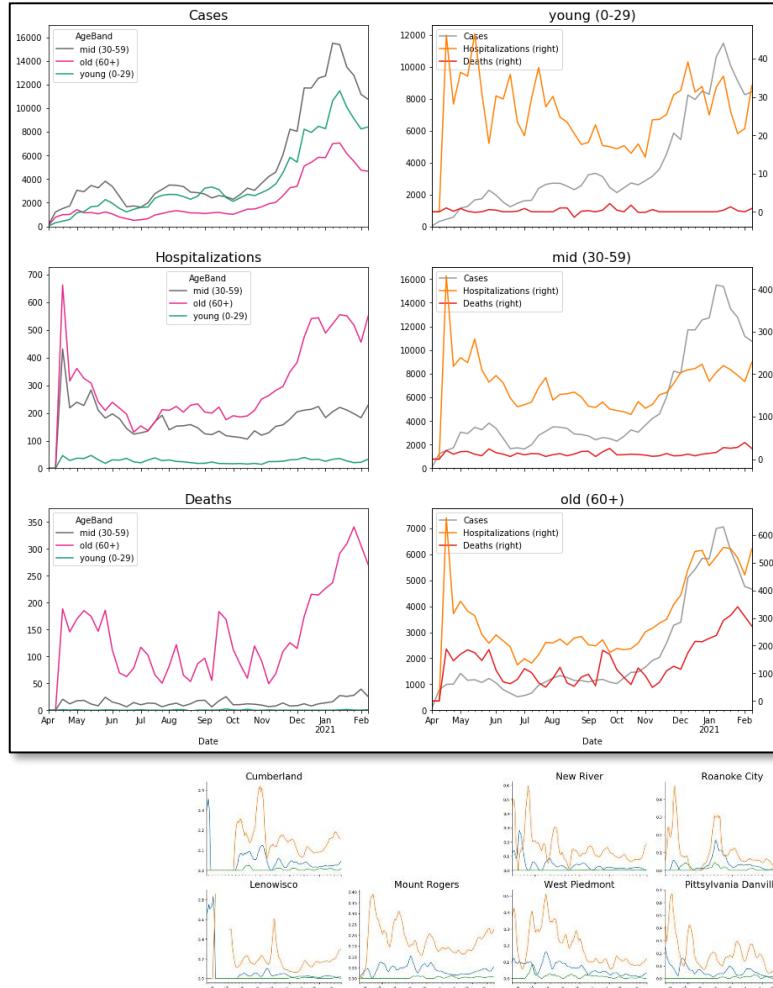
## Case rates by zip codes broken into income quintiles



# Shifting Hospitalization Rates

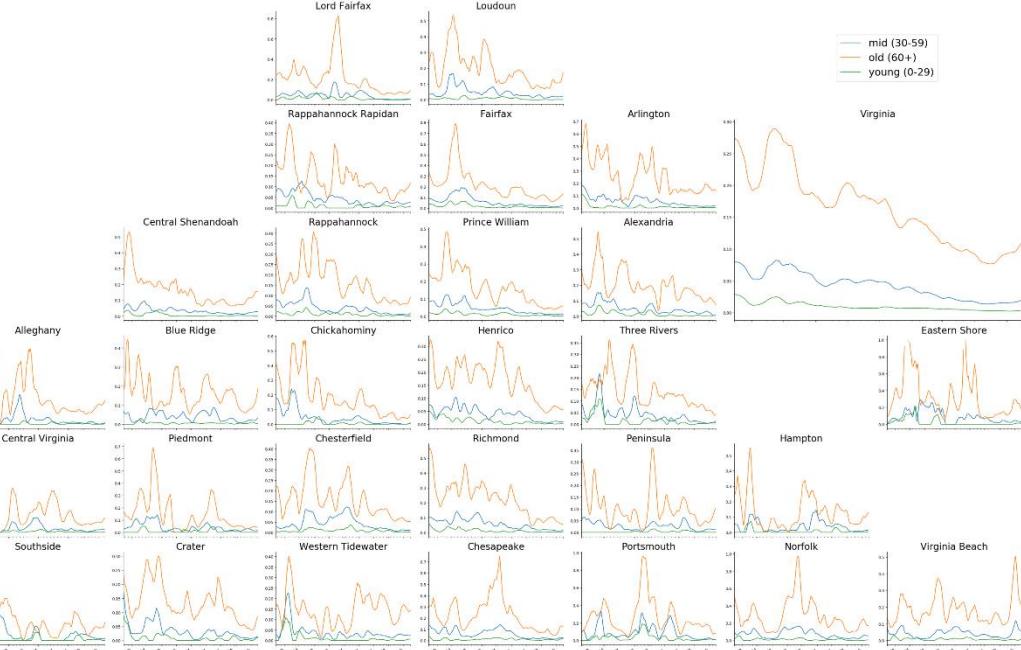
## Comparison of cases, hospitalizations, and deaths by age-group

- Over the course of the pandemic the ratios between these have shifted even within different age-groups
- Cases rise with minimal change in hospitalizations in middle age group
- More infections in the young but with no rise in hospitalizations
- Reflects the case detection biases by age and point in time during the pandemic



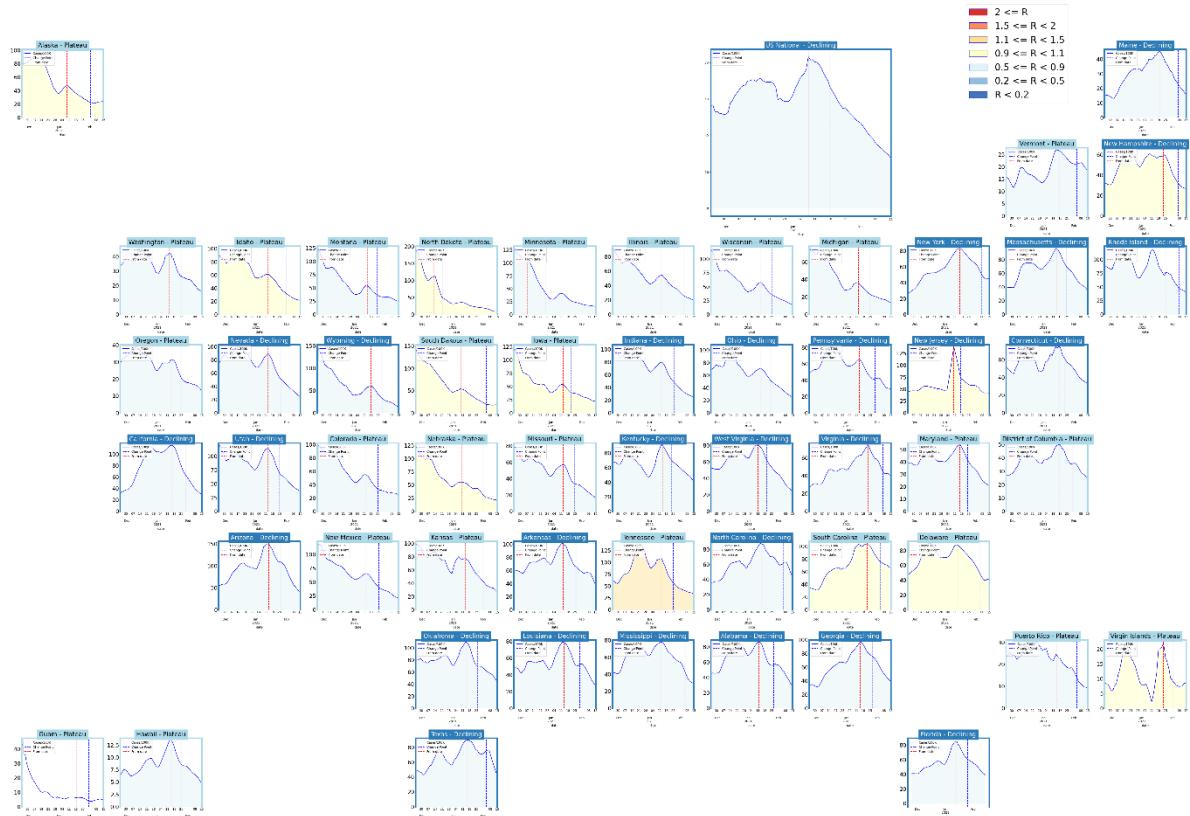
## Ratio of Cases to Hospitalizations (5 day shift) by Health District

- Many districts showing increase in last couple weeks in the older age-group



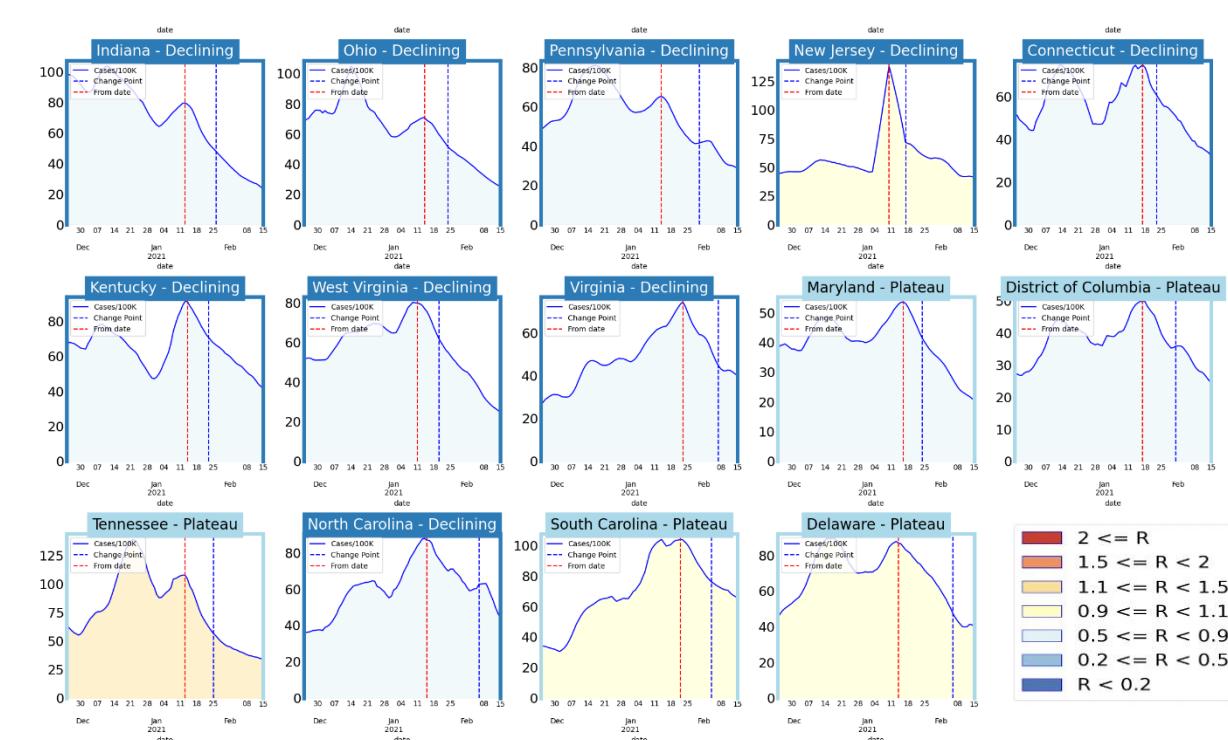
# Other State Comparisons

Trajectories of States



- All states are declining (27) or plateaued (27)
- Rates remain relatively high

Virginia and her neighbors

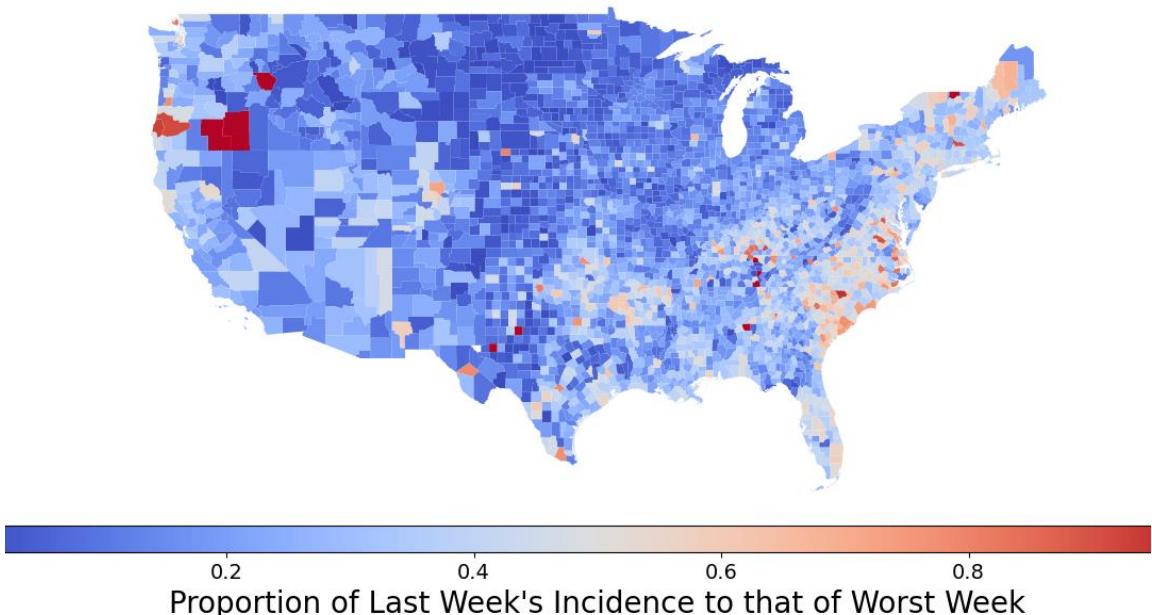


- VA and her neighbors are all declining or plateaued
- TN shows some growth (especially in some Appalachian counties)
- Rates remain high in most states however

# Current Week vs. Highest Week

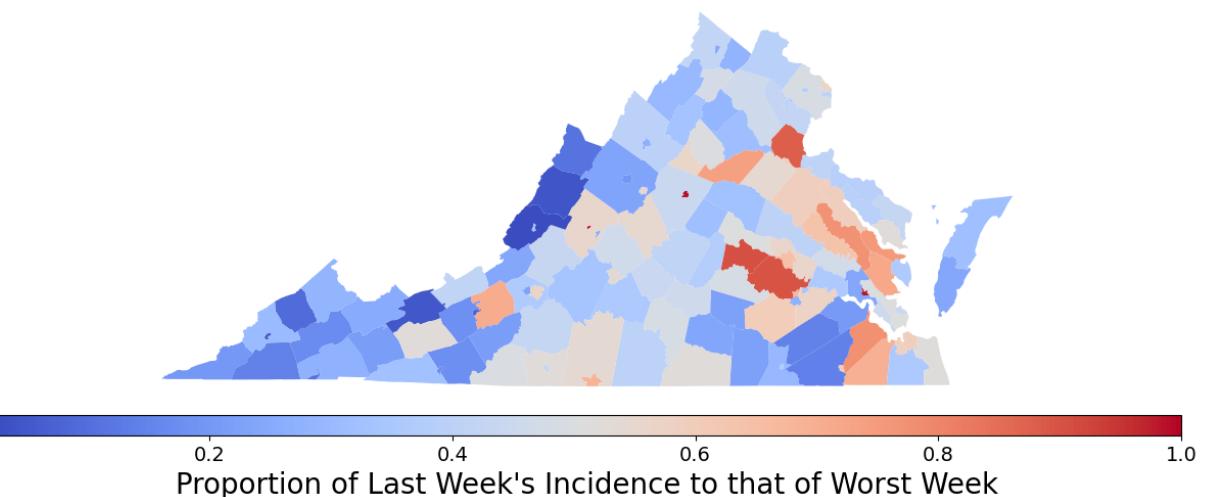
For all counties in the US

Recent Incidence Compared to Worst Week by County



Virginia's counties

Recent Incidence Compared to Worst Week by County



- 19% of US counties have a weekly case rate over 50% of the worst weekly case rate

- 46% of VA counties have a weekly case rate over 50% of the worst weekly case rate

# Zip code level weekly Case Rate (per 100K)

## Case Rates in the last week by zip code

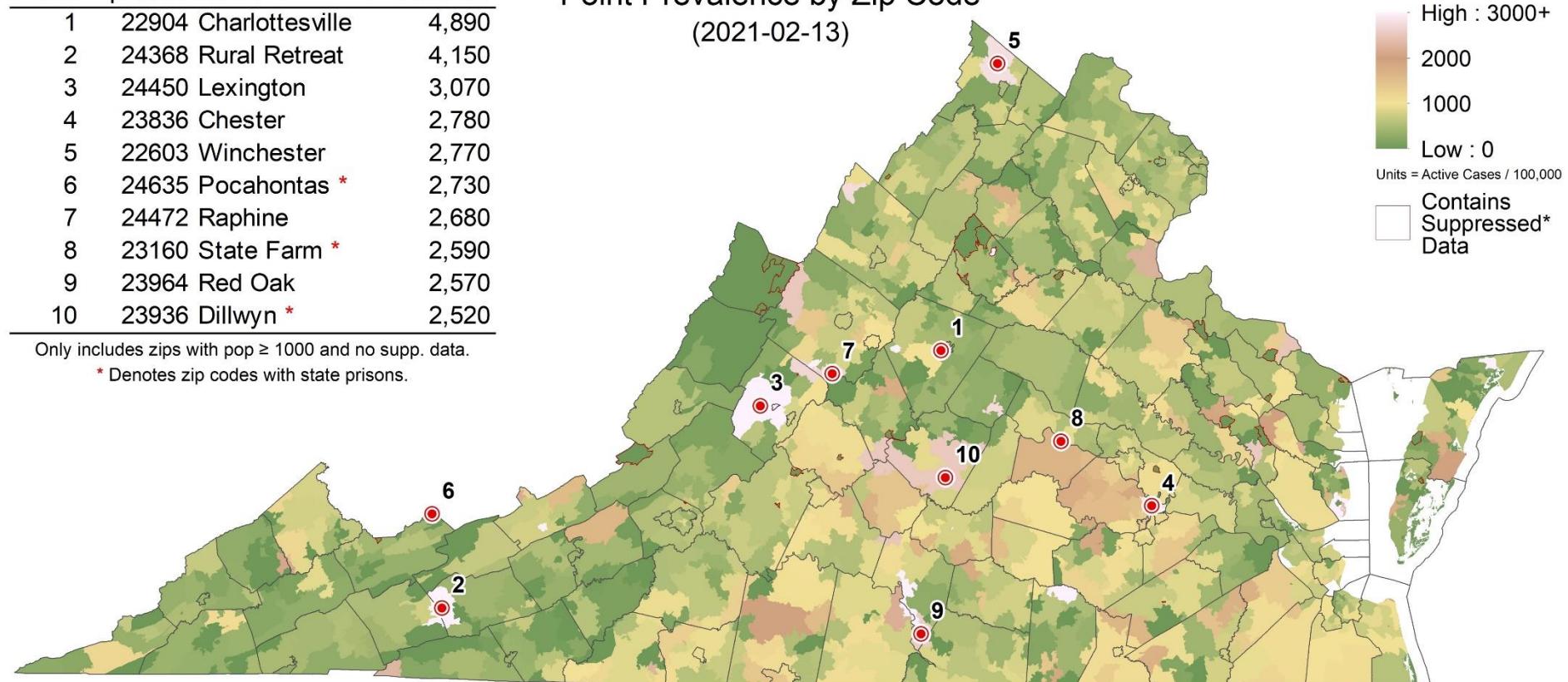
- Prisons continue to be highlighted in the top ten
- Concentrations of high rates scattered across the Commonwealth
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code Name	Prevalence
1	22904 Charlottesville	4,890
2	24368 Rural Retreat	4,150
3	24450 Lexington	3,070
4	23836 Chester	2,780
5	22603 Winchester	2,770
6	24635 Pocahontas *	2,730
7	24472 Raphine	2,680
8	23160 State Farm *	2,590
9	23964 Red Oak	2,570
10	23936 Dillwyn *	2,520

Only includes zips with pop  $\geq 1000$  and no supp. data.

\* Denotes zip codes with state prisons.

Point Prevalence by Zip Code  
(2021-02-13)



# Risk of Exposure by Group Size

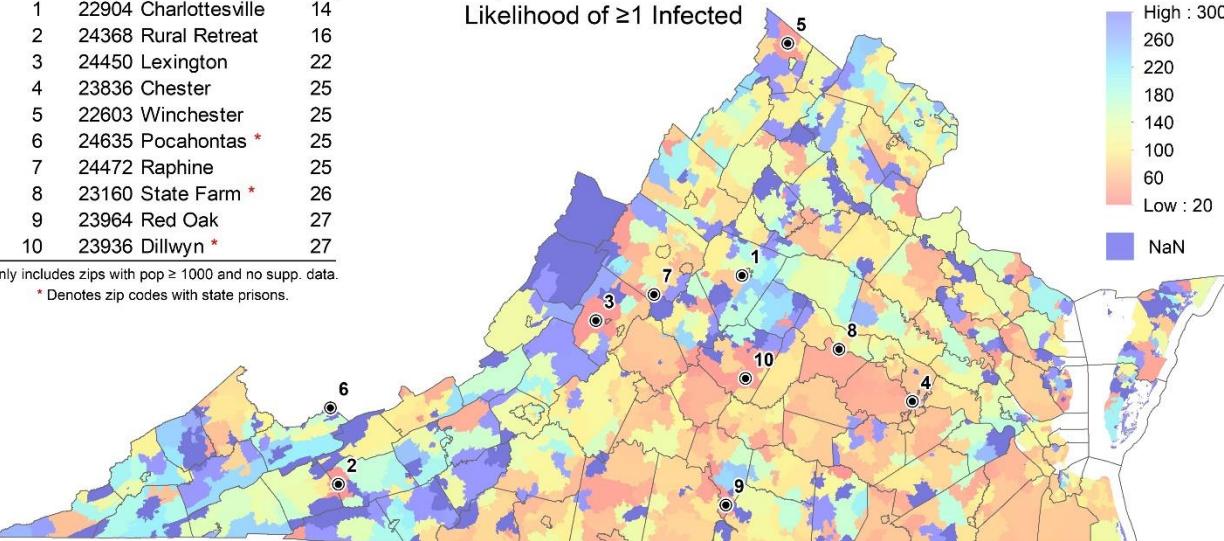
**Case Prevalence in the last week by zip code used to calculate risk of encountering someone infected in a gathering of randomly selected people (group size 25)**

- 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 14 in Hanover, 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	22904 Charlottesville	14
2	24368 Rural Retreat	16
3	24450 Lexington	22
4	23836 Chester	25
5	22603 Winchester	25
6	24635 Pocahontas *	25
7	24472 Raphine	25
8	23160 State Farm *	26
9	23964 Red Oak	27
10	23936 Dillwyn *	27

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

Group Size Needed for 50% Likelihood of  $\geq 1$  Infected

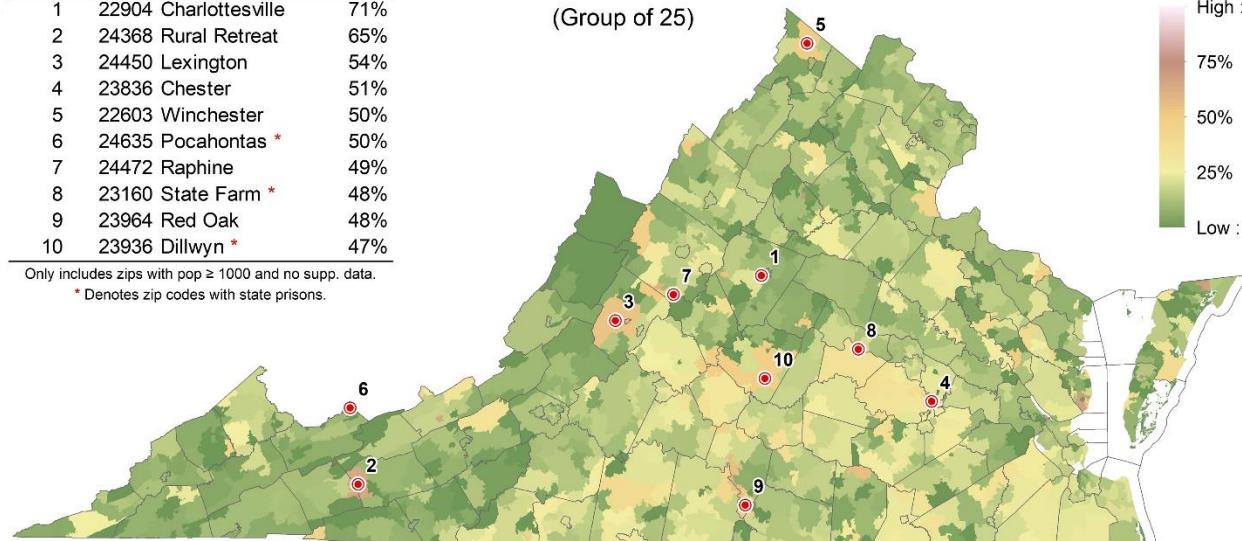


Group Size  
High : 300+  
260  
220  
180  
140  
100  
60  
Low : 20  
NaN

Group Size	Rank	Zip Code Name	Likelihood
High : 300+	1	22904 Charlottesville	71%
260	2	24368 Rural Retreat	65%
220	3	24450 Lexington	54%
180	4	23836 Chester	51%
140	5	22603 Winchester	50%
100	6	24635 Pocahontas *	50%
60	7	24472 Raphine	49%
Low : 20	8	23160 State Farm *	48%
Low : 20	9	23964 Red Oak	48%
Low : 20	10	23936 Dillwyn *	47%

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

Likelihood of  $\geq 1$  Infected Members  
(Group of 25)



Likelihood  
High : 1  
75%  
50%  
25%  
Low : 0

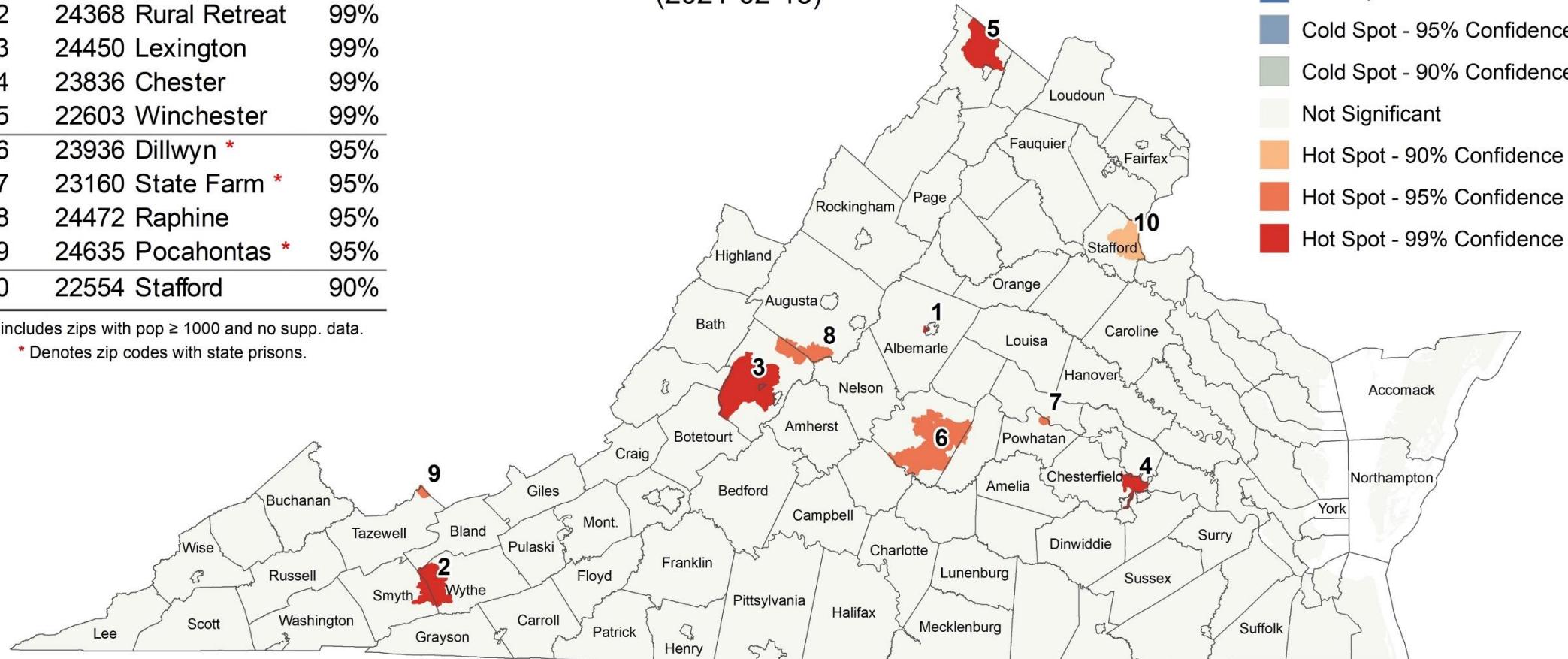
# Current Spatial Hot Spots

Spot	Zip Code	Name	Conf.
1	22904	Charlottesville	99%
2	24368	Rural Retreat	99%
3	24450	Lexington	99%
4	23836	Chester	99%
5	22603	Winchester	99%
6	23936	Dillwyn *	95%
7	23160	State Farm *	95%
8	24472	Raphine	95%
9	24635	Pocahontas *	95%
10	22554	Stafford	90%

Only includes zips with pop  $\geq 1000$  and no supp. data.

\* Denotes zip codes with state prisons.

Point Prevalence Hot Spots by Zip Code  
(2021-02-13)



Hot Spots compare the weekly case prevalence to other zip codes in the surrounding area to identify areas with statistically significant deviations

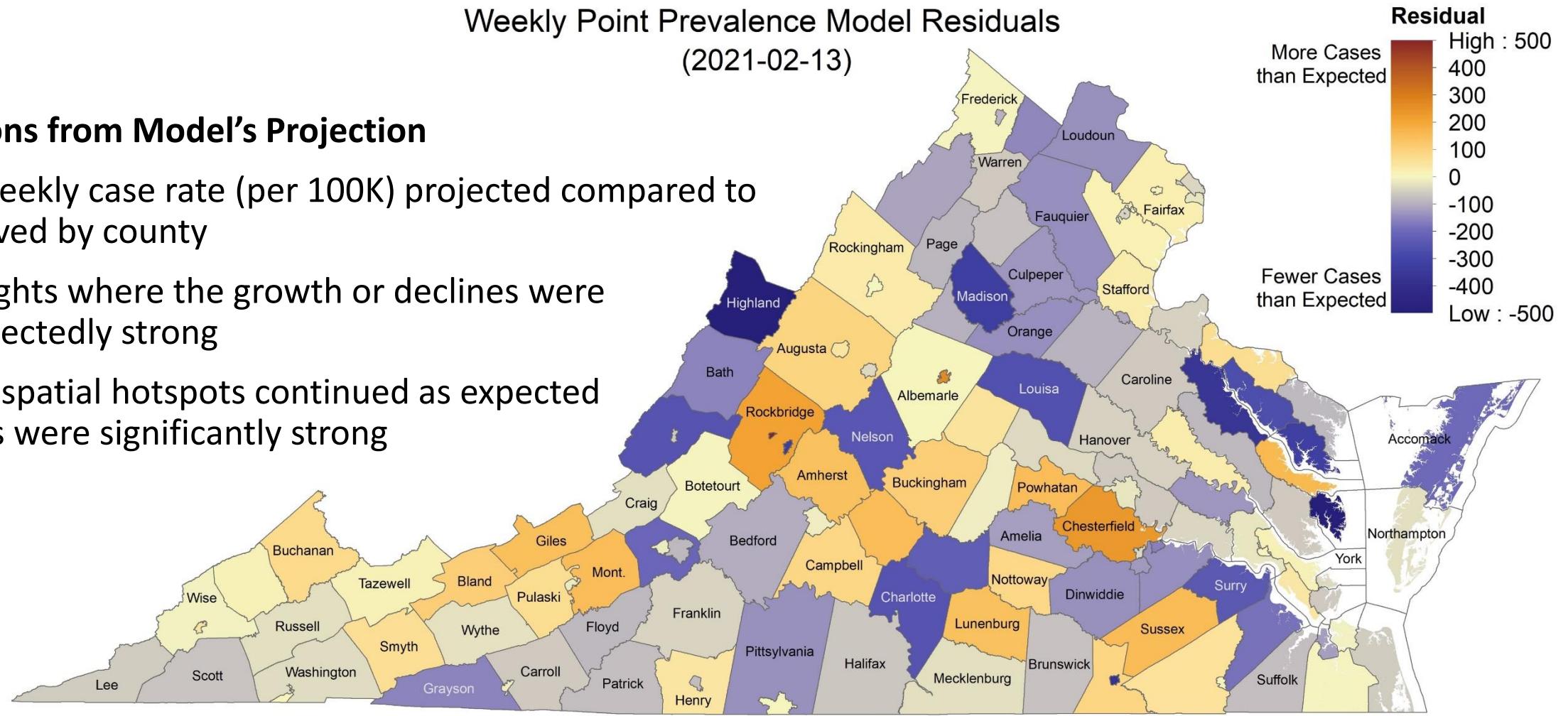


# Deviations from Model's Expectations

## 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  
(2021-02-13)



# New variants of SARS-CoV2

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

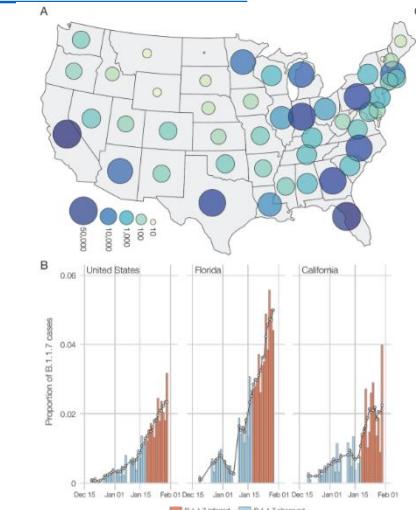
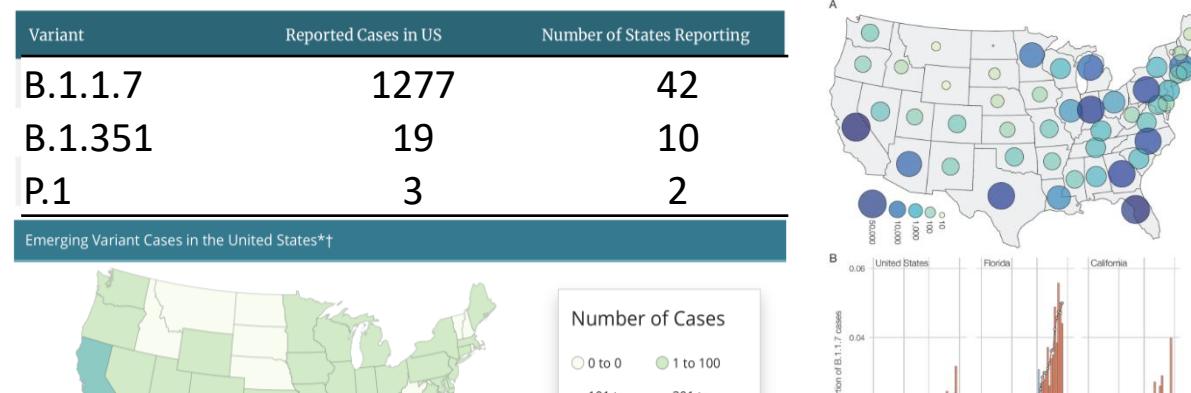
- Current evidence supports that new variants can:
  - Increase transmissibility
  - Increase severity (more hospitalizations and/or deaths)
  - Limit immunity from prior infection and vaccination

## Lineage B.1.1.7

- B.1.1.7 has been detected in Virginia as well as in at least 1277 cases across 42 states as of Feb 16<sup>th</sup> (avg delay of 10-20 days from isolation to reporting), will continue to grow rapidly
- Updated estimates based on US growth rates estimate it will predominate (eg reach 50% frequency) by mid to late March and is 35%-45% more transmissible.
- An update to previous study now estimates 40-80% more transmissible though did not support increased severity
- Study in Lancet also finds B117 infections have no appreciably different clinical course

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



U.S. is on a similar trajectory as other countries where B.1.1.7 rapidly became dominant  
[Andersen et al.](#)

# New variants of SARS-CoV2

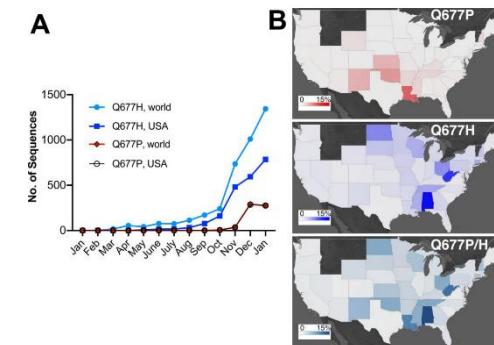
## Lineage B.1.351

- Emerging strain initially identified in South Africa shows signs of vaccine escape, currently 19 reported cases in 10 states (including Virginia) as of Feb 16<sup>th</sup>
- New Experiments show SARS-CoV-2 variants B.1.351 and B.1.1.248 escape from therapeutic antibodies and antibodies induced by infection and vaccination, though an additional study demonstrated that a single boosting dose of mRNA vaccine restores response
- Moderna and Pfizer vaccine demonstrated to have robust response to this variant, and thus likely to remain highly effective, though Novavax and Johnson & Johnson vaccine demonstrated reduced efficacy in trial arm conducted in South Africa when this strain was circulating

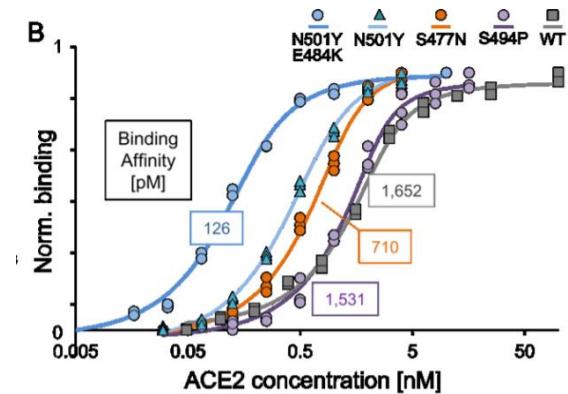
## Additional Variants

- Lineage P.1 (similar mutations as in B.1.1.7 and B.1.351):** First case reported in Minnesota on Monday Jan 25<sup>th</sup>, now 3 cases in 2 states has caused a resurgence of hospitalizations in Manaus, Brazil continues this despite estimated ¾ of the population infected
- Lineage B.1.429 (similar mutations as in B.1.1.7 and B.1.351):** Initially found in Southern California, coincided with surge in Nov and Dec, found in over half of sequenced samples in LA

## Additional variant frequently arising



Mutation at position 677 in Spike has appeared at least 7 times in US-focused clusters in the past few months



Convergent evolution towards more transmissible variants currently being observed recreated through in vitro evolution, may provide picture of next mutations to look for: "we project that the Q498R mutation will appear in the future"

# Model Update – Adaptive Fitting

---



# Adaptive Fitting Approach

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

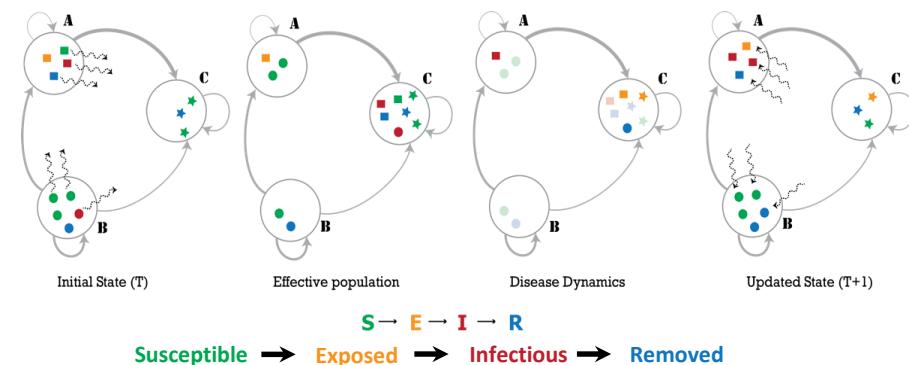
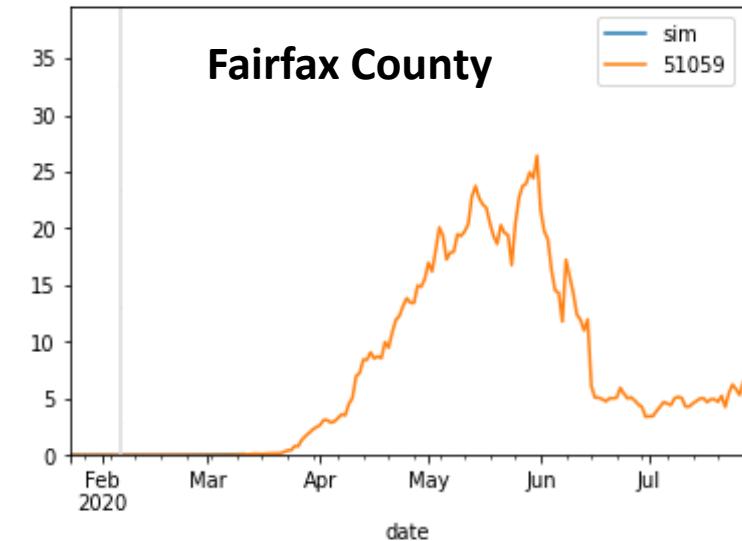
- Allows history to be precisely captured, and used to guide bounds on projections

**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:

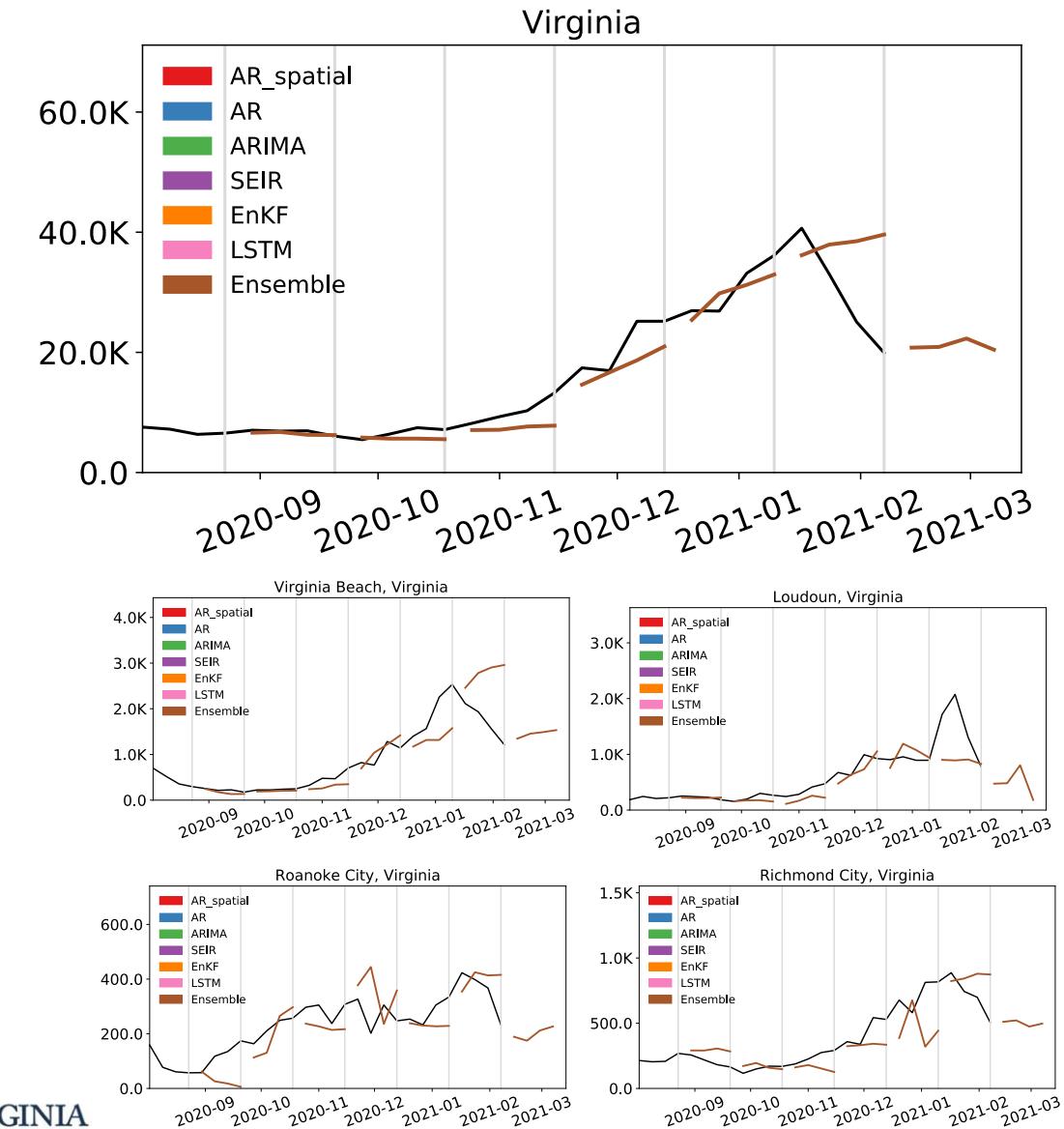
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

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.



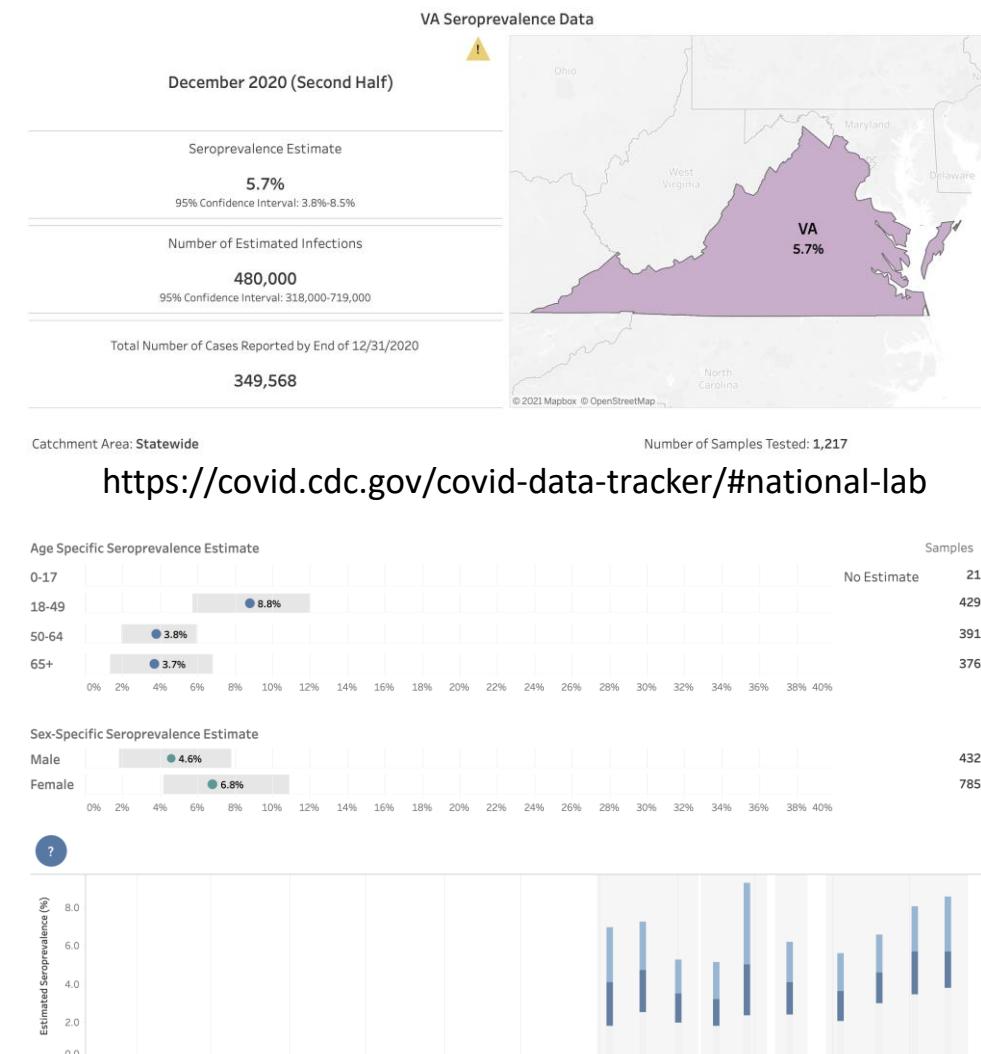
# Seroprevalence updates to model design

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

- CDC Nationwide Commercial Laboratory Seroprevalence Survey estimated 5.7% [3.8% – 8.5%] seroprevalence as of Dec 10<sup>th</sup> – 23<sup>rd</sup> from 4.6% a month earlier

**These findings are equivalent to an ascertainment ratio of ~3x, with bounds of (1x to 7x)**

- Thus for 3x there are 3 total infections in the population for every confirmed case
- 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:

Dashboard Updated: 2/16/2021  
Data entered by 5:00 PM the prior day.

Cases, Hospitalizations and Deaths					
Total Cases*	Total Hospitalizations**		Total Deaths		
<b>553,308</b>	<b>23,042</b>		<b>7,037</b>		
(New Cases: 1,770) <sup>▲</sup>	Confirmed†	Probable†	Confirmed†	Probable†	Confirmed†
438,276	21,905	115,032	1,137	6,047	990

\* 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.

<sup>▲</sup>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
<b>2,491</b>	<b>61,043</b>

\* 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**
<b>5,633,818</b>	<b>9.1%</b>

\* 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
<b>17</b>	<b>0</b>

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

Accessed 8:30am February 17, 2021

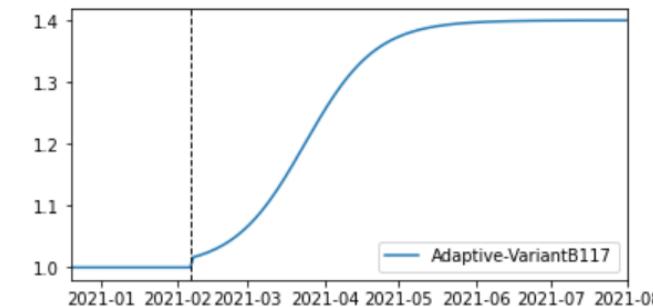
<https://www.vdh.virginia.gov/coronavirus/>

# Scenarios – Seasonal Effects

- Variety of factors continue to drive transmission rates
  - Seasonal impact of weather patterns, travel and gatherings related to holidays, fatigue with infection control practices
- Plausible levels of transmission can be bounded by past experience
  - Assess transmission levels at the county level since May 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
- New planning Scenarios:
  - **Best of the Past:** Lowest level of transmission (10<sup>th</sup> percentile)
  - **Fatigued Control:** Highest level of transmission (95<sup>th</sup> 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 40% increase from the current baseline projection
  - **Emergence timing:** Gradually assumes predominance over the next 6 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 increases gradually over 4 months to level 40% more transmissible

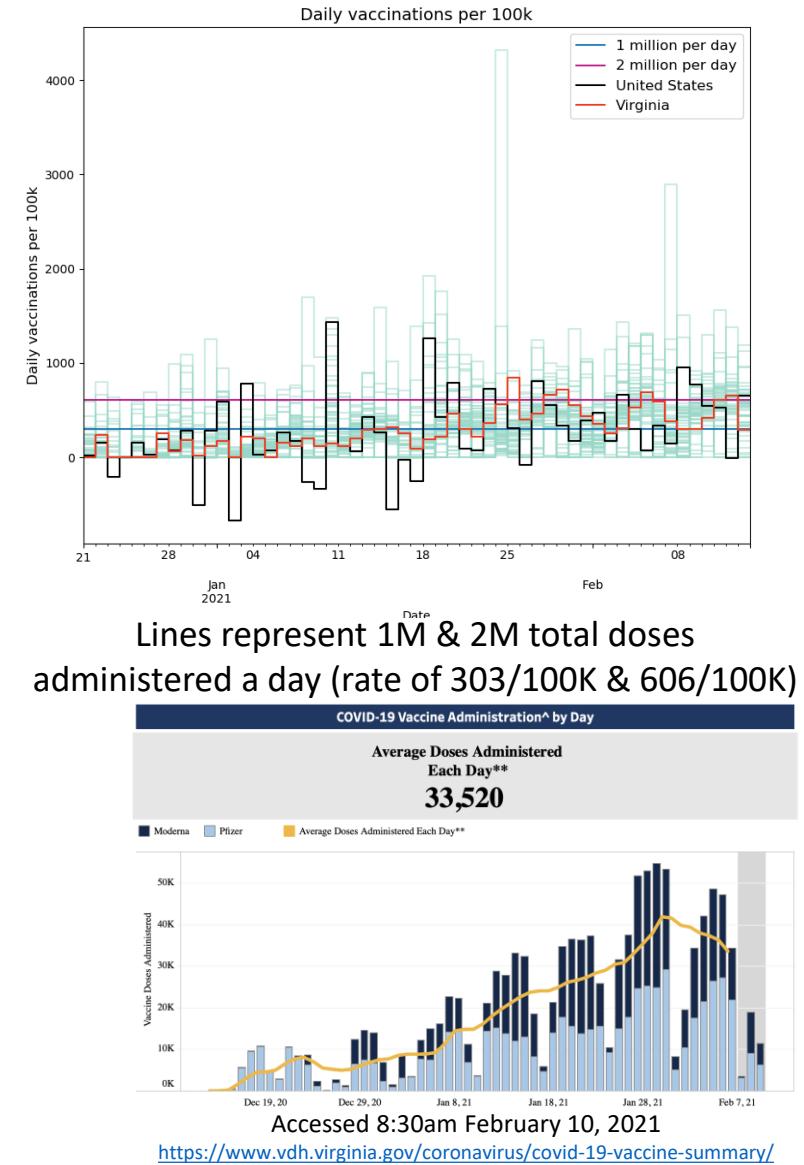


# Scenarios – Vaccines

## VA Vaccination Rates

- Vaccination has started, and efforts are underway to increase its pace
  - Exact achievable rollouts and level of coverage are unknown, though coming into focus
- Vaccine efficacy varies over course of vaccine
  - FDA EUAs show 50% efficacy achieved 2 weeks after 1<sup>st</sup> dose, and 95% 2 weeks after 2<sup>nd</sup> dose
  - Assuming 3.5 week (average of Pfizer and Moderna) gap between doses
- Vaccine hesitancy poses a future problem
  - Currently demand far outpaces supply so we assume all courses will be administered until we reach the hesitancy threshold, for 50% this is several months in the future.

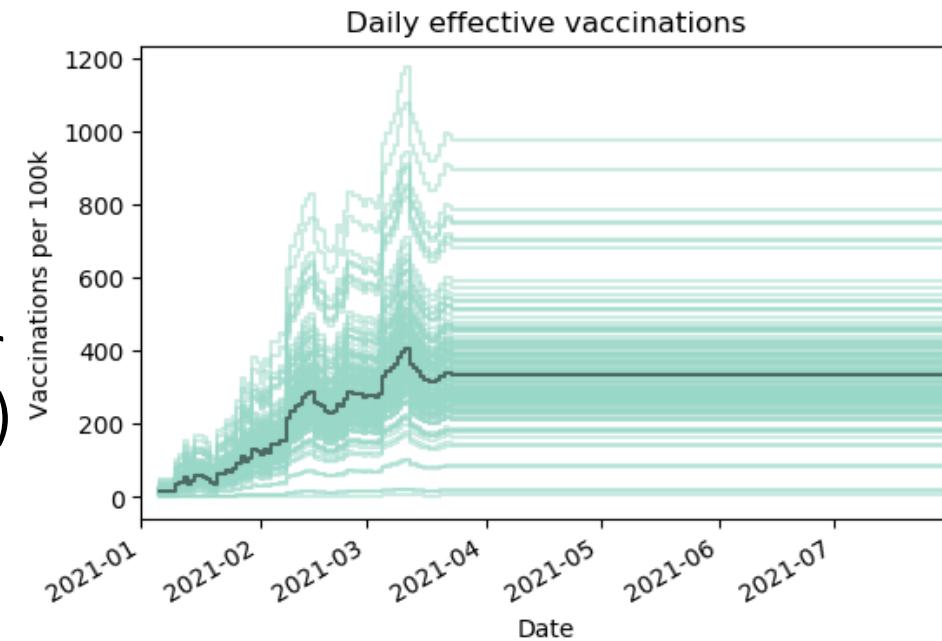
Current rollouts and scenarios inspired by  
MIDAS Network COVID-19 Scenario Hub:  
<https://github.com/midas-network/covid19-scenario-modeling-hub>



# Scenarios – Vaccines

- Administration schedule uses actual administration and expected for the future
  - Use history of state-specific doses administered as captured by [Bloomberg](#) (up to Jan 19<sup>th</sup>) and [CDC](#) (Jan 20<sup>th</sup> and on)
  - Adjustments made to make the vaccine specific for each county (as obtained through VDH dashboard) vax data in data package.
  - Future courses based on sustaining daily average of most recent week
    - **Rate:** 229 doses per 100K per day (~20K total per day), which is down from last week's levels
    - **Location:** Per capita distribution across all counties

**Modeled Vaccine Induced Immunity**



All US states, median 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 updated 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-BestPast:** Best of the past control seasonal effects
  - If we revert to best control 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
- **Adaptive-BestPast-VariantB117:** Best of the past control vs. txm boost from B.1.1.7

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



# Model Results

---

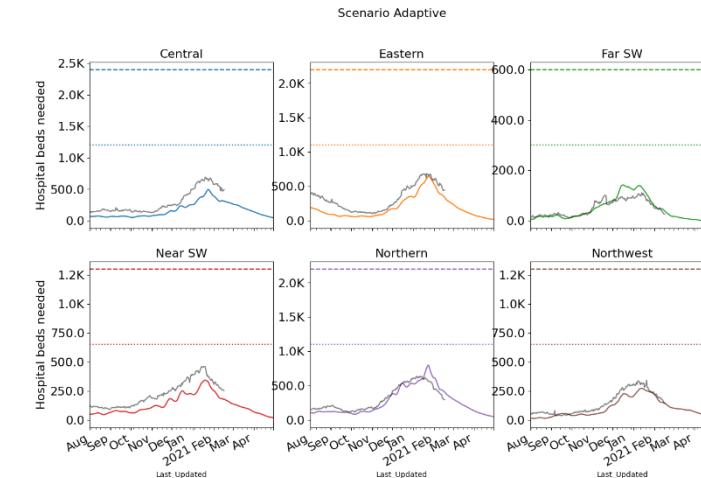
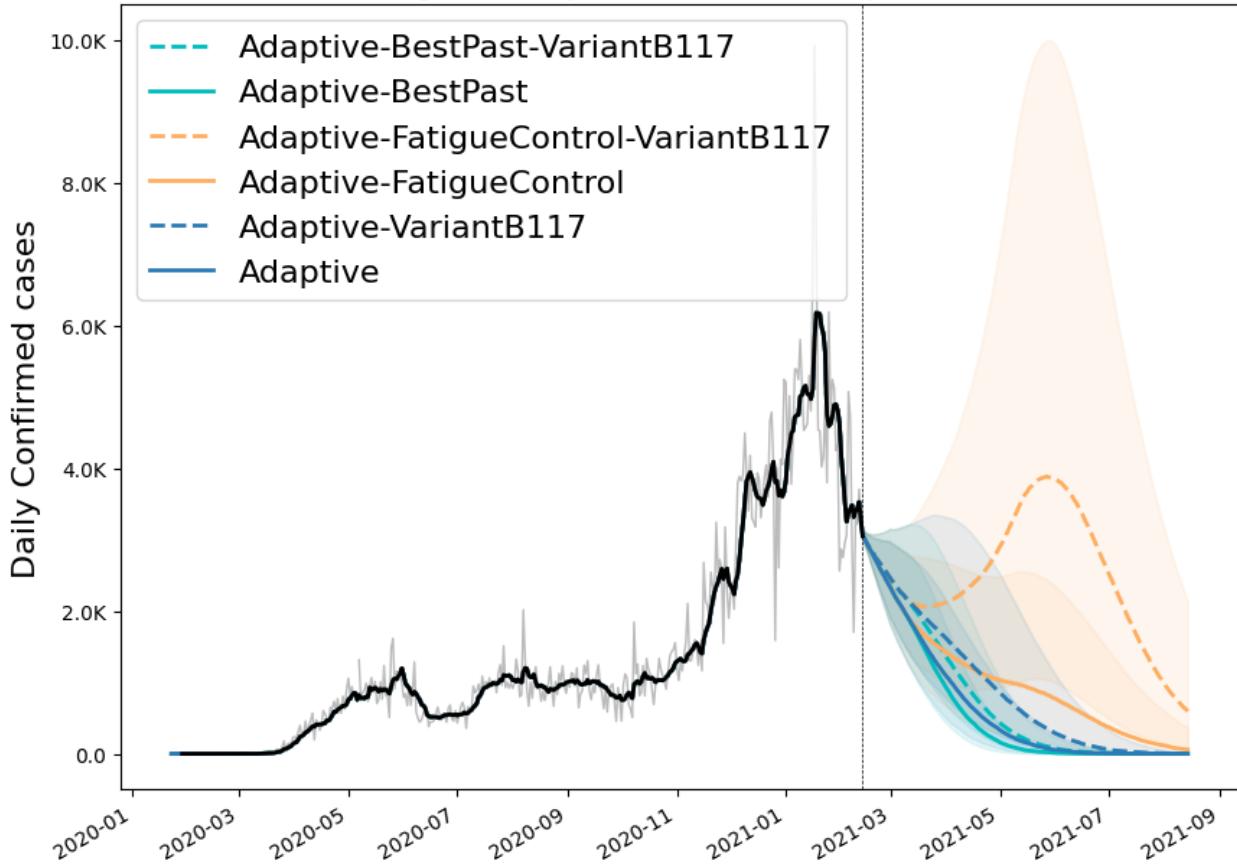


# Outcome Projections

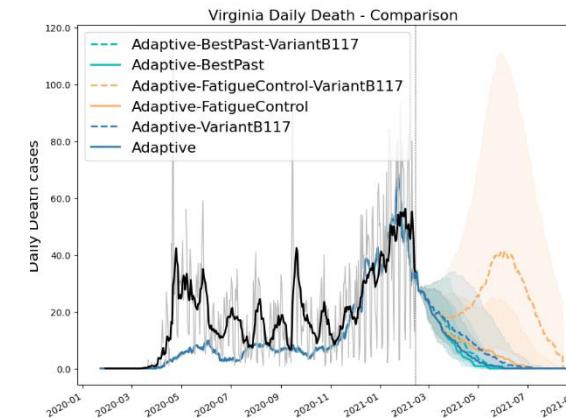
## Estimated Hospital Occupancy

### Confirmed cases

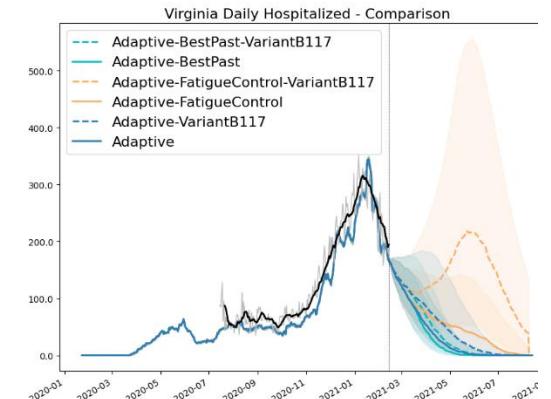
Virginia Daily Confirmed - Comparison



### Daily Deaths



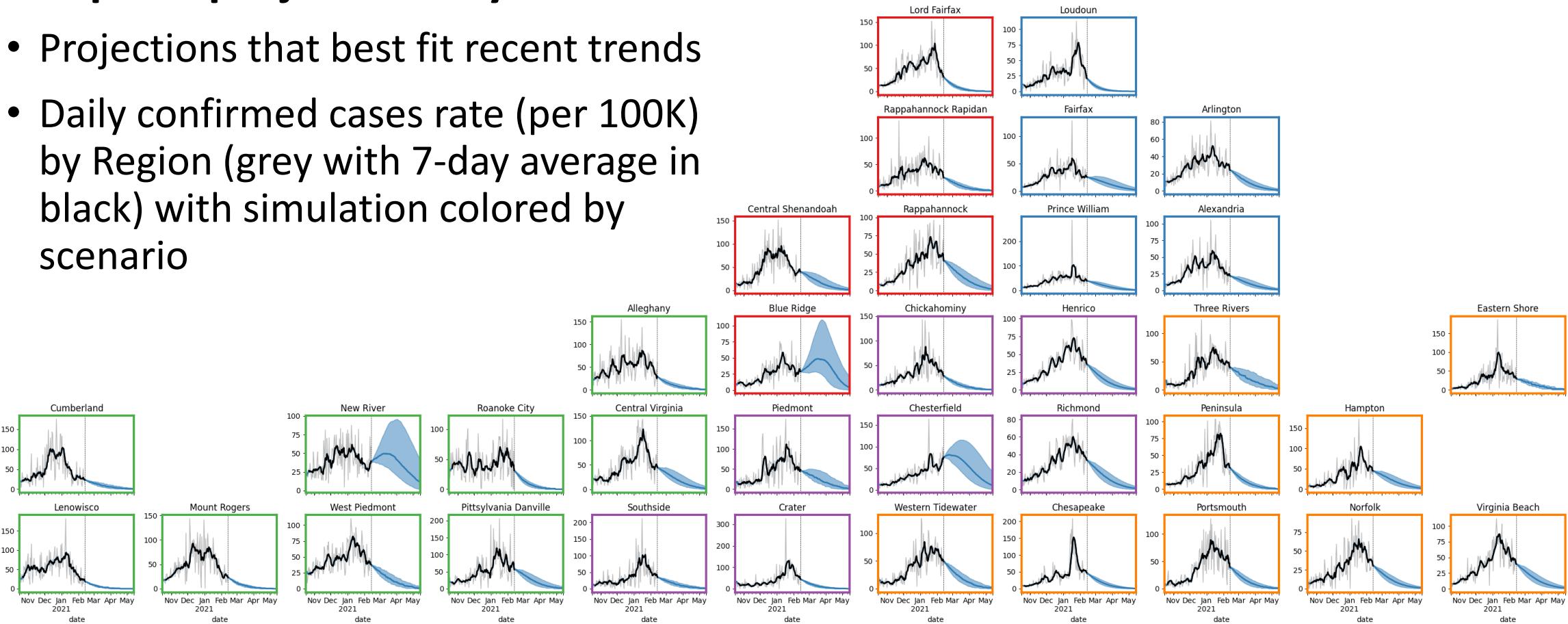
### Daily Hospitalized



# District Level Projections: Adaptive

## Adaptive projections by District

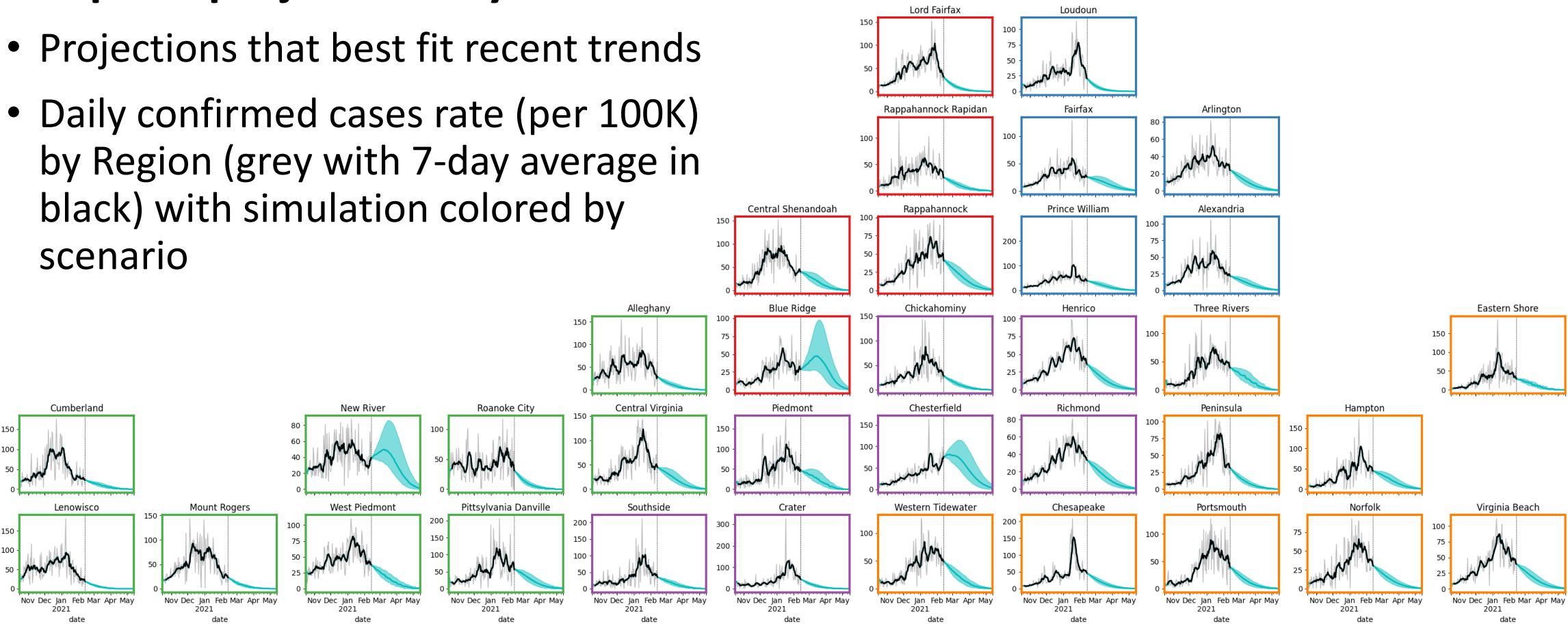
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



# District Level Projections: Adaptive-BestPast

## Adaptive projections by District

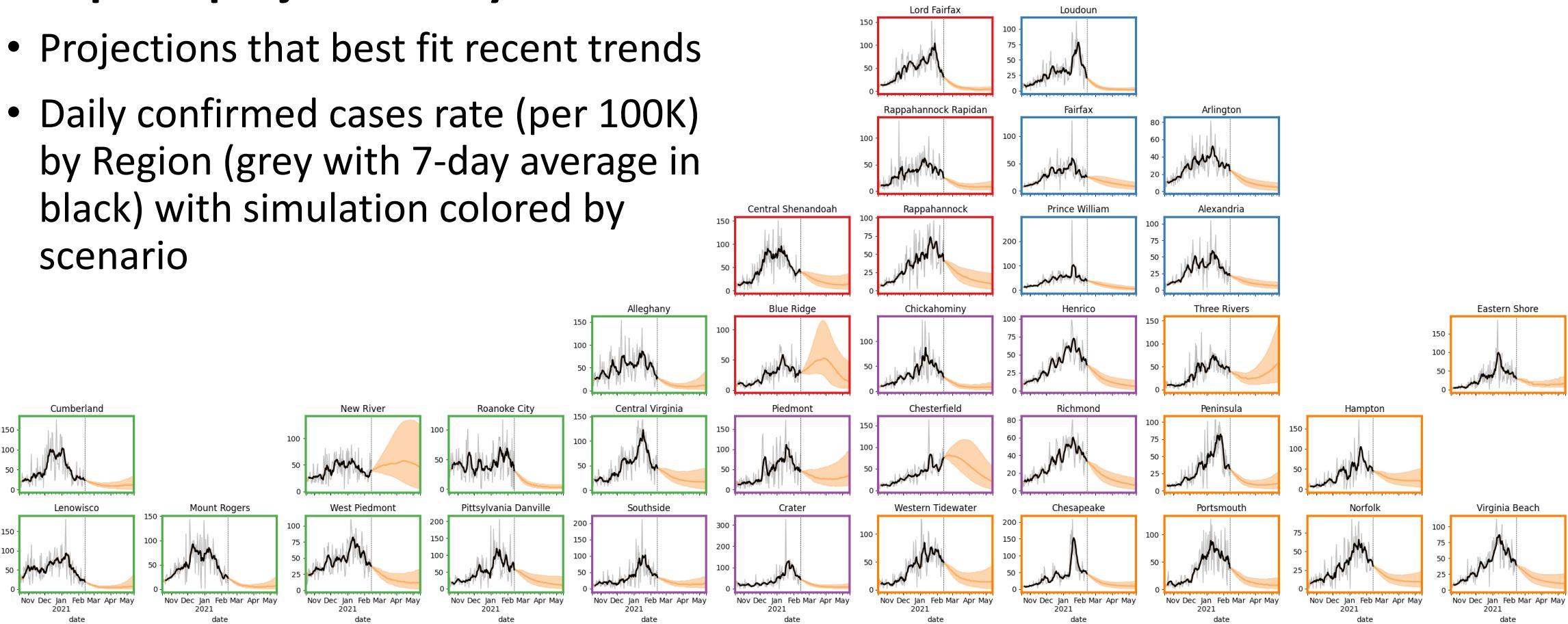
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



# District Level Projections: Adaptive-FatigueControl

## Adaptive projections by District

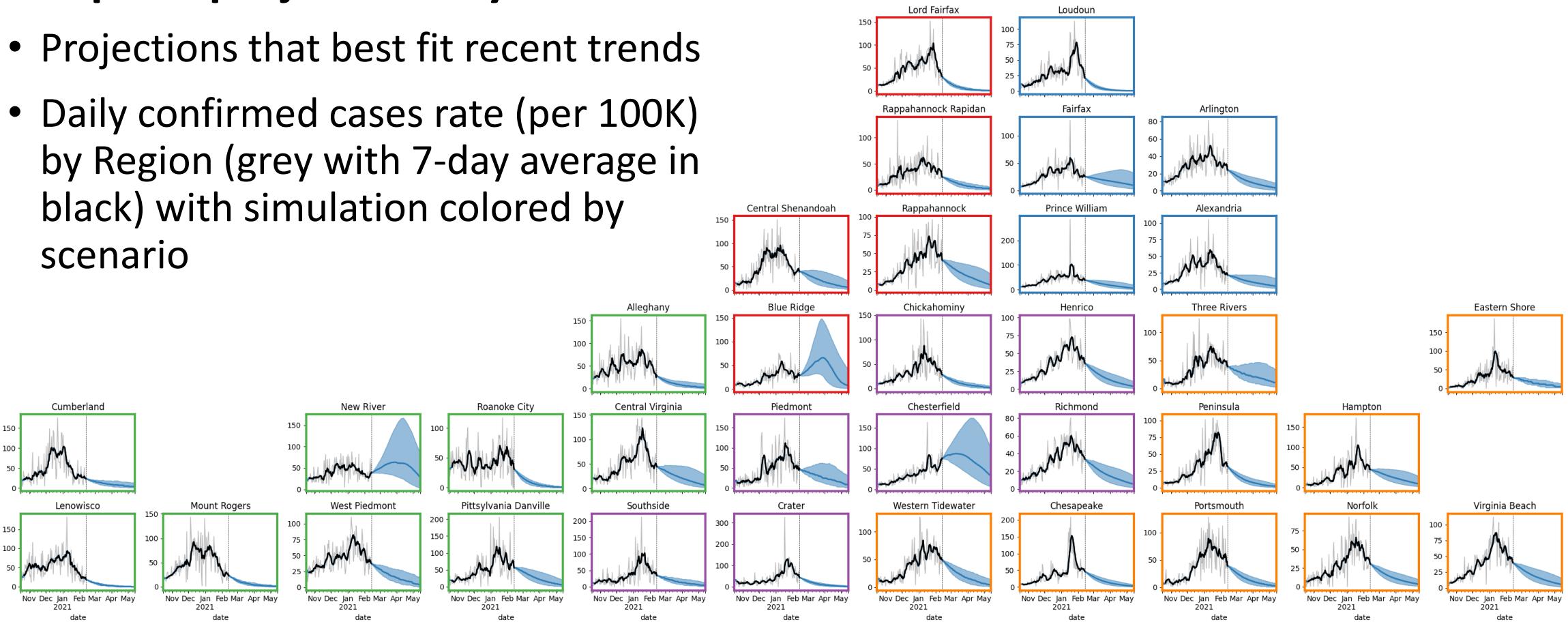
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



# District Level Projections: Adaptive-VariantB117

## Adaptive projections by District

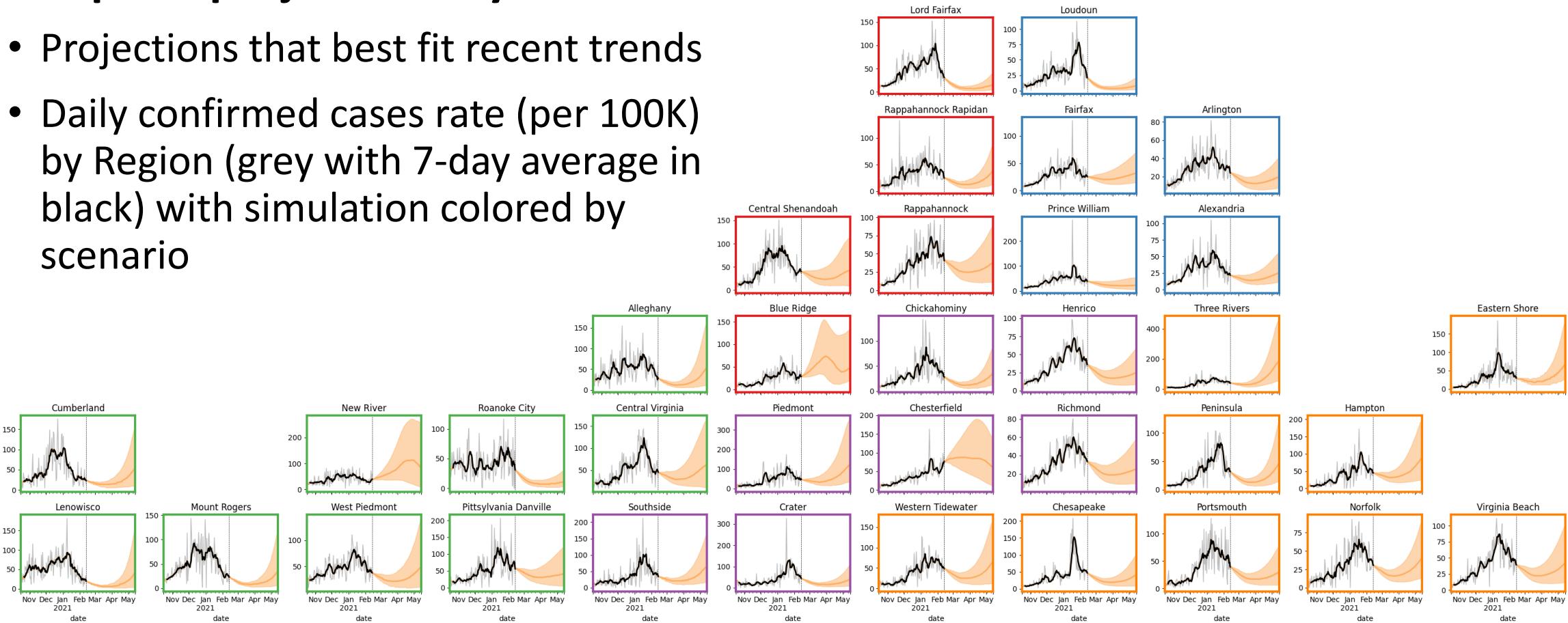
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



# District Level Projections: Adaptive-FatigueControl-VariantB117

## Adaptive projections by District

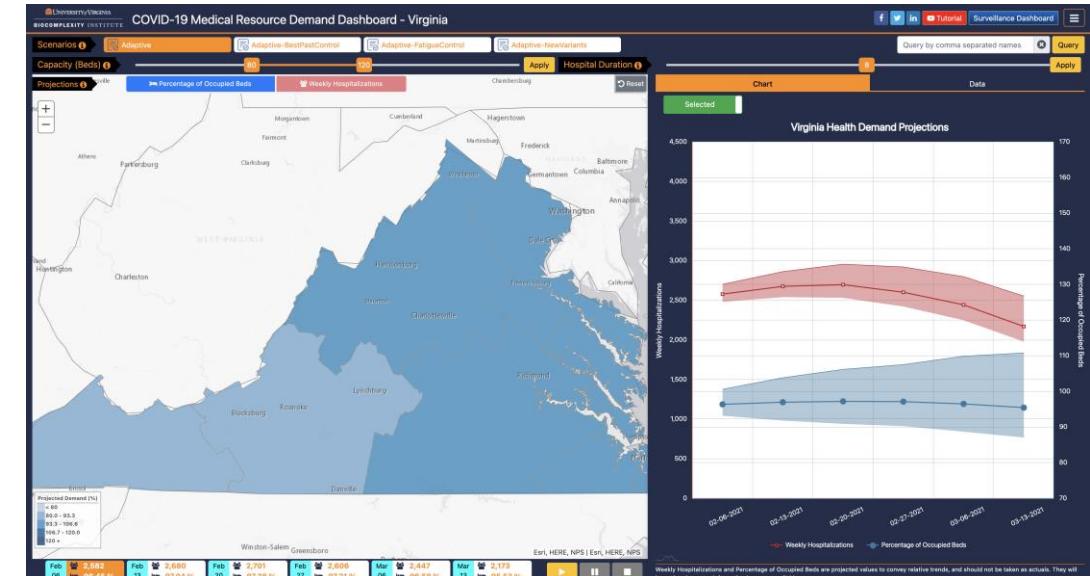
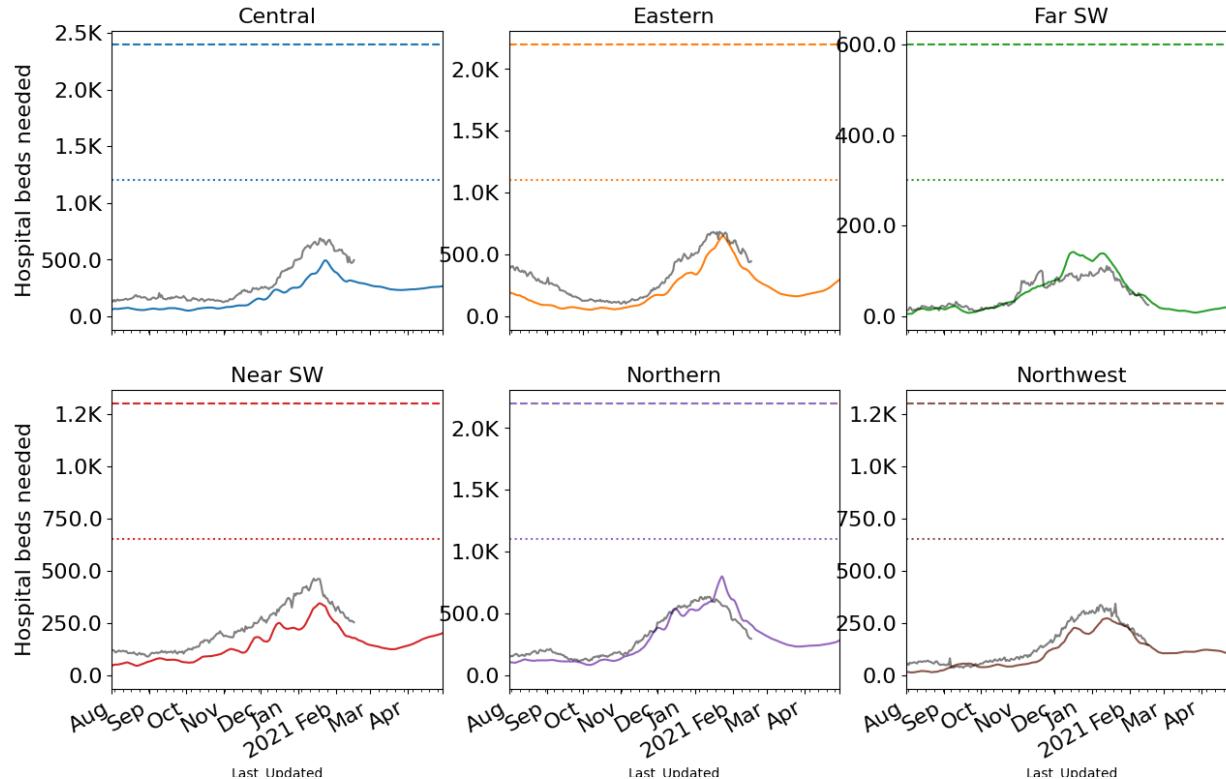
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



# 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-Variant scenario:

- Surge bed capacity is unlikely to be reached in coming 4 months

\* Assumes average length of stay of 8 days

17-Feb-21

# Weekly Cases and Hospitalizations

**Weekly confirmed cases**

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-BestPast	Adaptive-VariantB117	Adaptive-Fatigued Control -VariantB117
2/14/21	23,028	23,028	23,030	23,030	23,028
2/21/21	19,738	19,749	19,751	19,872	19,880
2/28/21	17,419	17,426	17,437	18,075	18,076
3/7/21	15,199	15,204	15,212	16,378	16,371
3/14/21	13,178	13,264	13,118	14,953	15,062
3/21/21	11,180	11,880	10,832	13,651	14,482
3/28/21	9,260	10,834	8,493	12,459	14,532
4/4/21	7,582	9,924	6,423	11,248	14,880
4/11/21	6,006	9,088	4,588	10,002	15,550
4/18/21	4,609	8,386	3,156	8,742	16,558
4/25/21	3,469	7,768	2,079	7,505	17,858
5/2/21	2,556	7,324	1,316	6,280	19,734

**Weekly Hospitalizations**

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-BestPast	Adaptive-VariantB117	Adaptive-Fatigued Control -VariantB117
2/14/21	1,280	1,280	1,280	1,280	1,280
2/21/21	1,087	1,087	1,087	1,095	1,095
2/28/21	936	936	937	971	971
3/7/21	821	822	821	883	886
3/14/21	701	704	698	805	815
3/21/21	599	632	585	728	774
3/28/21	492	580	446	674	777
4/4/21	389	535	318	610	821
4/11/21	303	475	225	529	856
4/18/21	226	432	144	460	903
4/25/21	164	409	94	396	966
5/2/21	116	382	53	324	1,075



# Key Takeaways

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

- **Case rate growth in Virginia continues to decline with a few hotspots emerging**
- VA mean weekly incidence down to 34/100K from 39/100K, US levels decline (to 23 from 29 per 100K)
- Case rates are still high, over a quarter of VA counties above half of their peak
- Projections are down across Commonwealth, though several districts are notably up
- Recent updates:
  - Variant B.1.1.7 scenarios included and added to control-based scenarios
  - Further updates to vaccination schedules, with fitting now including partially vaccinated population and future vaccinations based on current levels instead of goals
- 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](mailto:brylew@virginia.edu)

Srini Venkatramanan

[srini@virginia.edu](mailto:srini@virginia.edu)

Madhav Marathe

[marathe@virginia.edu](mailto:marathe@virginia.edu)

Chris Barrett

[ChrisBarrett@virginia.edu](mailto: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

Feb 6<sup>th</sup> Estimates

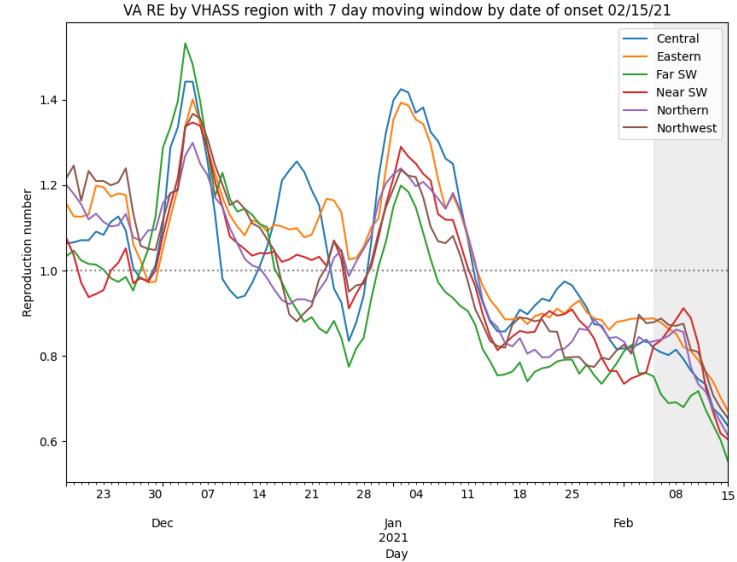
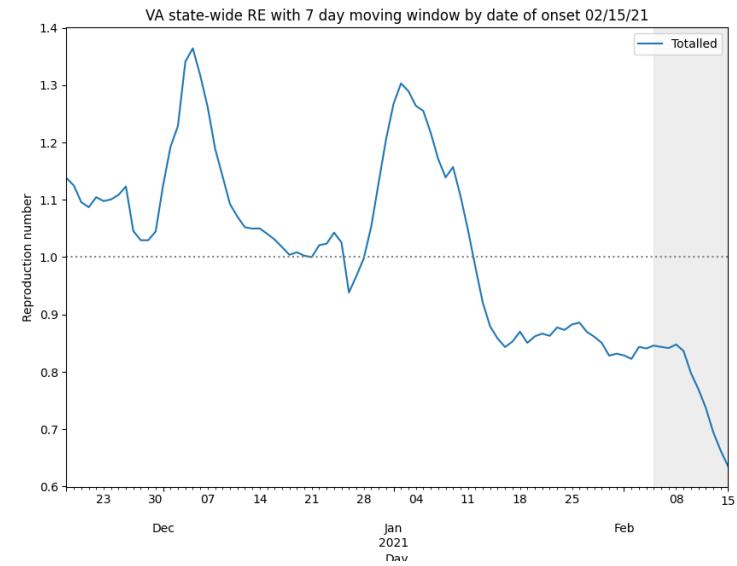
Region	Date of Onset	Date Onset Diff
	R <sub>e</sub>	Last Week
State-wide	0.843	-0.078
Central	0.808	-0.023
Eastern	0.877	0.009
Far SW	0.709	-0.020
Near SW	0.837	0.121
Northern	0.838	0.033
Northwest	0.887	0.132

## Methodology

- Wallinga-Teunis method (EpiEstim<sup>1</sup>) 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,

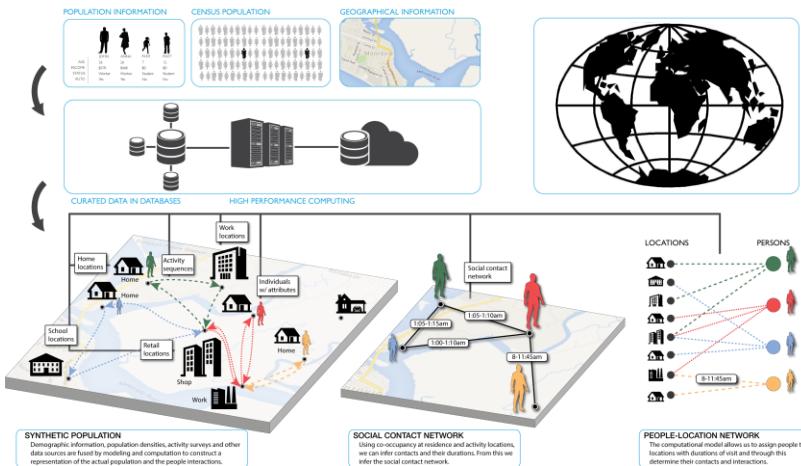
<https://doi.org/10.1093/aje/kwt133>



# Agent-based Model (ABM)

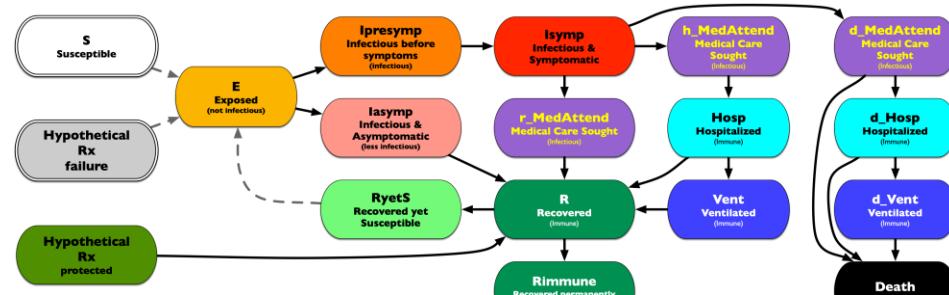
## EpiHiper: Distributed network-based stochastic disease transmission simulations

- 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

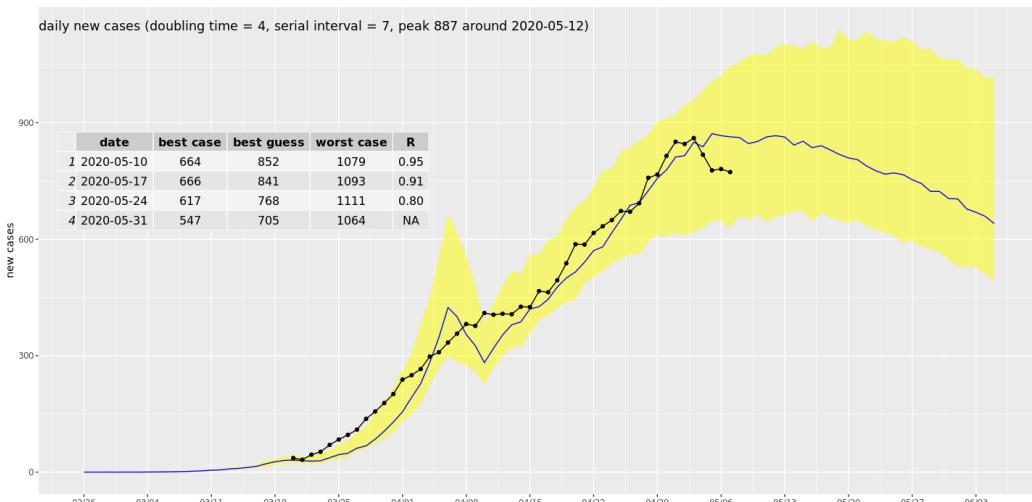


UNIVERSITY OF VIRGINIA

# ABM Social Distancing Rebound Study Design

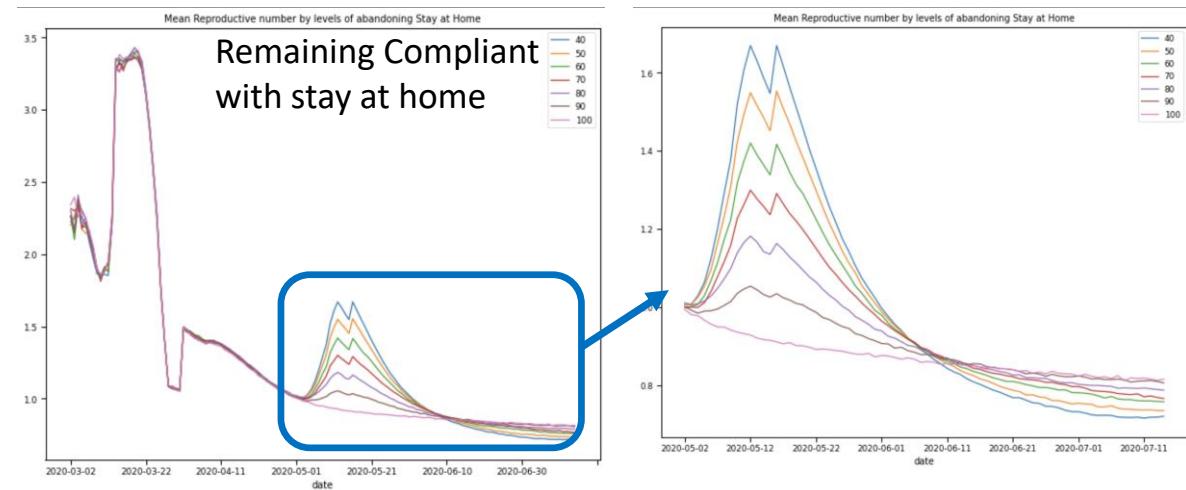
## Study of "Stay Home" policy adherence

- 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 1/6<sup>th</sup> return to pre-pandemic levels