

Network Systems
Science & Advanced
Computing

Biocomplexity Institute
& Initiative

University of Virginia

Estimation of COVID-19 Impact in Virginia

January 6th, 2021

(data current to January 4th-5th)

Biocomplexity Institute Technical report: TR 2021-002



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, 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 has fluctuated through the holidays and is up overall.**
- VA mean weekly incidence (52/100K) up (from 42) as national levels rebound (to 58/100K from 48/100K).
- Projections are mixed across commonwealth but generally up as well.
- Recent updates:
 - Preliminary estimates for vaccination impact
 - Planning scenarios shifted to early January (Jan 8)
 - Added a 3 week “Strong Control” control strategy to scenarios
- Behavioral changes can outpace impact of optimistic vaccine rollout and prevent significantly more cases by Spring.
- The situation is changing rapidly. Models will be updated regularly.



Situation Assessment

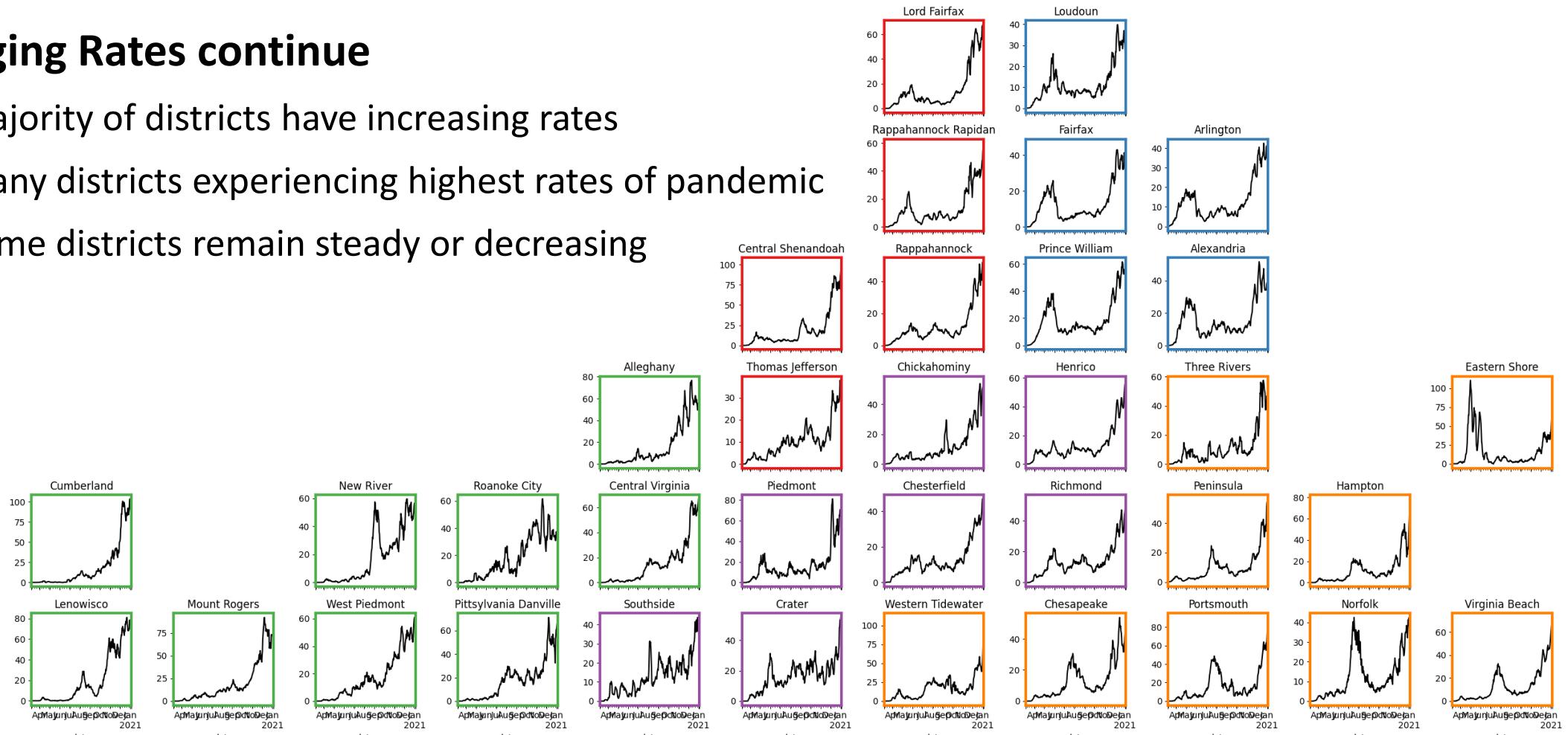


BIOCOMPLEXITY INSTITUTE

Case Rate (per 100k) by VDH District

Surging Rates continue

- Majority of districts have increasing rates
- Many districts experiencing highest rates of pandemic
- Some districts remain steady or decreasing

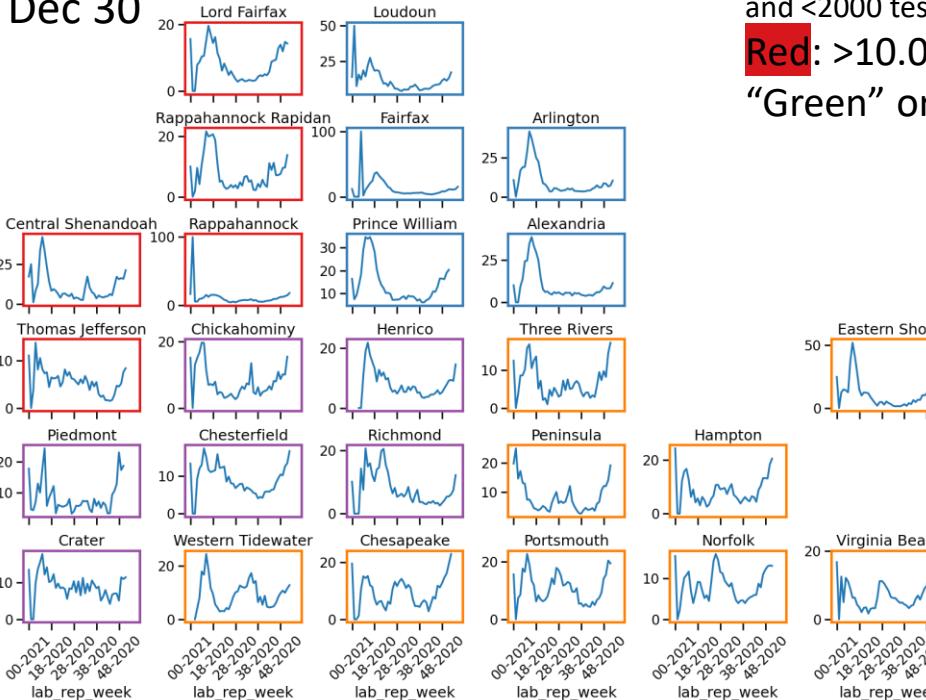
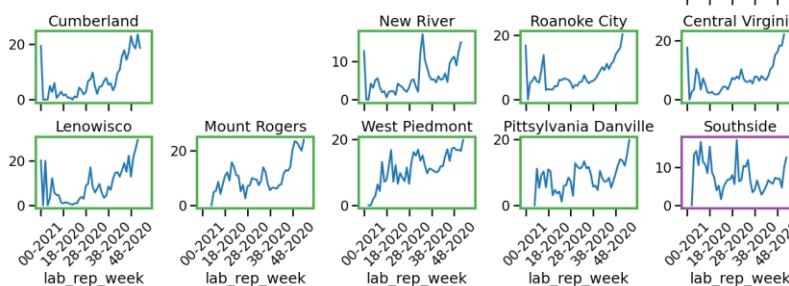


UNIVERSITY OF VIRGINIA

Test Positivity by VDH District

Weekly changes in test positivity by district

- Increasing levels in many districts throughout the commonwealth with many districts above 10% for several weeks
- 120 counties reporting over 10% on Dec 30

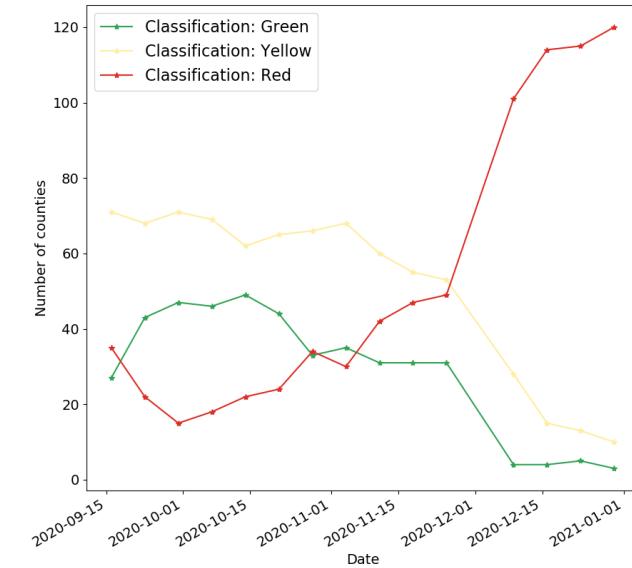


County level test positivity rates for RT-PCR tests.

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”

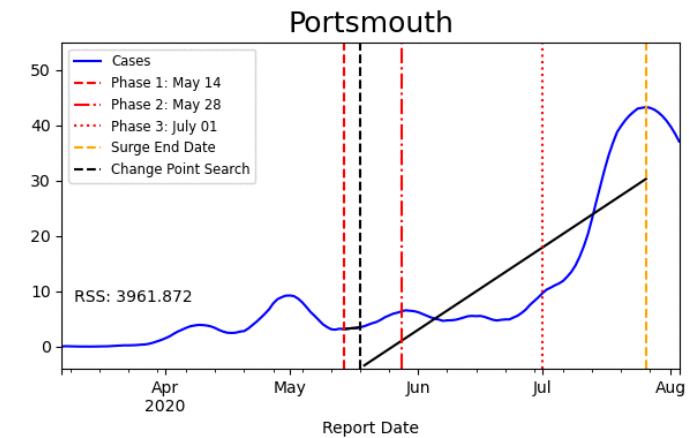


District Trajectories

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



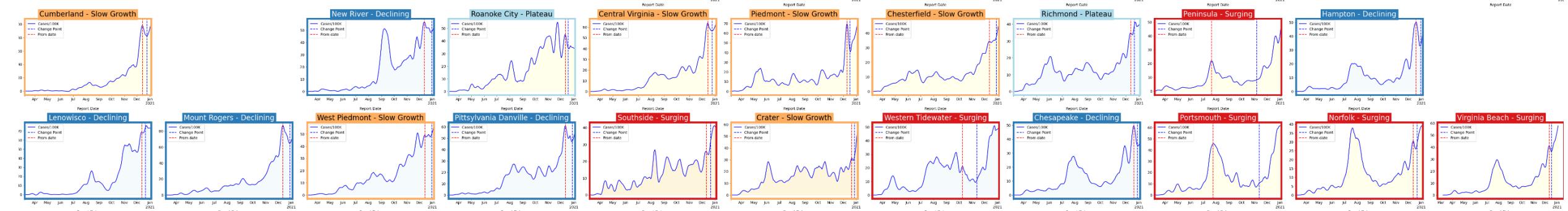
Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	10 (12)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	3 (4)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	13 (9)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	9 (10)



District Trajectories

Status	# Districts (prev week)
Declining	10 (12)
Plateau	3 (4)
Slow Growth	13 (9)
In Surge	9 (10)

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



Estimating Daily Reproductive Number

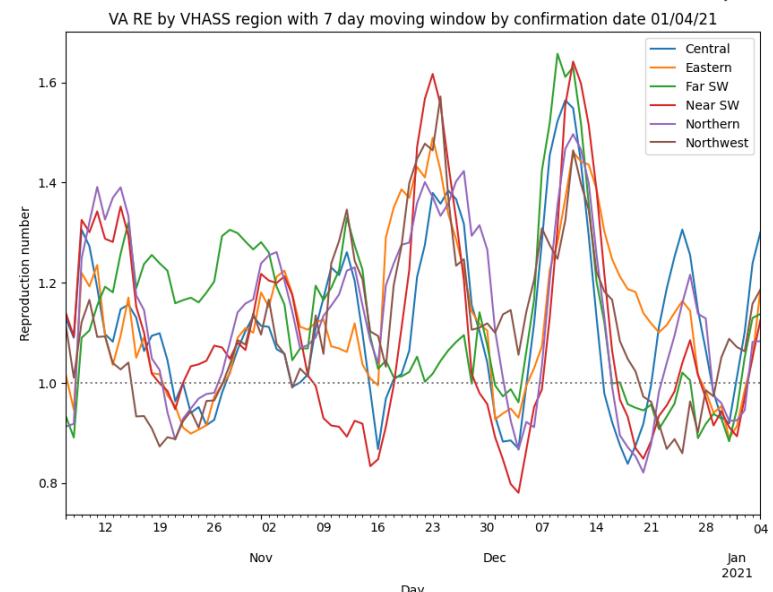
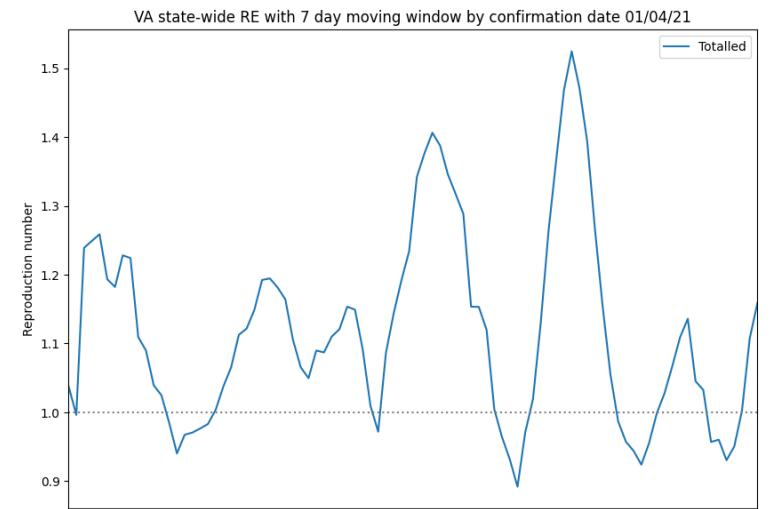
Jan 4th Estimates

Region	Date Confirmed	Date Confirmed R _e	Diff Last Week
State-wide		1.159	0.127
Central		1.300	0.235
Eastern		1.185	0.202
Far SW		1.137	0.220
Near SW		1.125	0.155
Northern		1.083	-0.045
Northwest		1.186	0.201

Methodology

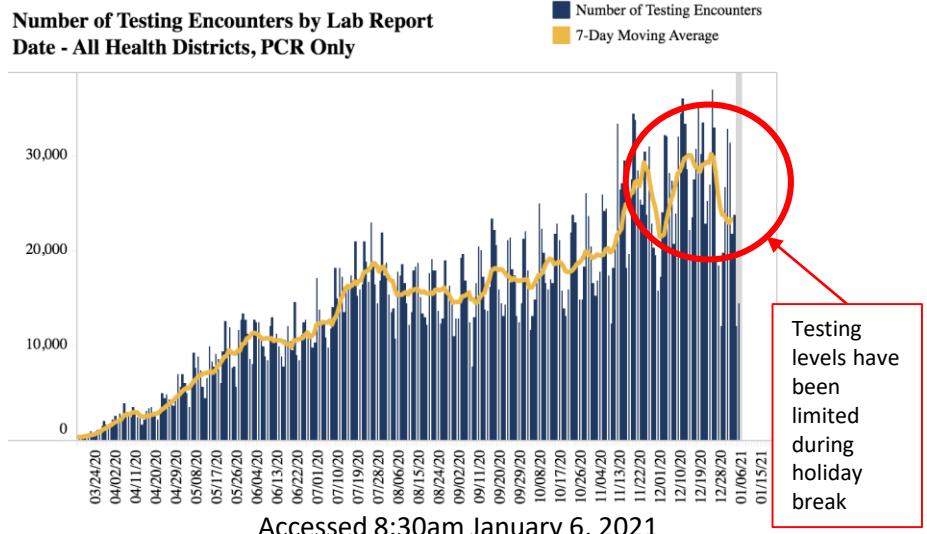
- Wallinga-Teunis method (EpiEstim¹) for cases by confirmation date
- Serial interval: 6 days (2 day std dev)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

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>

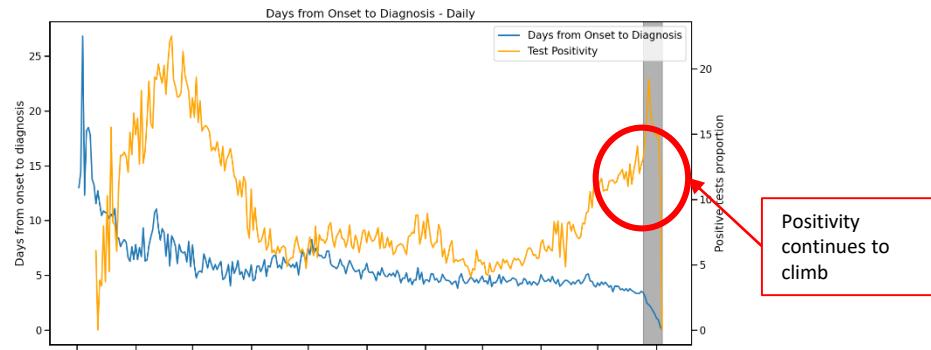


Changes in Case Detection

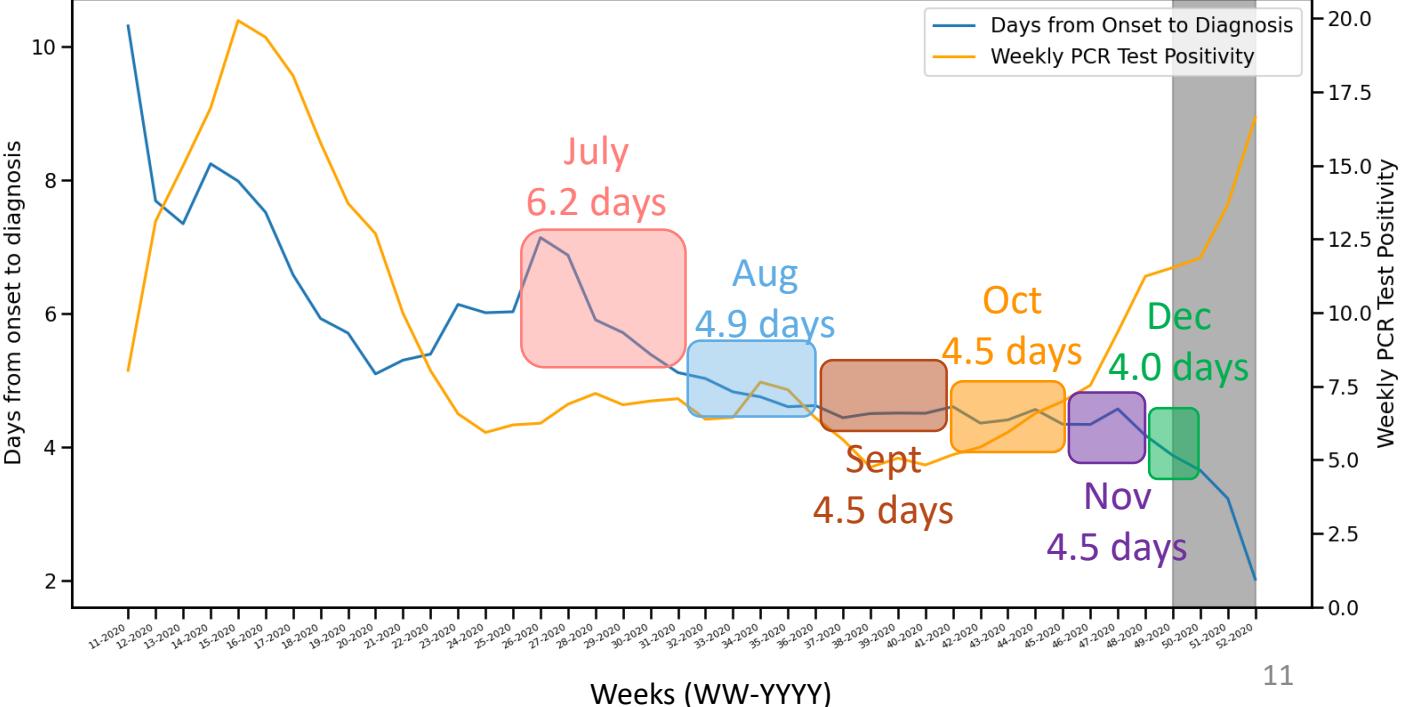
Timeframe (weeks)	Mean days	% difference from overall mean
April (13-16)	7.8	44%
May (17-21)	5.7	6%
June (22-25)	5.9	9%
July (26-30)	6.2	15%
Aug (31-34)	4.9	-9%
Sept (35-38)	4.5	-16%
Oct (39-43)	4.5	-17%
Nov (44-47)	4.5	-18%
Dec (48-49)	4.0	-26%
Overall (13-49)	5.4	--



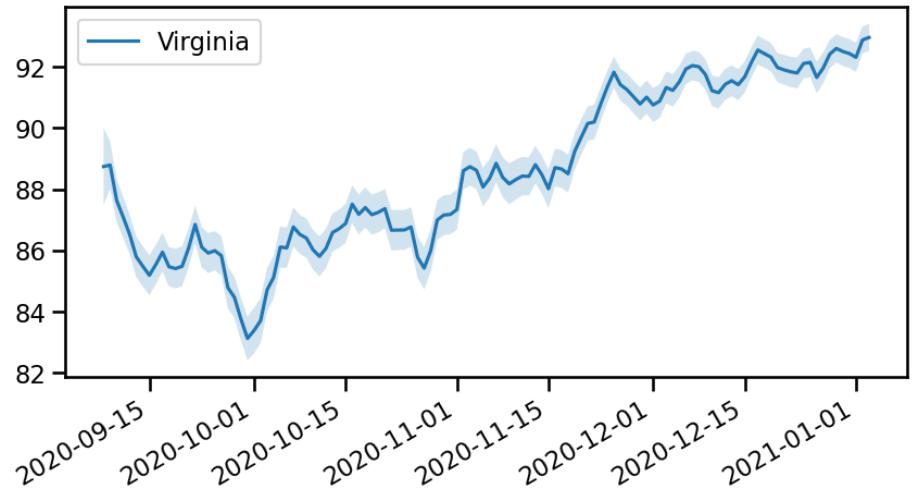
Test positivity vs. Onset to Diagnosis



Days from Onset to Diagnosis and Test Positivity - Weekly



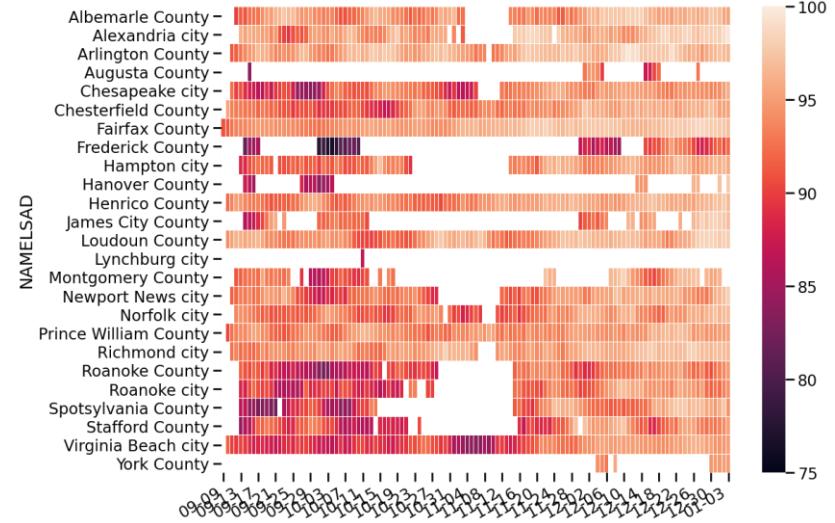
Mask usage in Virginia



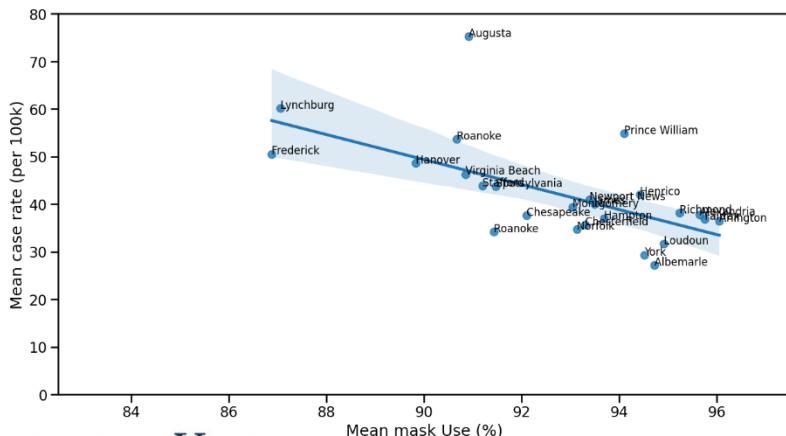
State level mask usage as reported via Facebook surveys over the past month shows ranges from 83% to 91%

- Relatively stable over time
- Limited 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.



Correlations seen among VA counties between mask use and case rate are now stronger due to surging growth

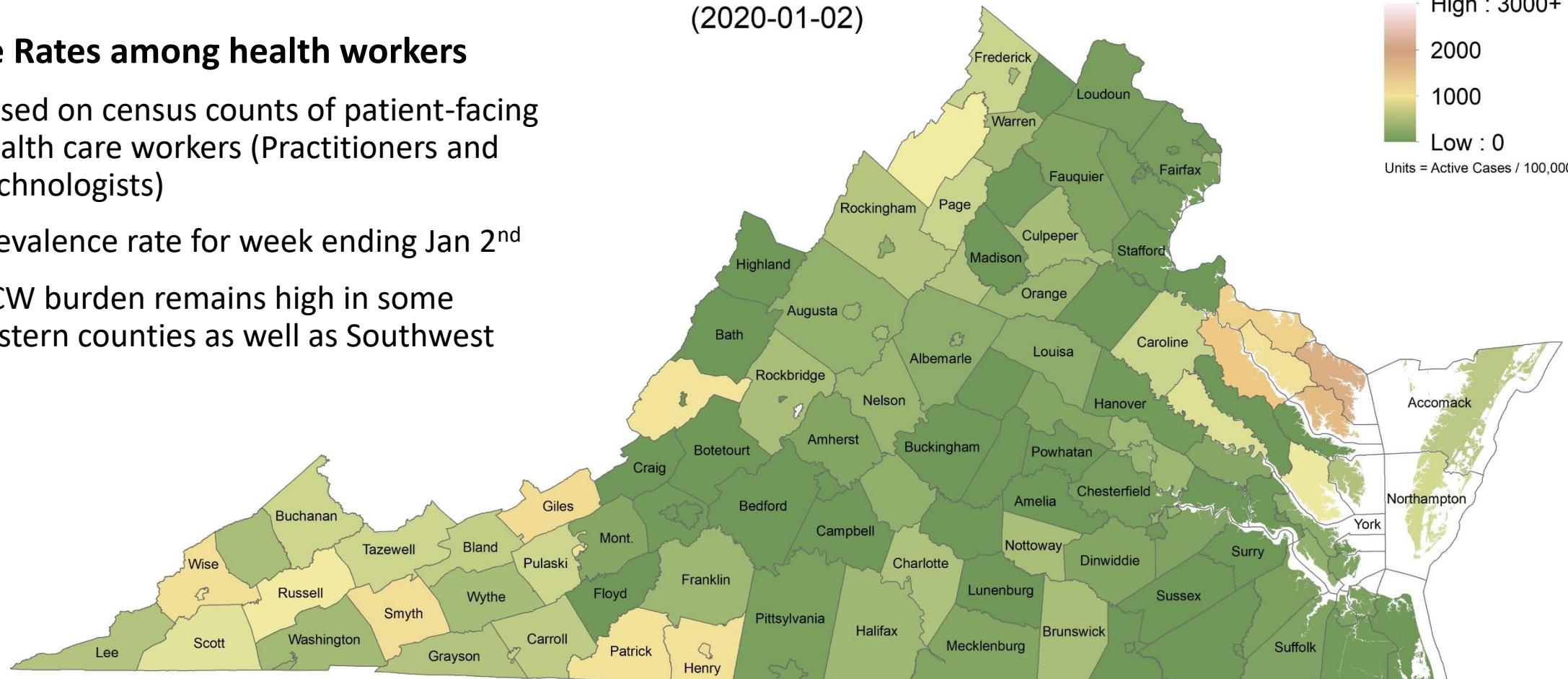
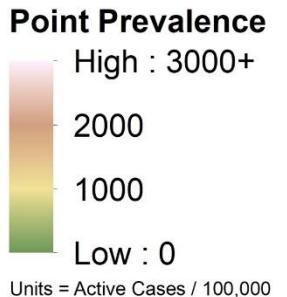
Slope: - 2.85; for every % we see a ~3/100K case rate difference

Health Care Worker Prevalence (per 100K)

Case Rates among health workers

- Based on census counts of patient-facing health care workers (Practitioners and Technologists)
- Prevalence rate for week ending Jan 2nd
- HCW burden remains high in some Eastern counties as well as Southwest

HCW Point Prevalence by Zip Code
(2020-01-02)

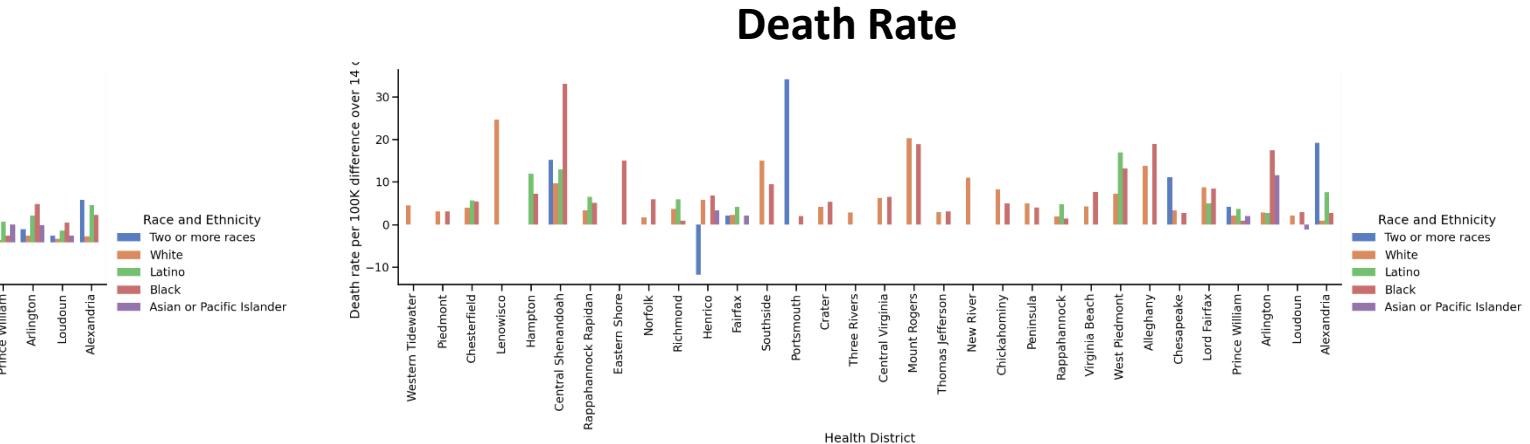
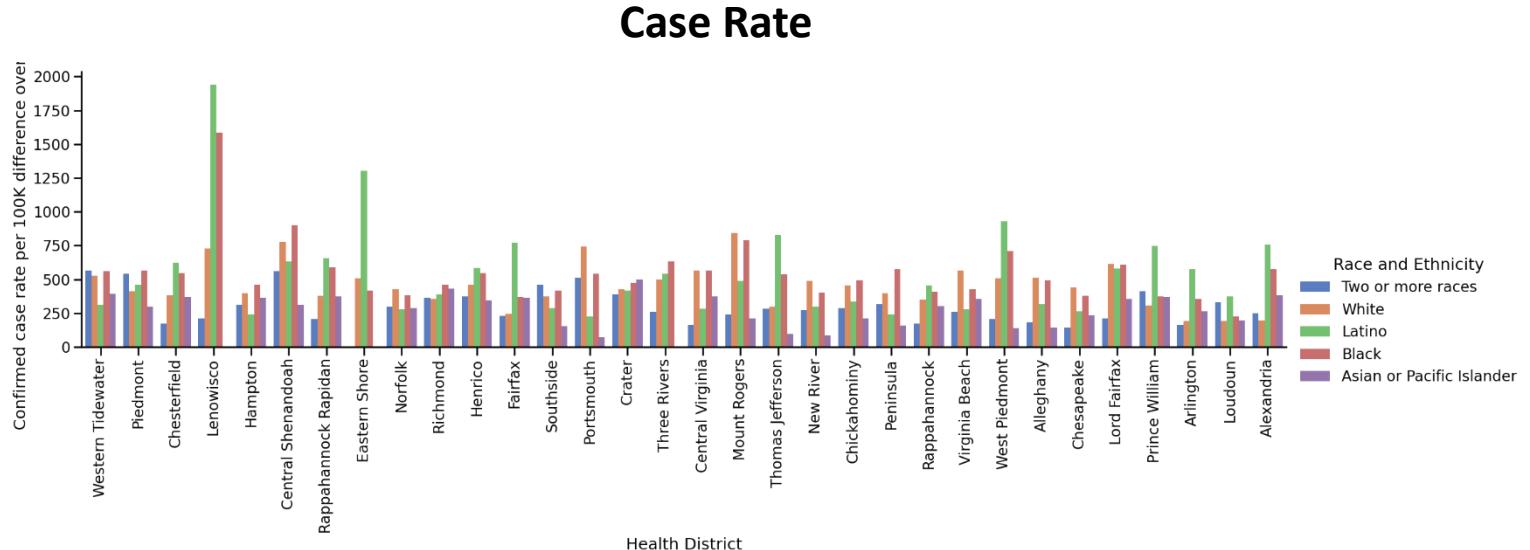
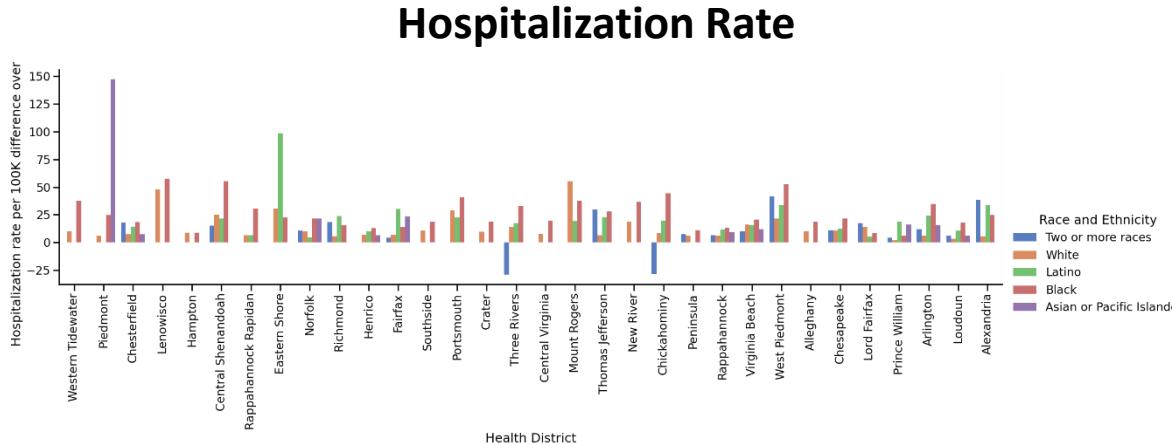


UNIVERSITY OF VIRGINIA

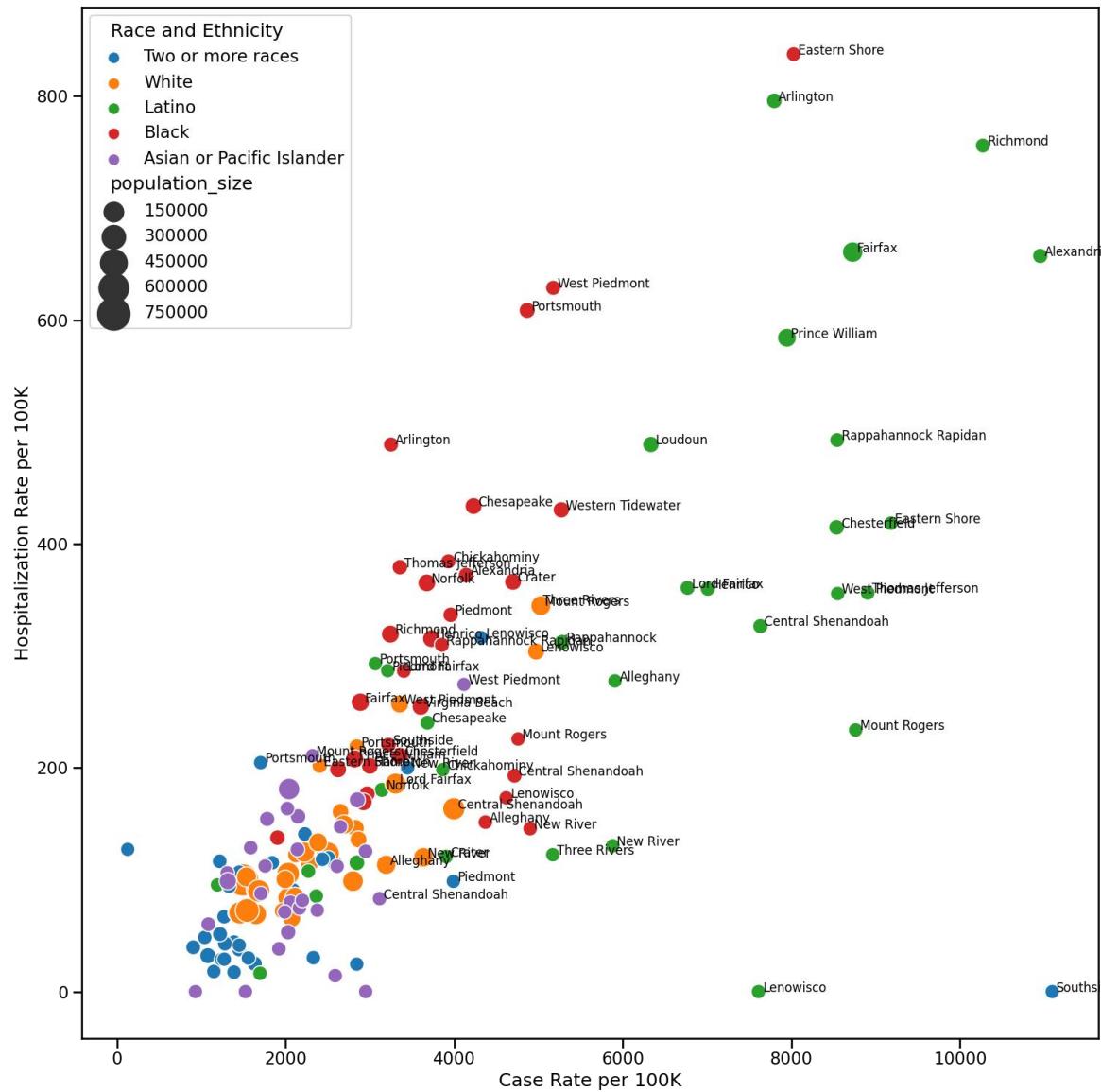
Race and Ethnicity – Recent Rate Changes (per 100K)

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



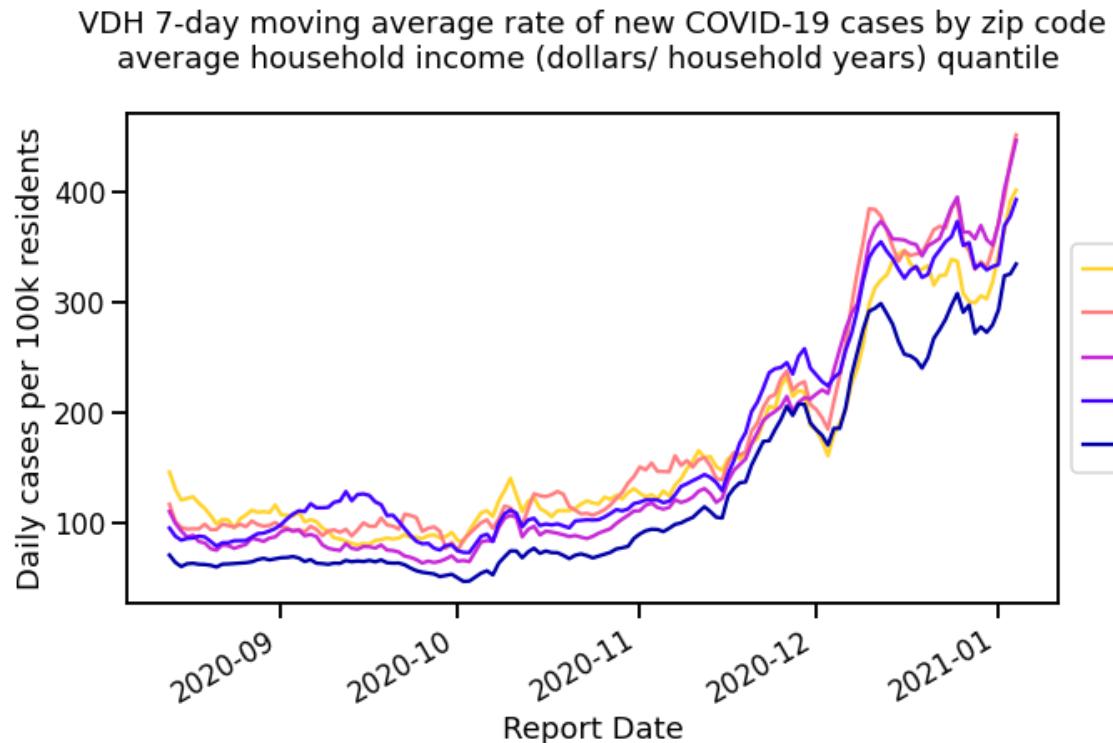
Race and Ethnicity cases per 100K



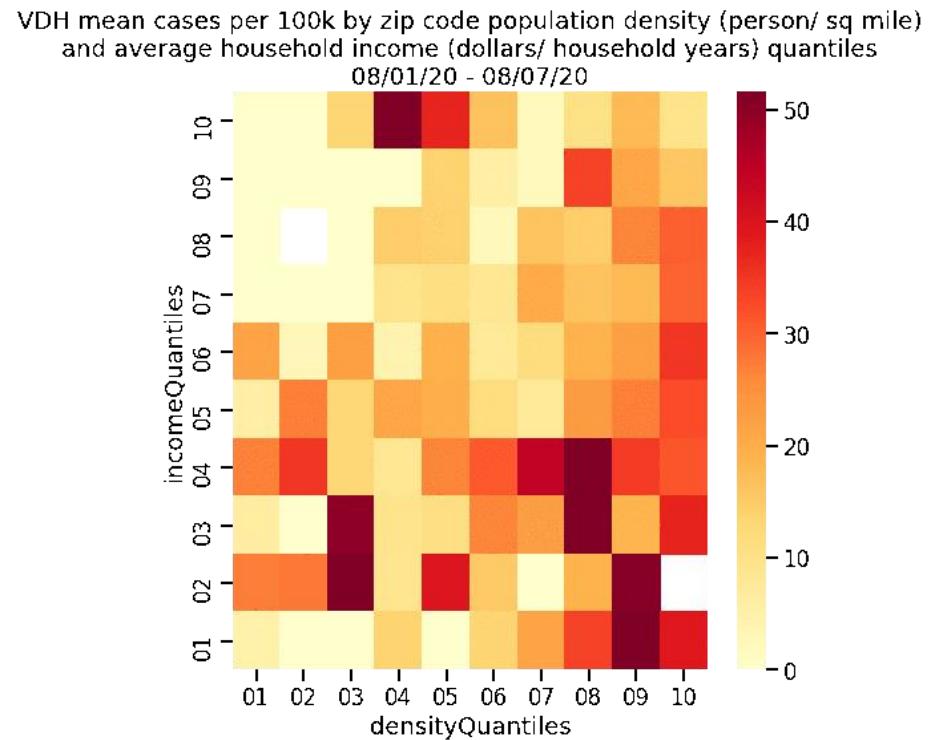
Rates per 100K of each Racial-Ethnic population by Health District

- 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 for clarity

Impact across Density and Income



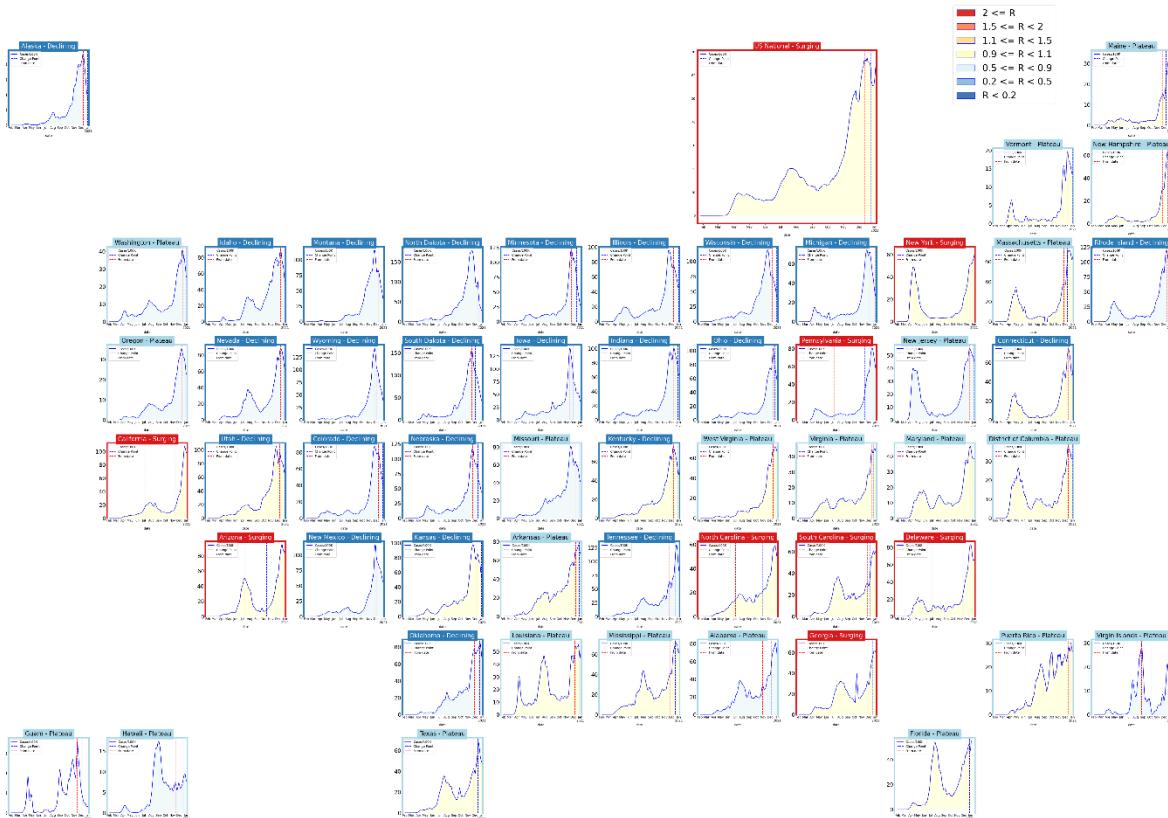
All zip codes show back into growth, wealthiest zip code now lags the rest significantly



Full evolution of pandemic, shows shifts from denser and wealthier zip codes to poorer and less dense zip codes

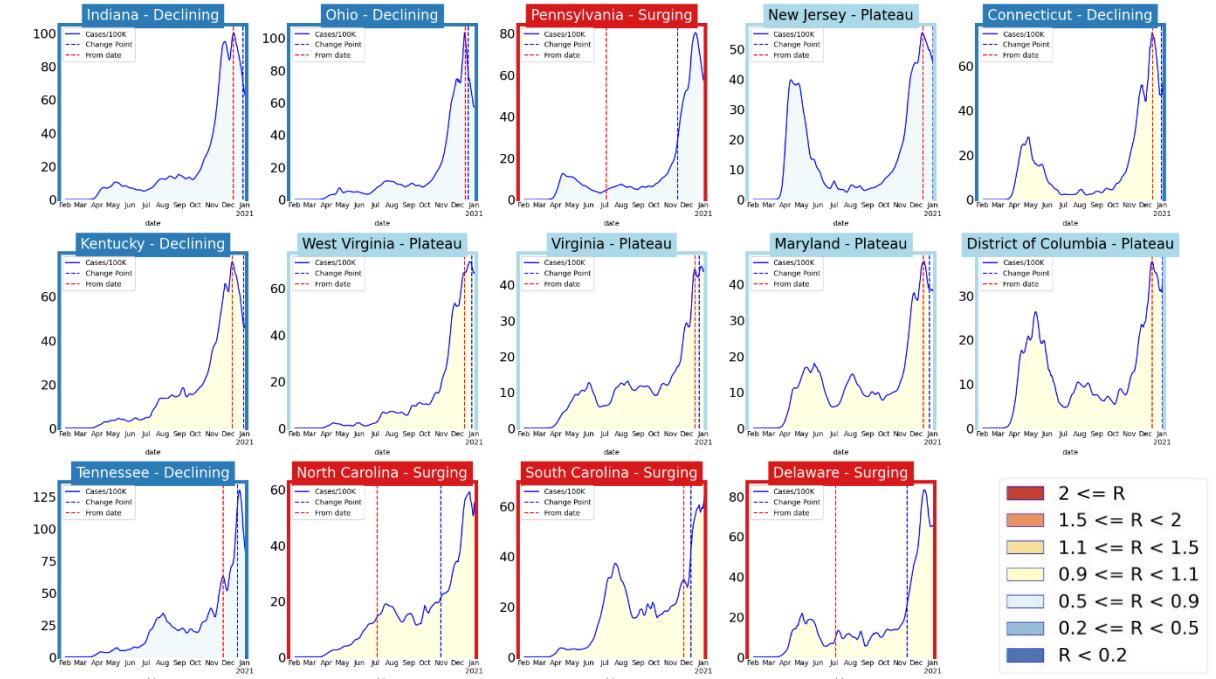
Other State Comparisons

Trajectories of States



- Many of the states with huge surges in past 6 weeks are subsiding

Virginia and her neighbors



- VA slows its growth and is currently plateaued at a high level
- Most surging states (only 8) are in and around mid-Atlantic
- Many neighbors have plateaued, or are declining

Zip code level weekly Case Rate (per 100K)

Case Rates in the last week by zip code

- Several of the top ten zip codes are home to prisons,
- Some counts are low and suppressed to protect anonymity, those are shown in white

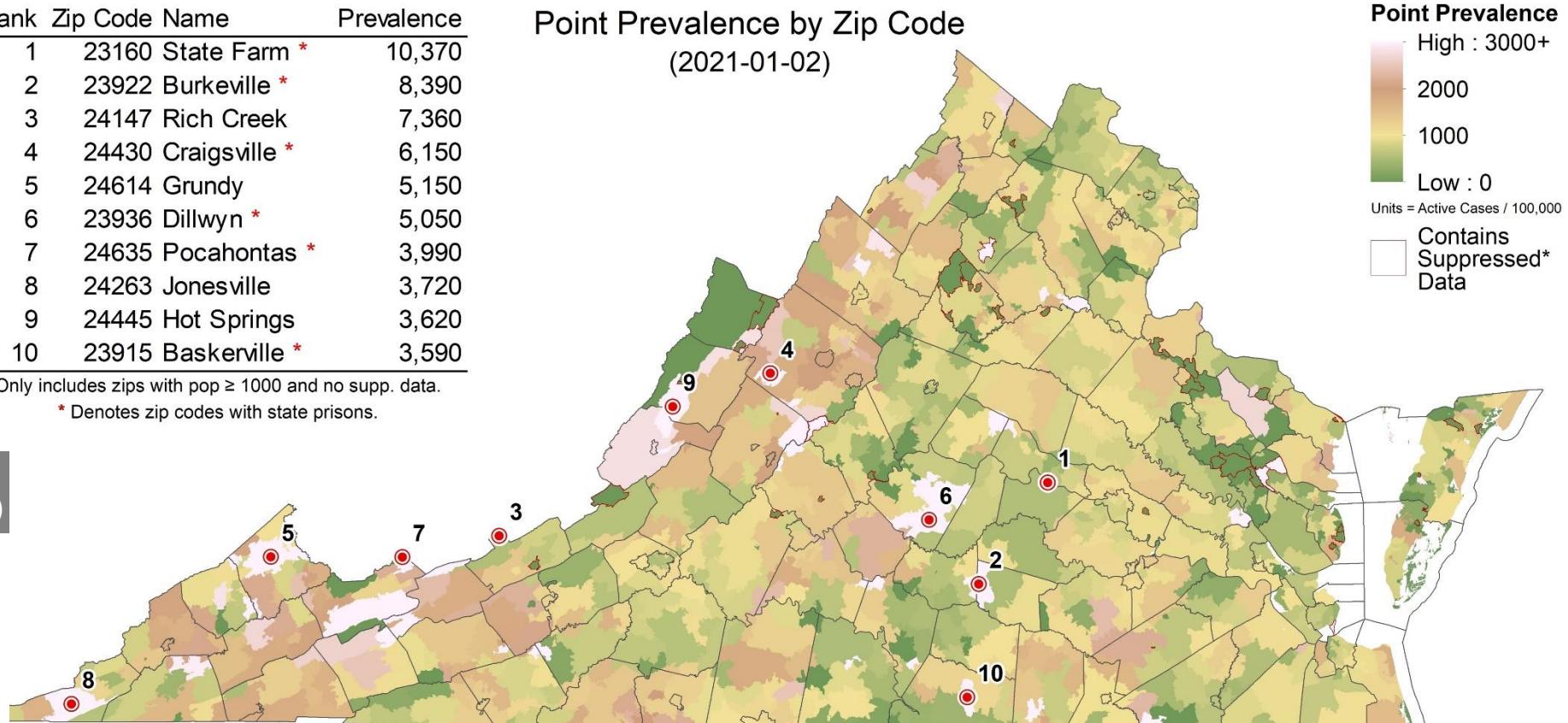
Rank	Zip Code	Name	Prevalence
1	23160	State Farm *	10,370
2	23922	Burkeville *	8,390
3	24147	Rich Creek	7,360
4	24430	Craigsville *	6,150
5	24614	Grundy	5,150
6	23936	Dillwyn *	5,050
7	24635	Pocahontas *	3,990
8	24263	Jonesville	3,720
9	24445	Hot Springs	3,620
10	23915	Baskerville *	3,590

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

* Denotes zip codes with state prisons.

Top 10 excluding prisons

Zip code	Name	Weekly Case Rate (per 100K)
24147	Rich Creek	7358
24614	Grundy	5149
24263	Jonesville	3715
24445	Hot Springs	3620
23084	Kents Store	3465
22834	Linville	3387
23011	Barhamsville	3148
24651	Tazewell	2973
24637	Pounding Mill	2967
22853	Timberville	2843



UNIVERSITY OF VIRGINIA

BIOCOMPLEXITY INSTITUTE

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)

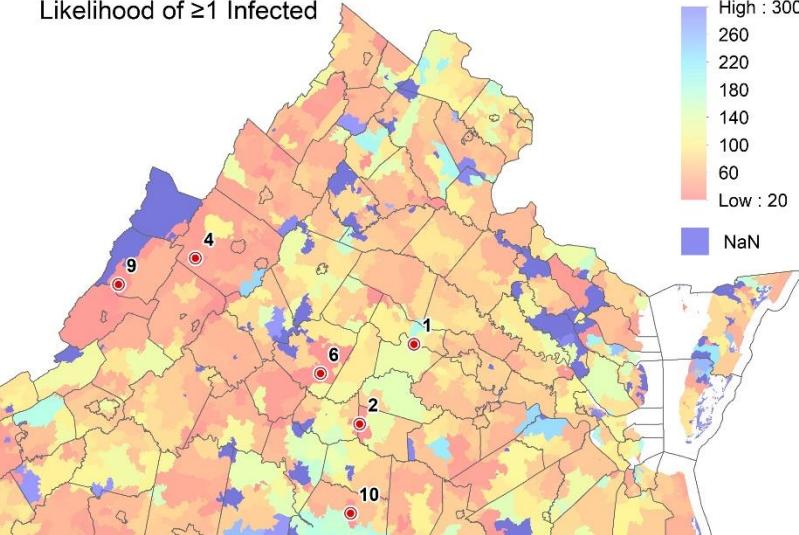
- Assumes 3 undetected infections per confirmed case (ascertainment rate from recent seroprevalence survey)
- On left, minimum size of a group with a 50% chance an individual is infected by zip code (eg in a group of 20 in Staunton, there is a 50% chance someone will be infected)
- Some zip codes have high likelihood of exposure even in groups of 25

Rank	Zip Code Name	Group Size
1	23160 State Farm *	6
2	23922 Burkeville *	8
3	24147 Rich Creek	9
4	24430 Craigsville *	11
5	24614 Grundy	13
6	23936 Dillwyn *	13
7	24635 Pocahontas *	17
8	24263 Jonesville	18
9	24445 Hot Springs	19
10	23915 Baskerville *	19

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

* Denotes zip codes with state prisons.

Group Size Needed for 50% Likelihood of ≥ 1 Infected



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

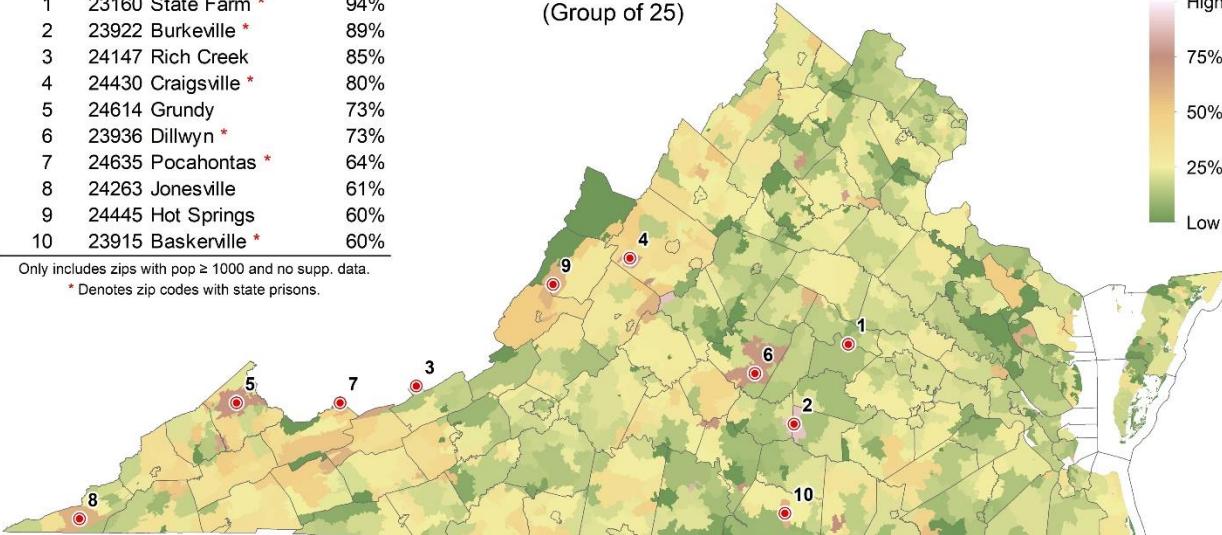
Rank Zip Code Name Likelihood

Rank	Zip Code Name	Likelihood
1	23160 State Farm *	94%
2	23922 Burkeville *	89%
3	24147 Rich Creek	85%
4	24430 Craigsville *	80%
5	24614 Grundy	73%
6	23936 Dillwyn *	73%
7	24635 Pocahontas *	64%
8	24263 Jonesville	61%
9	24445 Hot Springs	60%
10	23915 Baskerville *	60%

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

* Denotes zip codes with state prisons.

Likelihood of ≥ 1 Infected Members
(Group of 25)



Likelihood

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

New variants of SARS-CoV2

Emerging new variant with increased transmissibility but no evidence of higher severity

- Aliases: [Variant VUI 202012/01](#) and [Lineage B.1.1.7](#)
- Variant has been detected in CA, FL, CO, GA, and NY; most without travel history indicating local transmission
- This variant is still detected by PCR, and can be detected by proxy with an “S dropout”
- Evolution expected when virus under selective pressure
- Unlikely to alter efficacy of vaccines or other immune treatments
- NERVTAG suggests that “[*VUI-202012/01 demonstrates a substantial increase in transmissibility compared to other variants*](#)”
- Another South African variant (501Y.V2) has sparked concern as its mutations may change efficacy of vaccines and other immunological treatments



nextstrain.org

Model Update – Adaptive Fitting



Adaptive Fitting Approach

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

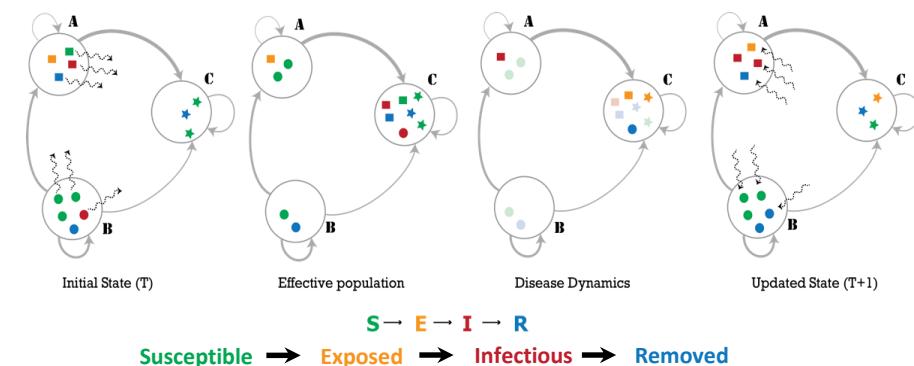
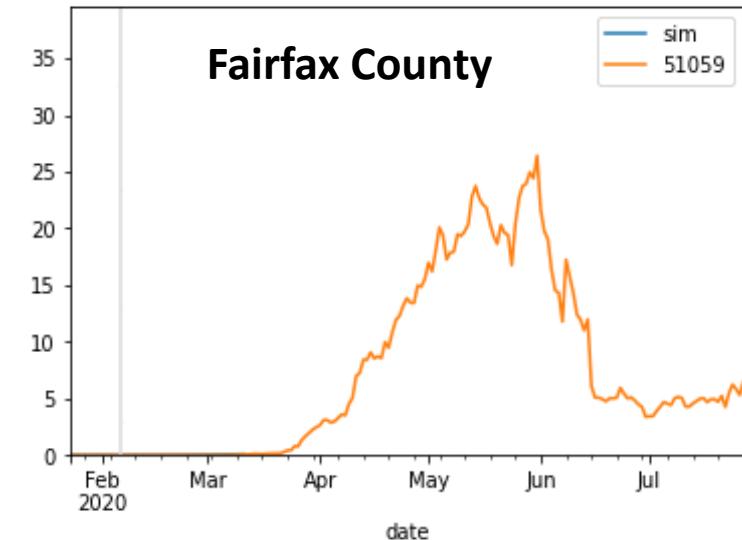
- Allows history to be precisely captured, and used to guide bounds on projections

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

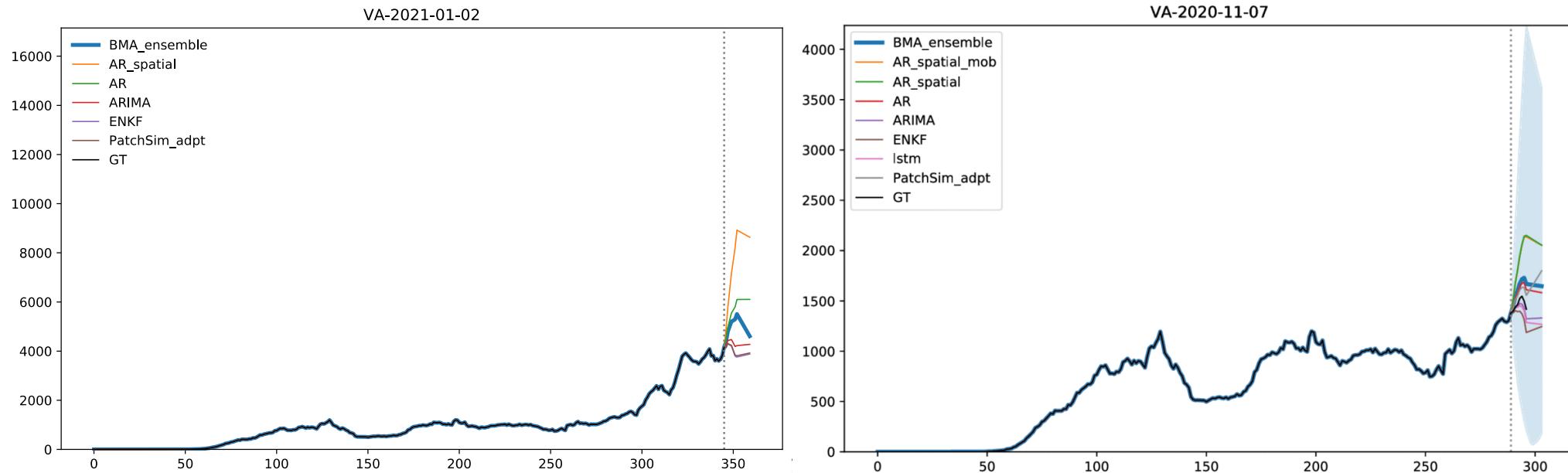
- Widespread pandemic eliminates sensitivity to initial conditions
- Uses steady 1 case per 10M population per day external seeding



Using Ensemble Model to Guide Projections

An ensemble methodology that combines the Adaptive Fitting and machine learning and statistical models has been developed and refined

- **Models:** Adaptive Fitting, ARIMA, LSTM, AR, spatially driven AR, Kalman Filters (ENKF)
- This approach facilitates the use of other data streams (weather, mobility, etc.)
- Ensemble provides scaffolding for the Adaptive Fitting's short-term projections



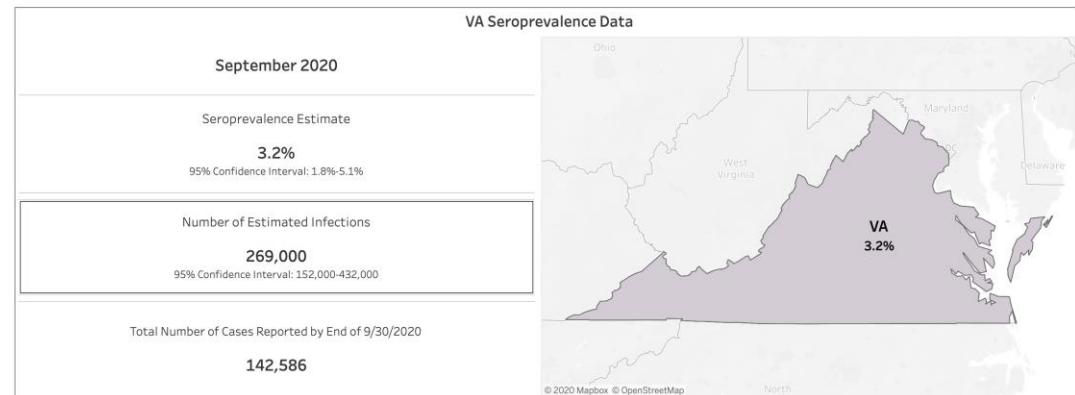
Seroprevalence updates to model design

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

- Virginia Serology Study estimated 2.4% of Virginians estimated infected (as of Aug 15th)
- CDC Nationwide Commercial Laboratory Seroprevalence Survey estimated 4.1% [2.4% – 6.2%] seroprevalence as of Oct 9th-21st up from 3.2% 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)



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

Virginia Coronavirus Serology Project Interim findings by region and statewide - July 22, 2020

Region	Number of participants	Number antibody positive	Crude prevalence per 100 participants	Weighted prevalence* per 100 population (95% CI)
Central	400	8	2.0	3.0 (0.5, 5.5)
East	707	9	1.3	1.5 (-0.2, 3.2)
Northern	819	36	4.4	4.2 (2.5, 5.9)
Northwest	756	11	1.5	0.9 (0.2, 1.6)
Southwest	431	3	0.7	1.0 (-0.2, 2.1)
Virginia	3,113	67	2.2	2.4 (1.6, 3.1)

* Weighted prevalence is reweighted by region, age, sex, race, ethnicity, and insurance status to match census population.

<https://www.vdh.virginia.gov/content/uploads/sites/8/2020/08/VDH-Serology-Projects-Update-8-13-2020.pdf>

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 14 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					
371,913	(New Cases: 4,377) [▲]	18,526		5,191					
Confirmed† 309,659	Probable† 62,254	Confirmed† 17,882	Probable† 644	Confirmed† 4,572	Probable† 619				
<small>* Includes both people with a positive test (Confirmed) and symptomatic with a known exposure to COVID-19 (Probable). ** Hospitalization status at time case was investigated by VDH. 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/ Source: Cases - Virginia Electronic Disease Surveillance System (VEDSS), data entered by 5:00 PM the prior day.</small>									
Outbreaks									
Total Outbreaks*		Outbreak Associated Cases							
1,982		45,992							
<small>* At least two (2) lab confirmed cases are required to classify an outbreak.</small>									
Testing (PCR Only)									
Testing Encounters PCR Only*			Current 7-Day Positivity Rate PCR Only**						
4,404,641			16.2%						
<small>* 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.</small>									
Multisystem Inflammatory Syndrome in Children									
Total Cases*		Total Deaths							
13		0							
<small>*Cases defined by CDC HAN case definition: https://emergency.cdc.gov/han/2020/han00432.asp</small>									

Accessed 8:30am January 6, 2021

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

Scenarios – Seasonal Effects and Vaccines

- Societal changes in the past month have led to an increase in transmission rates, these could continue to drive transmission
 - Seasonal impact of weather patterns, viral mutations, interactions at places of learning, travel related to holidays and traditional large family gatherings, fatigue with infection control practices
 - Population's behaviors determine the level of control of transmission we can achieve
- Vaccination has started, focus on priority groups may limit population level effects initially, though small impacts may be observed in early February
 - Initial rollout estimated at 12.5M people in US (~330K in VA) in January, then 25M (~660K) per month, assumes limited impact from any vaccinations in December.
 - Assume all available vaccine is administered and has 80% efficacy in 2 weeks (timing more sensitive than max efficacy in early stages)
 - Counterfactuals with no vaccine ("NoVax") are provided for comparison purposes

Scenarios – Seasonal Effects and Vaccines

- Three behavioral scenarios capture possible trajectories starting Dec 24th, 2020
 - **Adaptive:** No change from base projection
 - **Adaptive-StrongControl-3w:** 30% decrease in transmission starting Jan 8th, 2021 which lasts for 3 weeks, before returning to same transmission rate as Adaptive
 - **Adaptive-LessControl:** 15% increase in transmission starting Jan 8th, 2021
- Vaccinations are incorporated in “base” projections, counterfactuals without vaccinations provide lower bound on vaccines impact
 - **Adaptive-NoVax:** No change from base projection without vaccine
 - **Adaptive-NoVax-StrongControl-3w:** 30% decrease in transmission starting Jan 8th, 2021 which lasts for 3 weeks, before returning to same rate as Adaptive without vaccine
 - **Adaptive-NoVax-LessControl:** 15% increase in transmission starting Jan 8th, 2021 without vaccine



Model Results

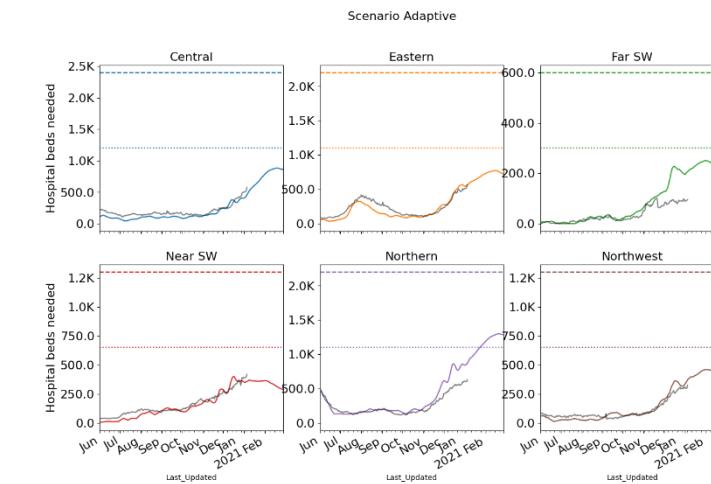
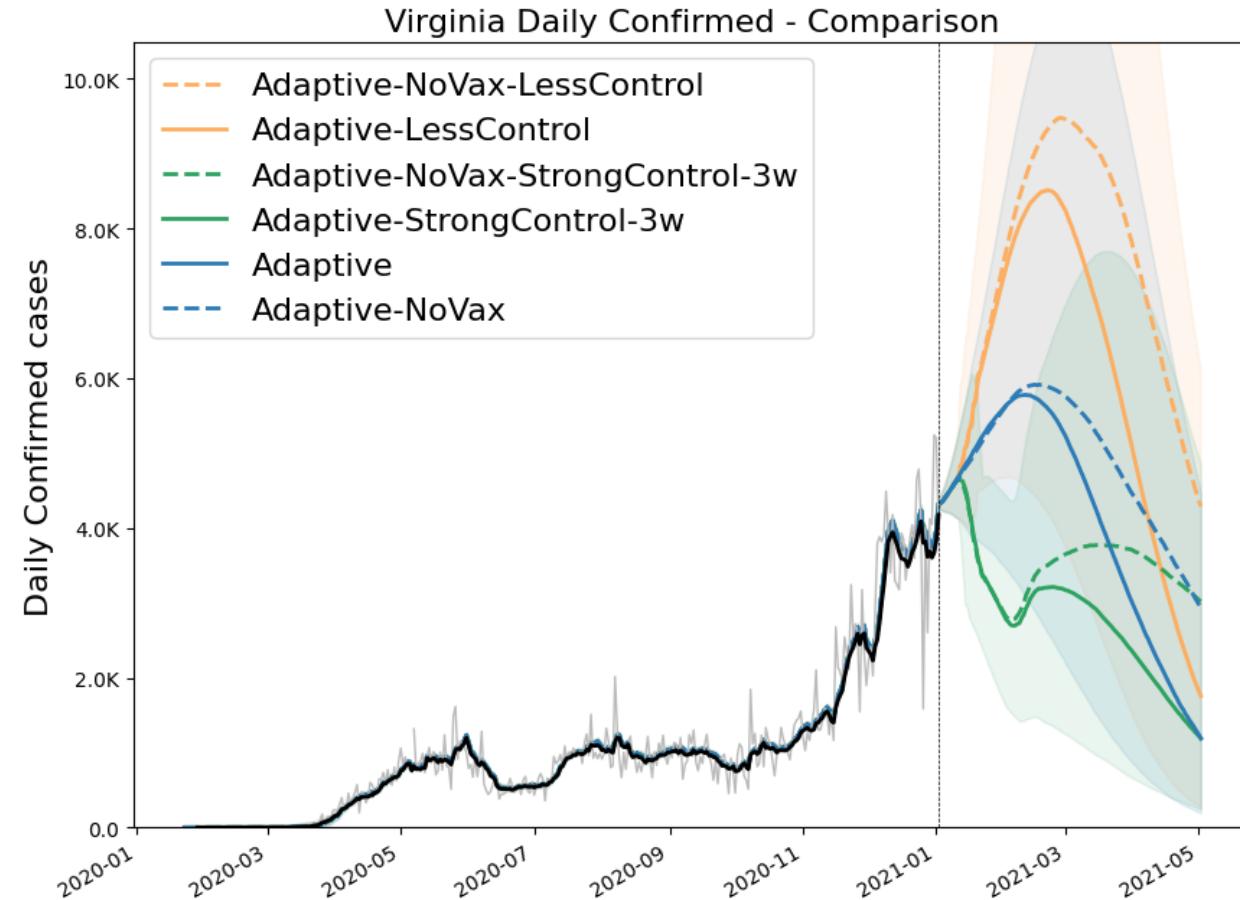


BIOCOMPLEXITY INSTITUTE

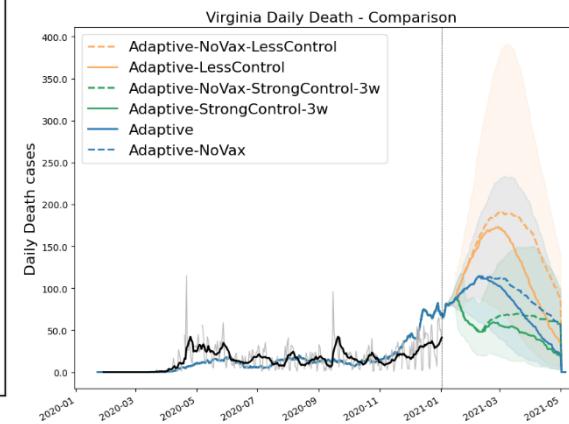
Outcome Projections

Estimated Hospital Occupancy

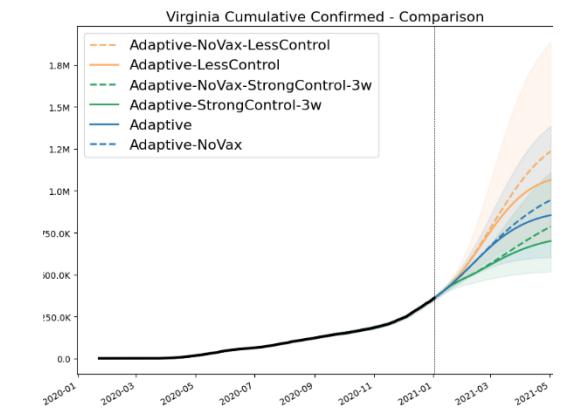
Confirmed cases



Daily Deaths



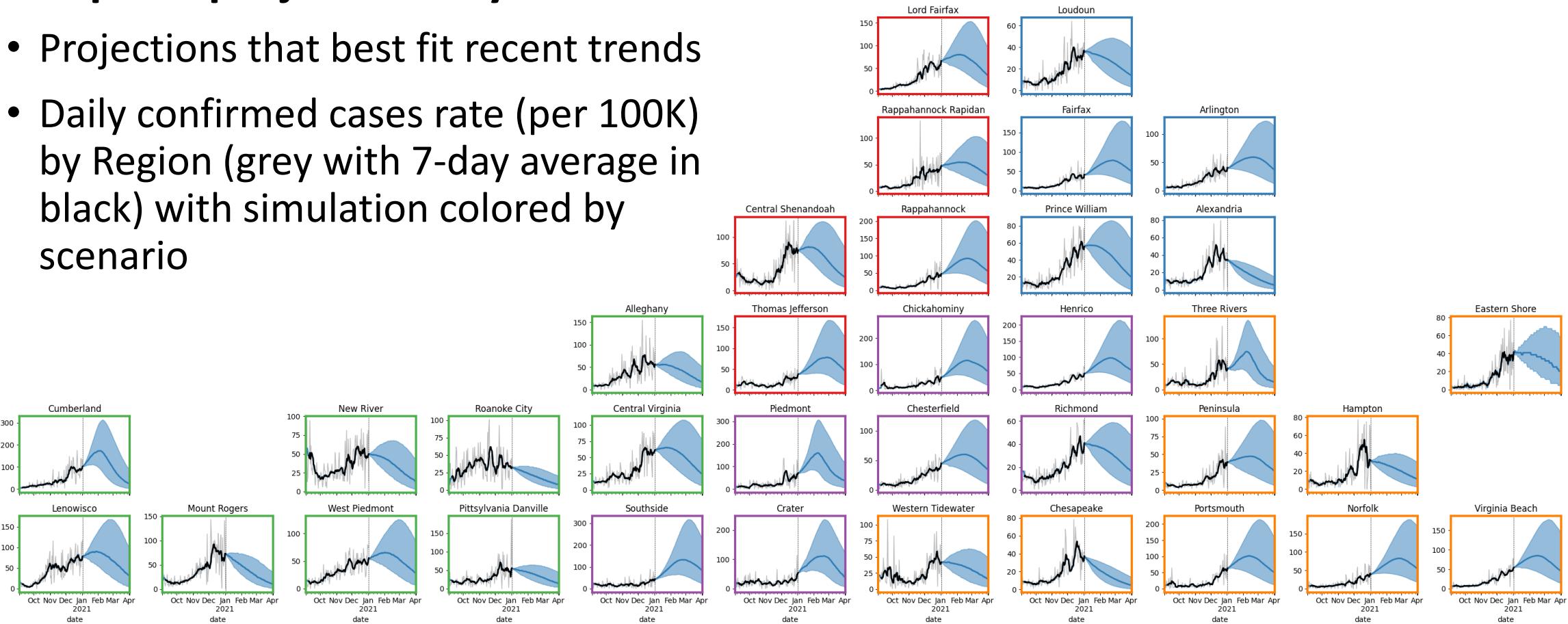
Cumulative Confirmed cases



District Level Projections: Adaptive

Adaptive projections by District

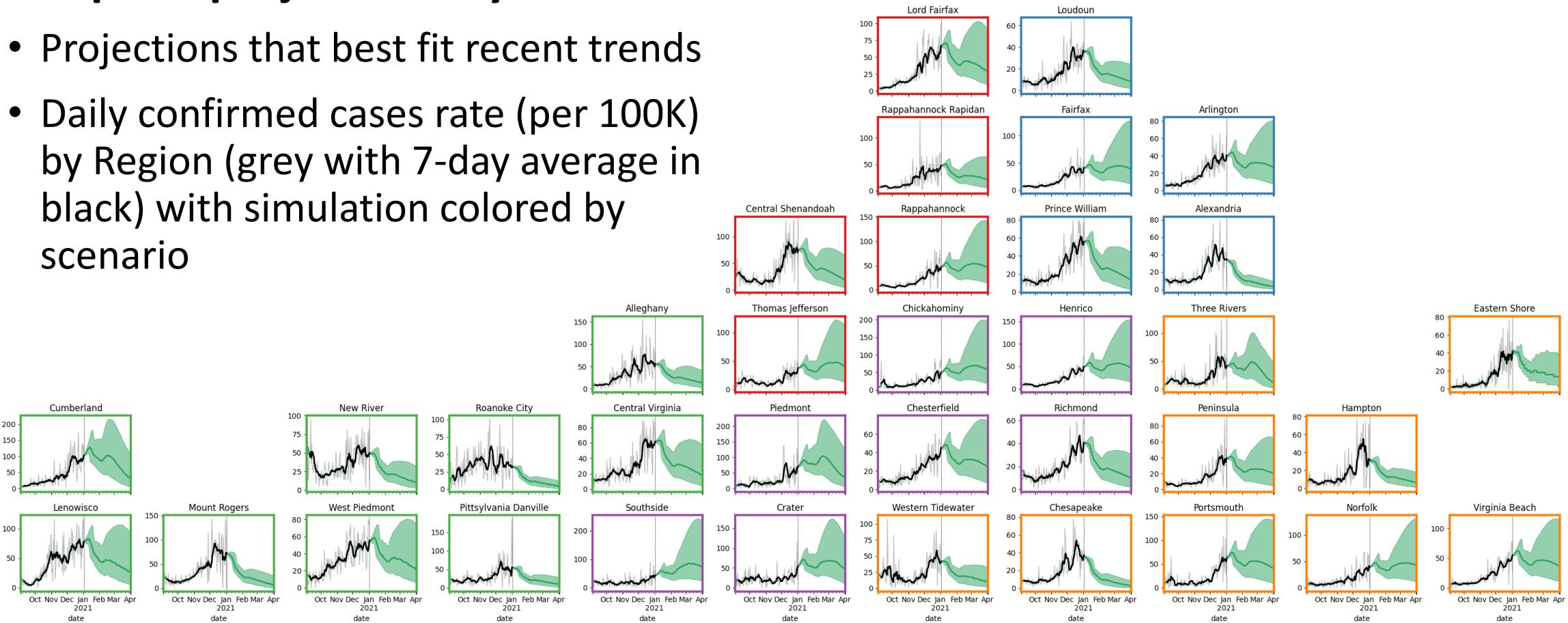
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-StrongControl-3w

Adaptive projections by District

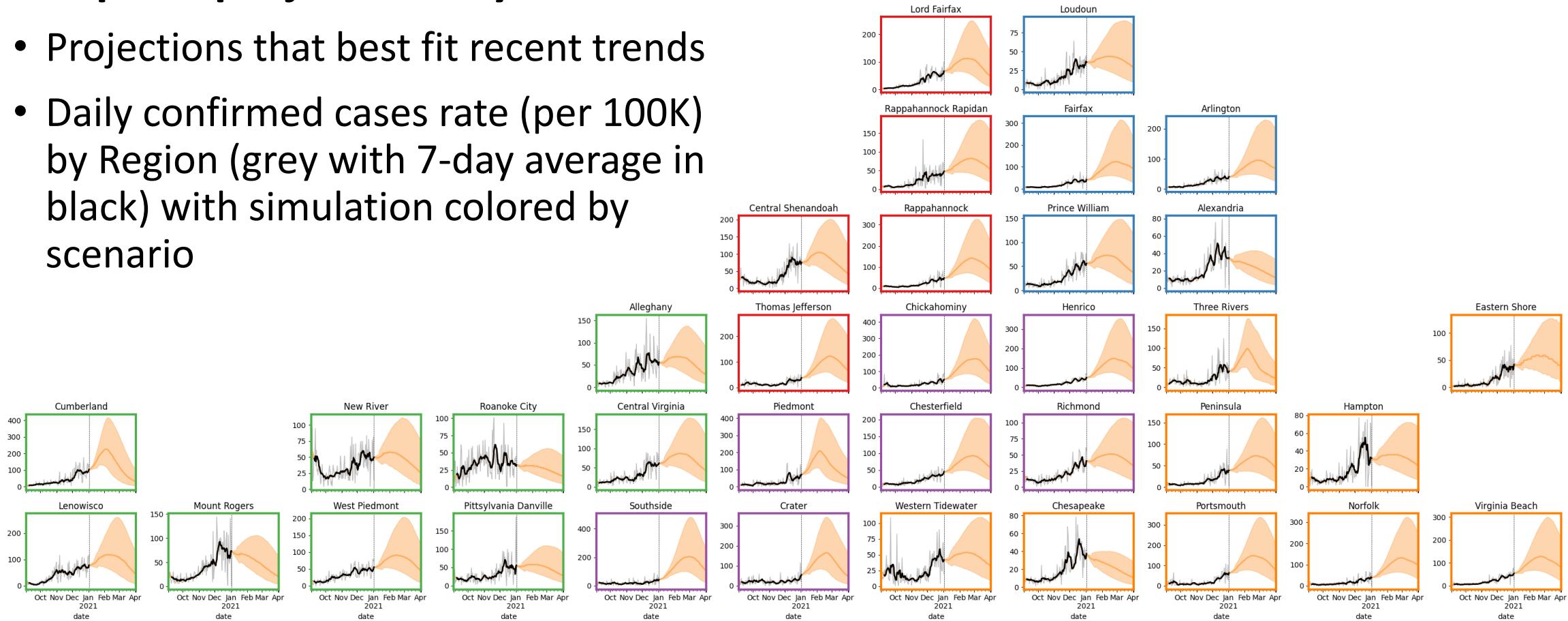
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-LessControl

Adaptive projections by District

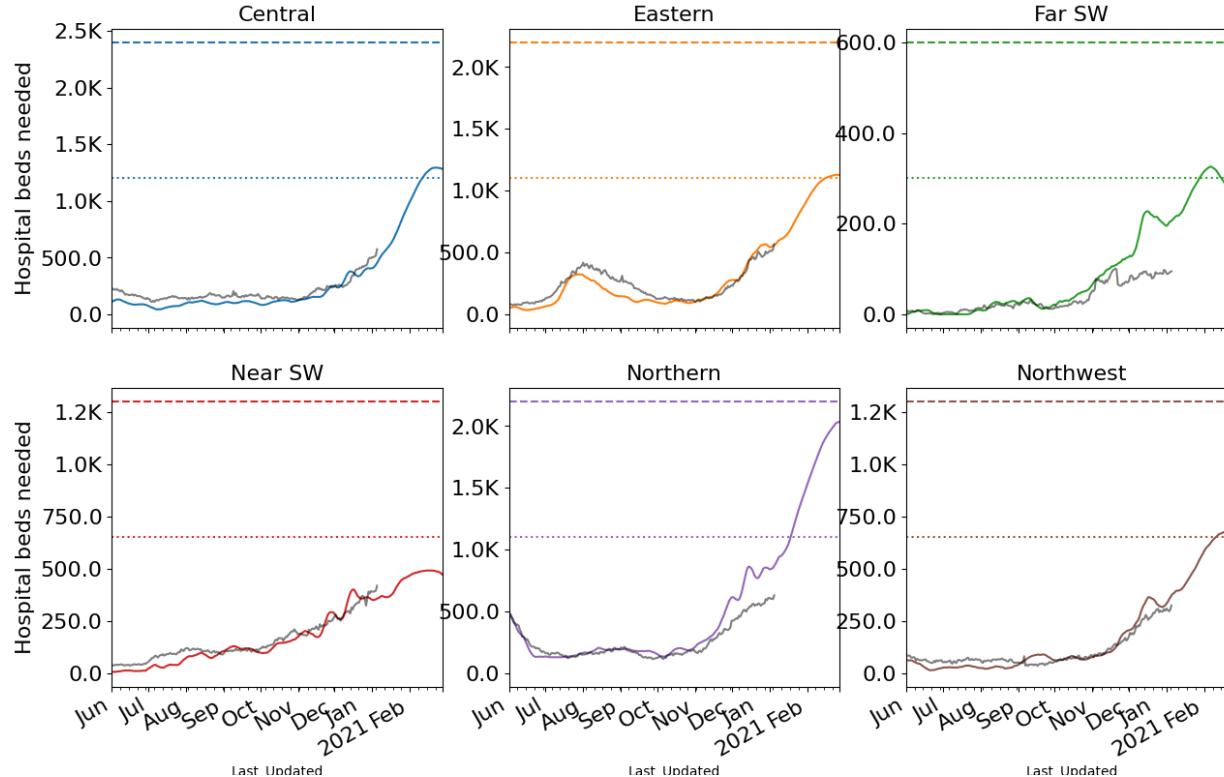
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



Hospital Demand and Bed Capacity by Region

Capacities* by Region – Adaptive-LessControl

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



Week Ending	Adaptive	Adaptive-LessControl
1/3/21	26,775	26,776
1/10/21	30,339	30,287
1/17/21	32,547	33,891
1/24/21	34,877	40,775
1/31/21	36,893	46,579
2/7/21	38,380	51,867
2/14/21	38,930	55,466
2/21/21	38,292	57,141
2/28/21	36,666	56,817
3/7/21	33,978	54,059
3/14/21	30,707	49,929
3/21/21	27,111	45,228

Weekly confirmed cases

If Adaptive-LessControl scenario persists:

- All regions approach initial bed capacity this winter
- Surge capacity approached in Northern region in Feb to early March

* Assumes average length of stay of 8 days

Key Takeaways

Projecting future cases precisely is impossible and unnecessary.

Even without perfect projections, we can confidently draw conclusions:

- **Case rate growth in Virginia has fluctuated through the holidays and is up overall.**
- VA mean weekly incidence (52/100K) up (from 42) as national levels rebound (to 58/100K from 48/100K).
- Projections are mixed across commonwealth but generally up as well.
- Recent updates:
 - Preliminary estimates for vaccination impact
 - Planning scenarios shifted to early January (Jan 8)
 - Added a 3 week “Strong Control” control strategy to scenarios
- Behavioral changes can outpace impact of optimistic vaccine rollout and prevent significantly more cases by Spring.
- The situation is changing rapidly. Models will 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

Estimating Daily Reproductive Number

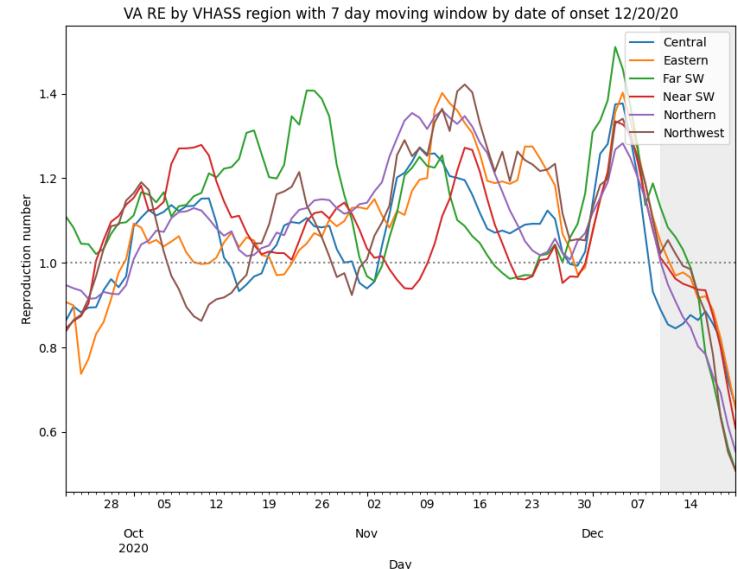
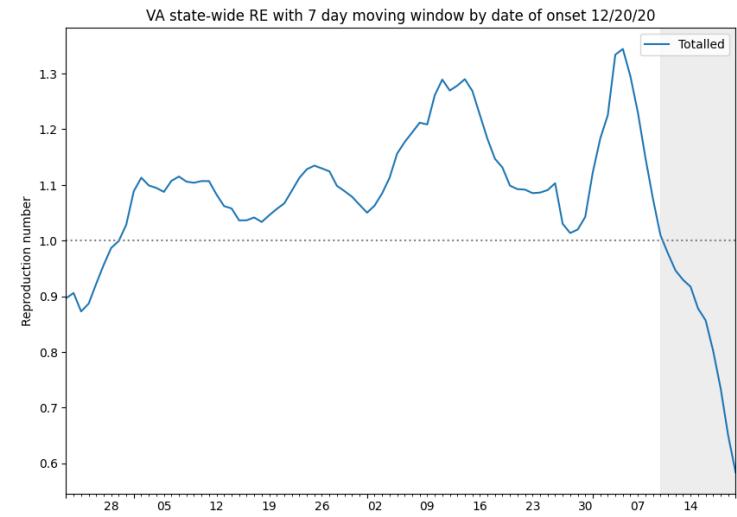
Dec 11th Estimates

Region	Date of Onset	Date Onset Diff
	R _e	Last Week
State-wide	0.977	-0.275
Central	0.854	-0.491
Eastern	1.009	-0.176
Far SW	1.083	-0.323
Near SW	0.988	-0.301
Northern	0.949	-0.253
Northwest	1.054	-0.193

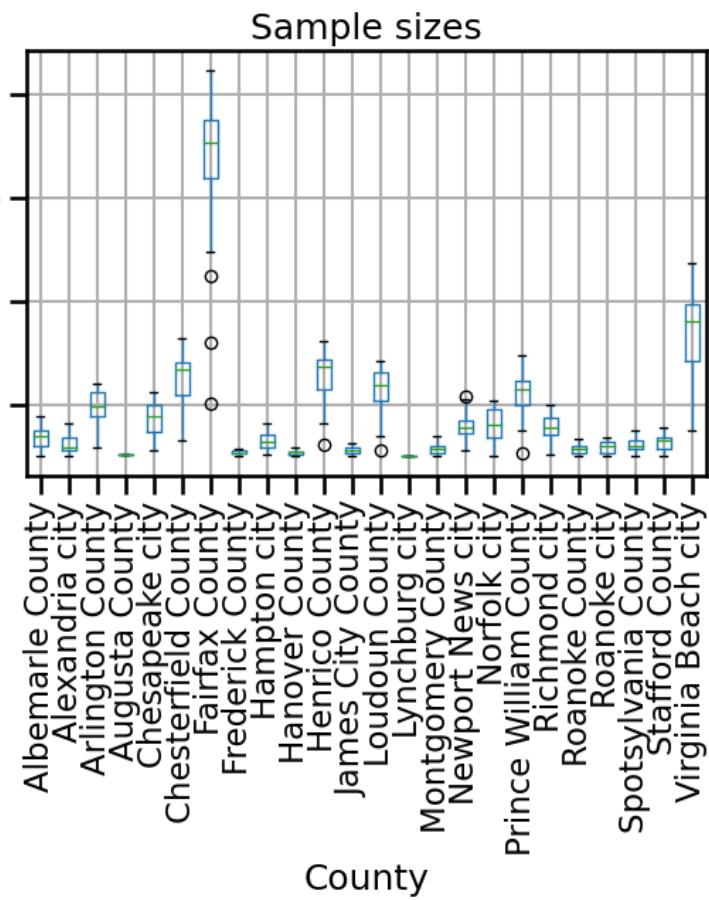
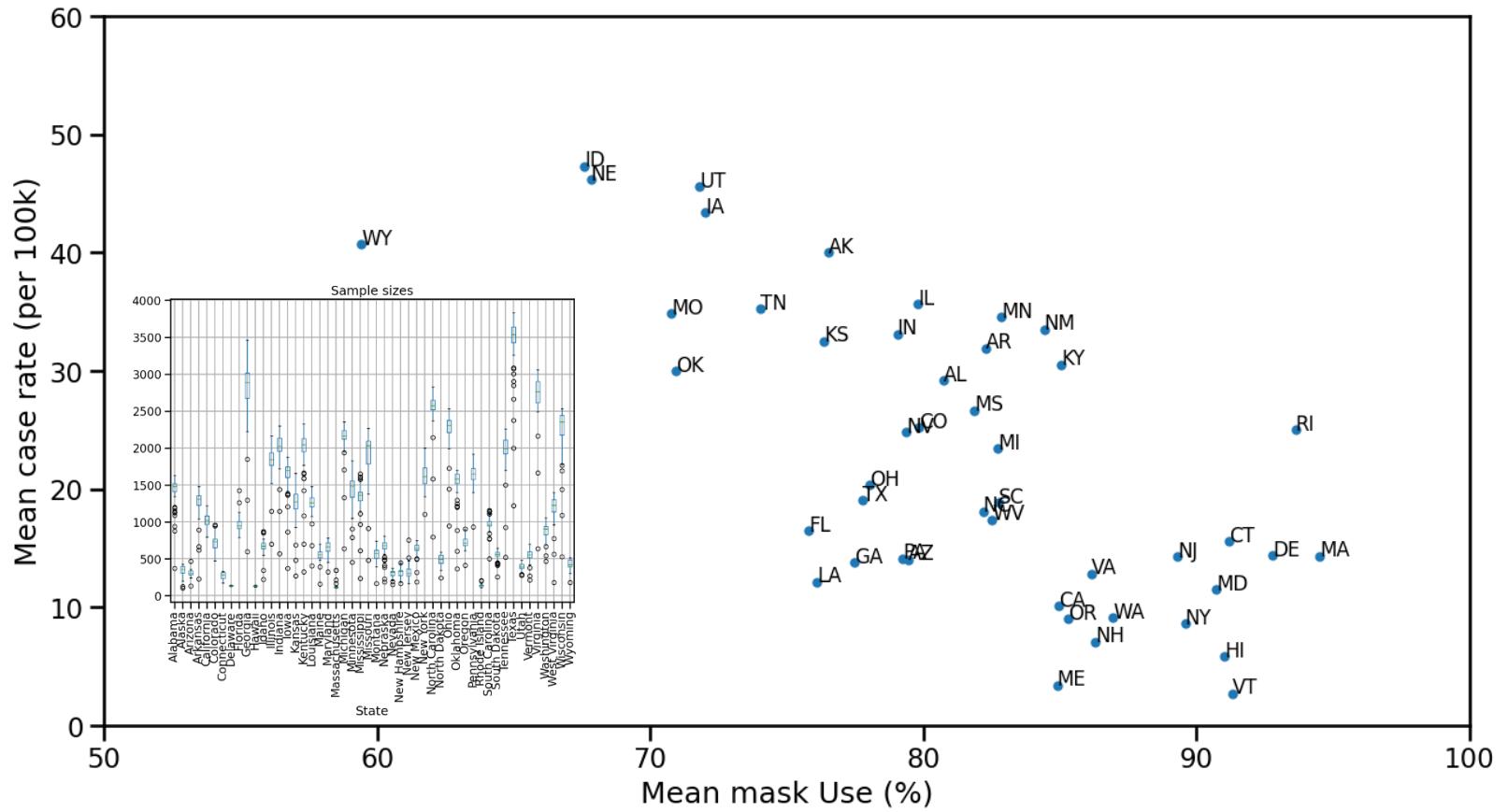
Methodology

- 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>



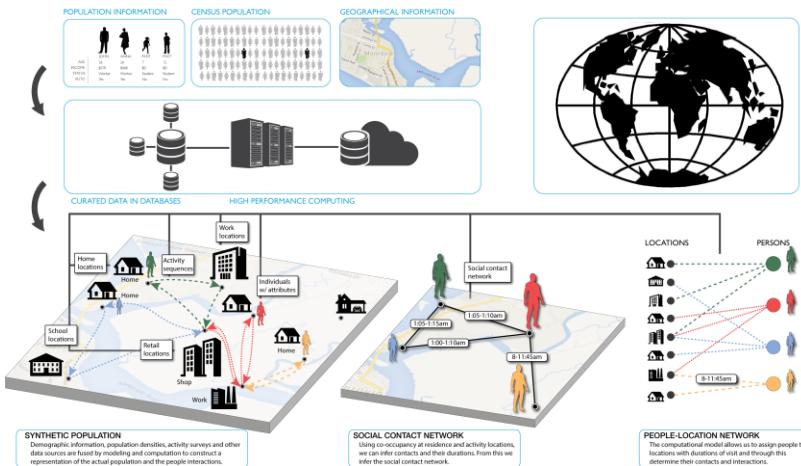
Mask usage sample sizes



Agent-based Model (ABM)

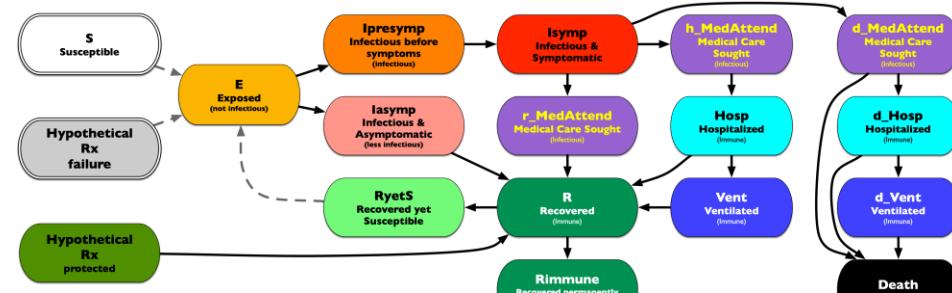
EpiHiper: Distributed network-based stochastic disease transmission simulations

- 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

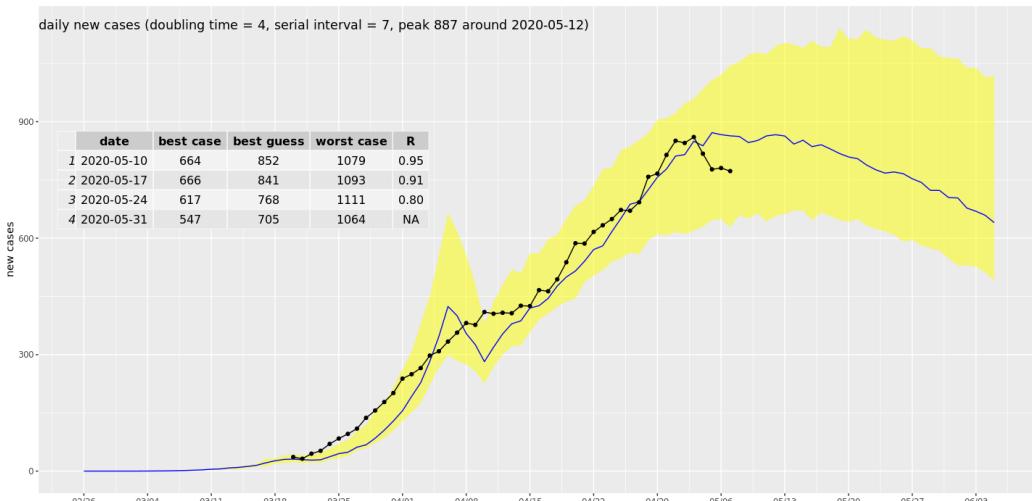


UNIVERSITY OF VIRGINIA

ABM Social Distancing Rebound Study Design

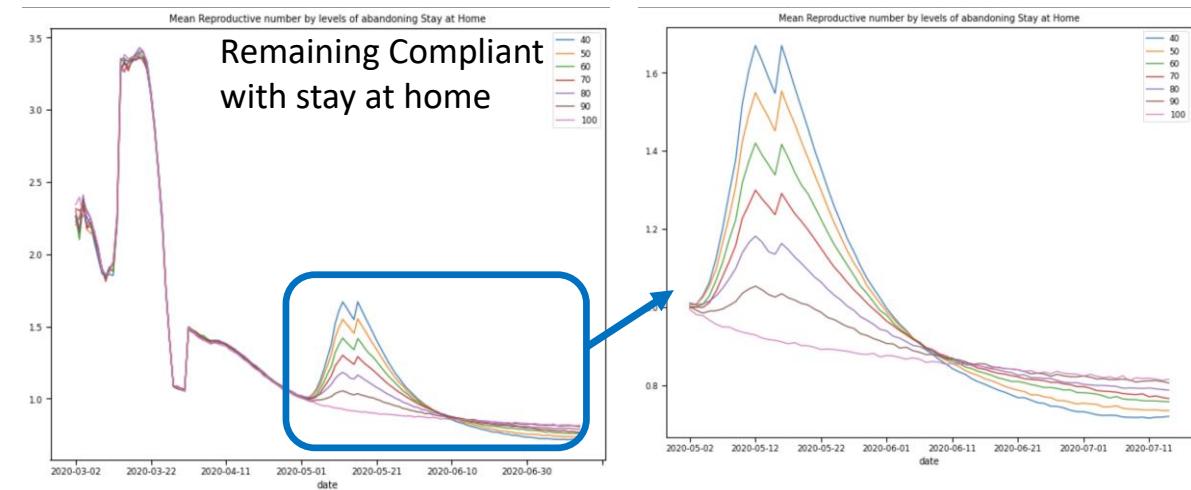
Study of "Stay Home" policy adherence

- 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

Medical Resource Demand Dashboard

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

