Network Systems Science & Advanced Computing

Biocomplexity Institute & Initiative

University of Virginia

Estimation of COVID-19 Impact in Virginia

March 10th, 2021

(data current to March 8th – 9th)

Biocomplexity Institute Technical report: TR 2021-025

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biocomplexity.virginia.edu

About Us

- ## Biocomplexity Institute at the University of Virginia
  - Using big data and simulations to understand massively interactive systems and solve societal problems
- ## Over 20 years of crafting and analyzing infectious disease models
  - Pandemic response for Influenza, Ebola, Zika, and others

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Overview

- **Goal**: Understand impact of COVID-19 mitigations in Virginia

- **Approach:**
  - Calibrate explanatory mechanistic model to observed cases
  - Project based on scenarios for next 4 months
  - Consider a range of possible mitigation effects in "what-if" scenarios

- **Outcomes:**
  - Ill, Confirmed, Hospitalized, ICU, Ventilated, Death
  - Geographic spread over time, case counts, healthcare burdens

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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 down to 16/100K from 19/100K, US levels plateau (to 19 from 18 per 100K)

- Significant progress made in last month, however 88% of VA counties above mean rate of Summer 2020

- Projections continue to be down but are flattening out across Commonwealth

- Recent updates:
  - Accelerated vaccine schedule 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
  - Ascertainment rate adjusted to better capture total infections to date

- The situation is changing rapidly. Models continue to be updated regularly.

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Situation Assessment

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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

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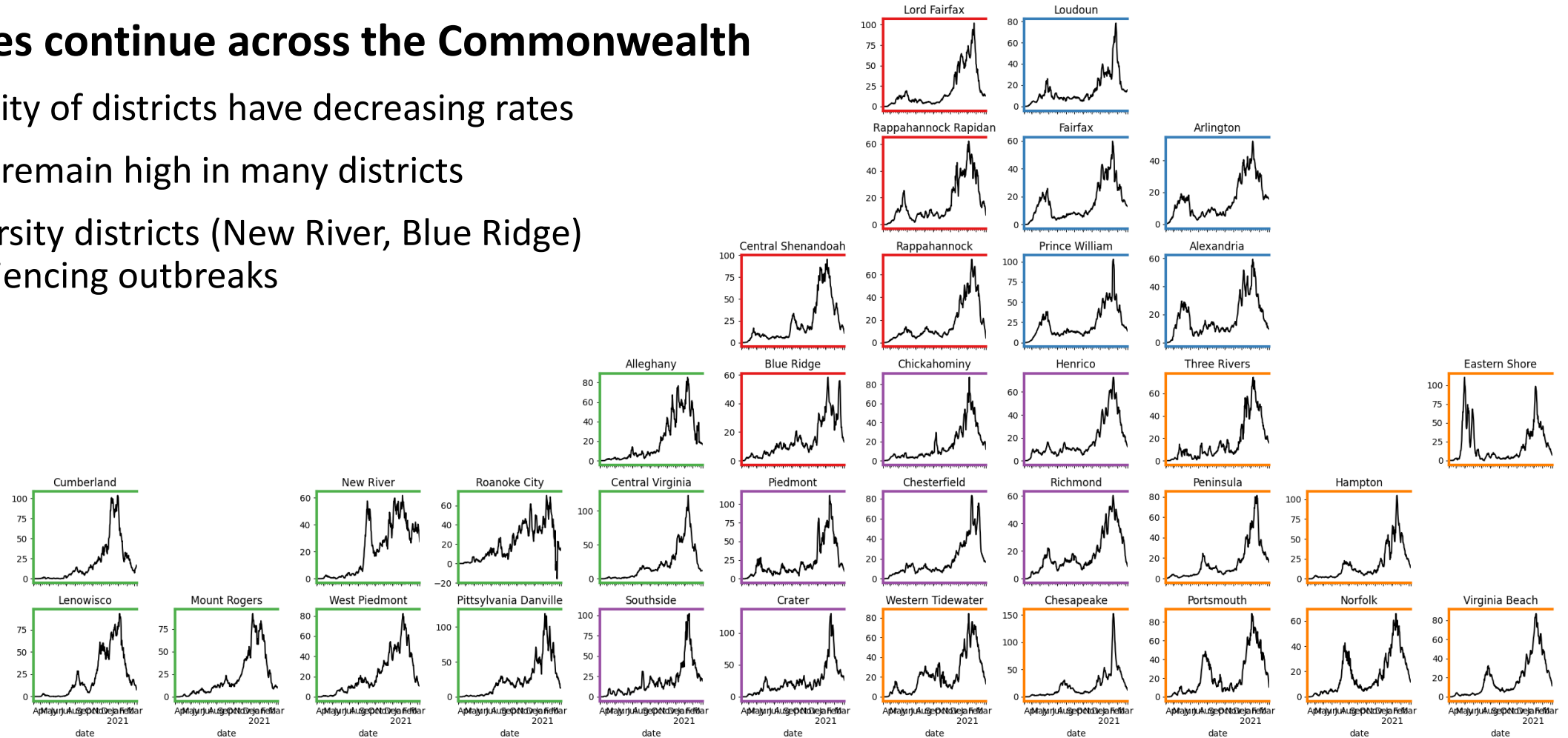
Test Positivity by VDH District

Weekly changes in test positivity by district

- Rates continue to decline

- 41 counties classified in the 'Red' category (as of Feb 24th) and are fewer than 'Yellow' for first time since late November
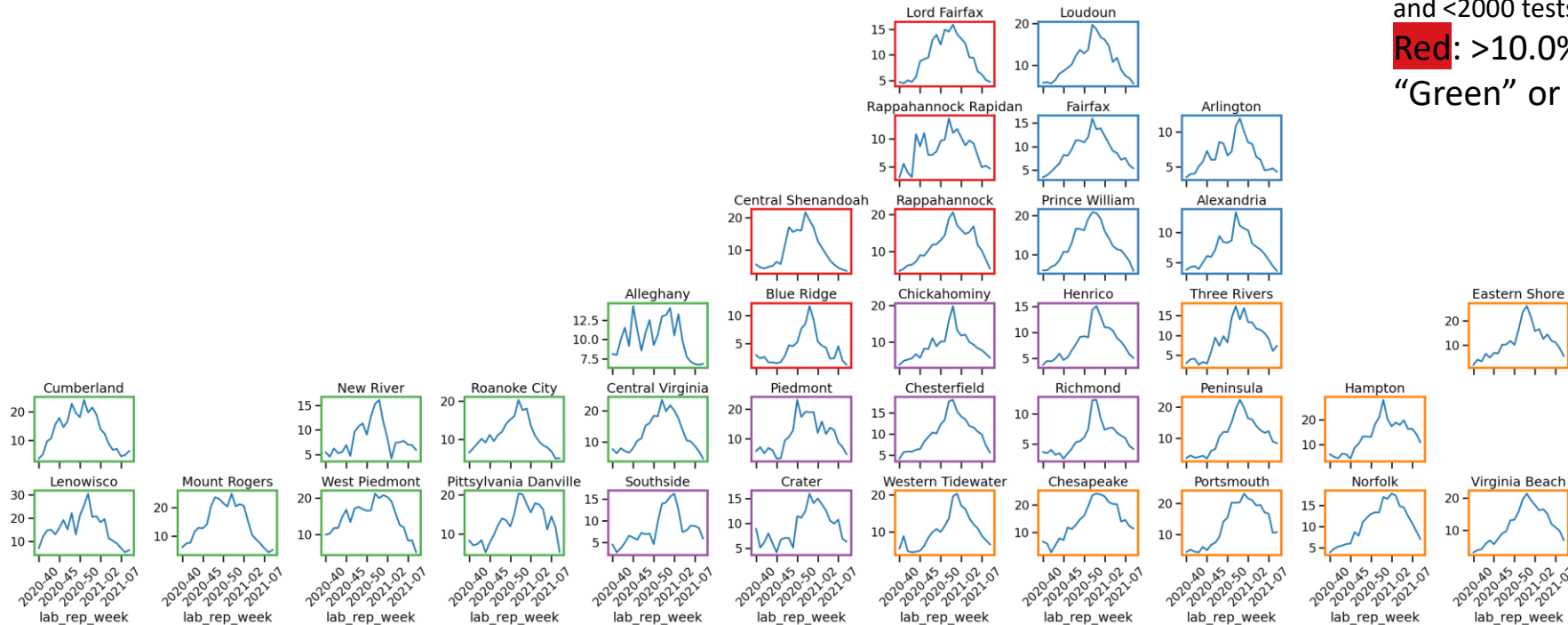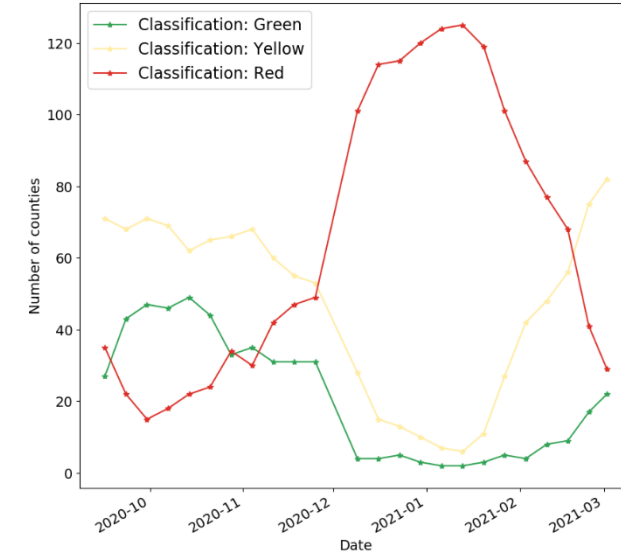
County level test positivity rates for RT-PCR tests.

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"

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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
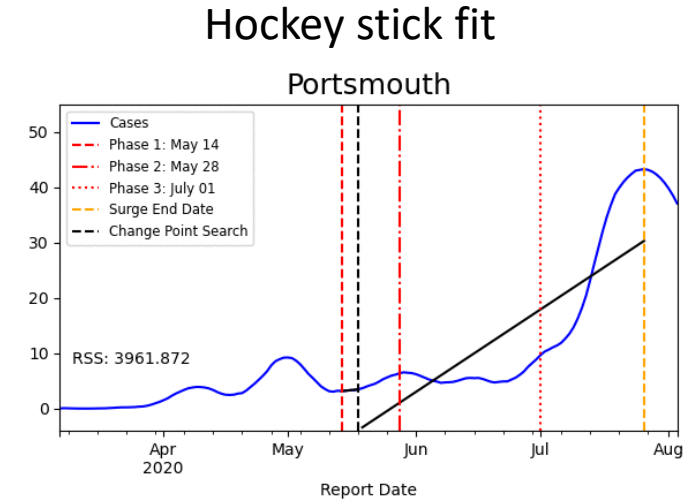
Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	29 (33)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	4 (2)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	2 (0)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	0 (0)

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District Trajectories – last 10 weeks

Status	# Districts (prev week)
Declining	29 (33)
Plateau	4 (2)
Slow Growth	2 (0)
In Surge	0 (0)

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

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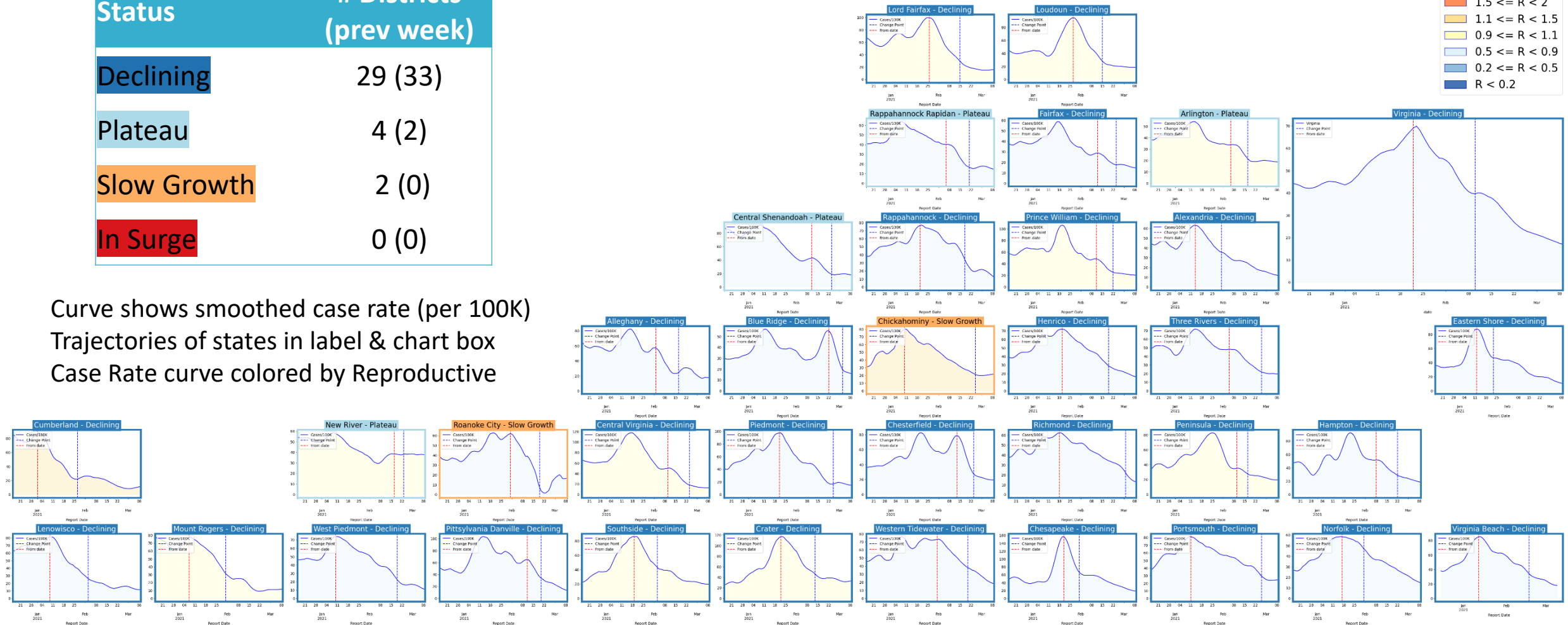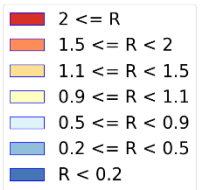
SARS-CoV2 Variants of Concern

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	3,283	49
B.1.351	91	21
P.1	15	9
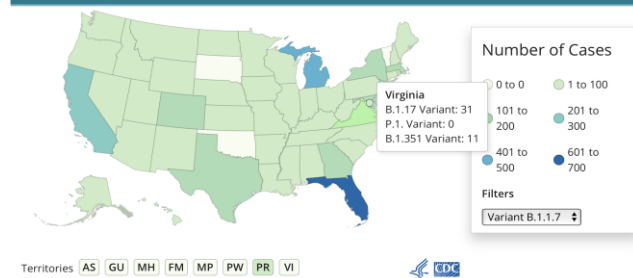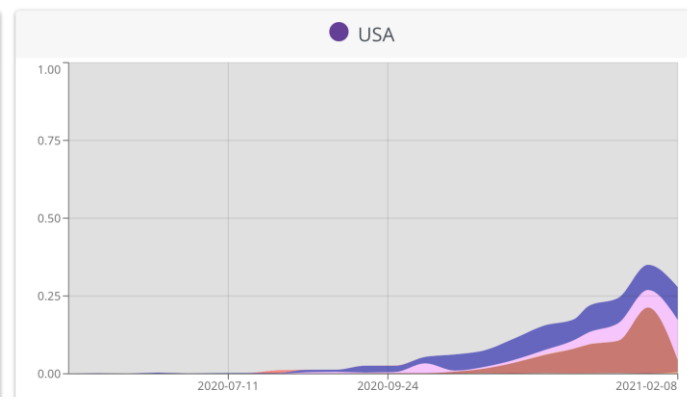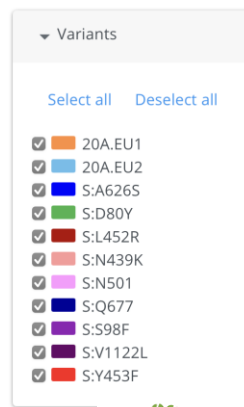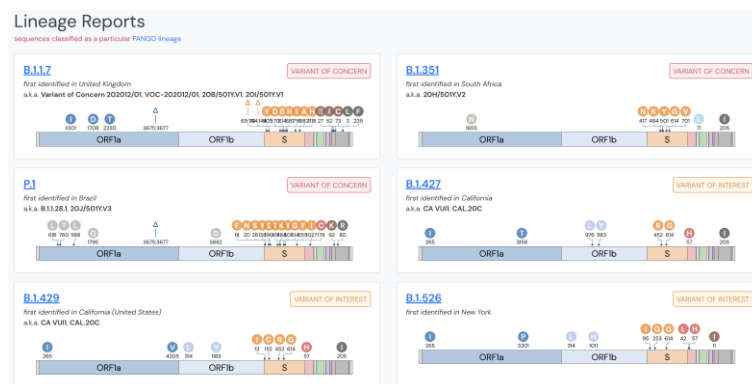
[CDC Variant Tracking](#)

[Outbreak Info](#)

[CoVariants.org](#)
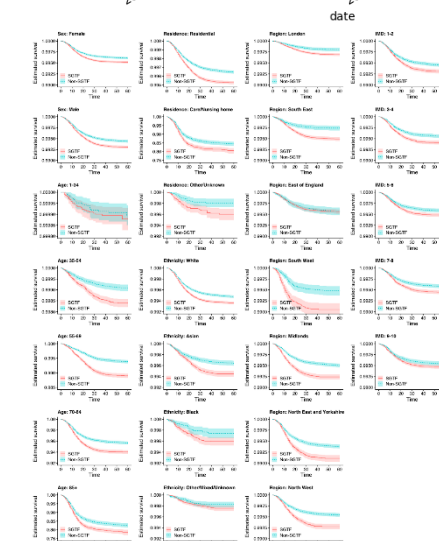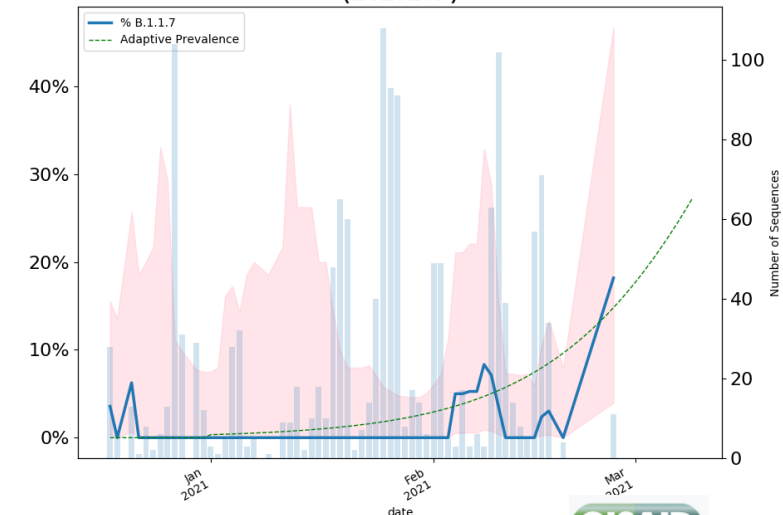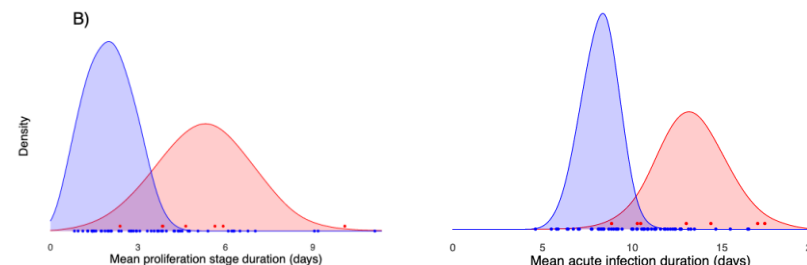
SARS-CoV2 Variants of Concern

Lineage B.1.1.7

- B.1.1.7 has been detected in Virginia and nearly all other states as of Mar 9th (10-20 day delay for genotyping), has continued to rapidly grow. Current estimates place national frequency at ~10% and Virginia at 16%

- Virginia appears to stay on target with estimates based on growth rates indicating it will predominate (eg reach 50% frequency) by mid to late March and is 35%-45% more transmissible

- 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 Rassmussen et al. study estimates B.1.1.7 to have the highest "fitness" advantage of all observed variants and mutations of note

Virginia - 18.2%
(B.1.1.7)

GISAID

outbreak.info

Outbreak Info

Reveals an increase in COVID-19 mortality associated with lineage B.1.1.7. When controlling for factors that could confound the association between B.1.1.7 infection and death, find increased mortality with B.1.1.7 which is consistent with earlier reports Medrxiv


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 46 reported cases in 14 states (including Virginia, 21 in South Carolina) as of Feb 23rd

- 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

- Has been detected in the past in VA and neighbors but not in the last month
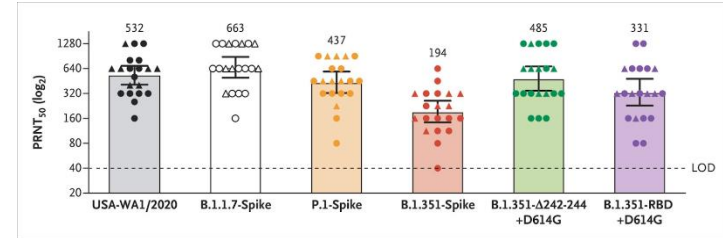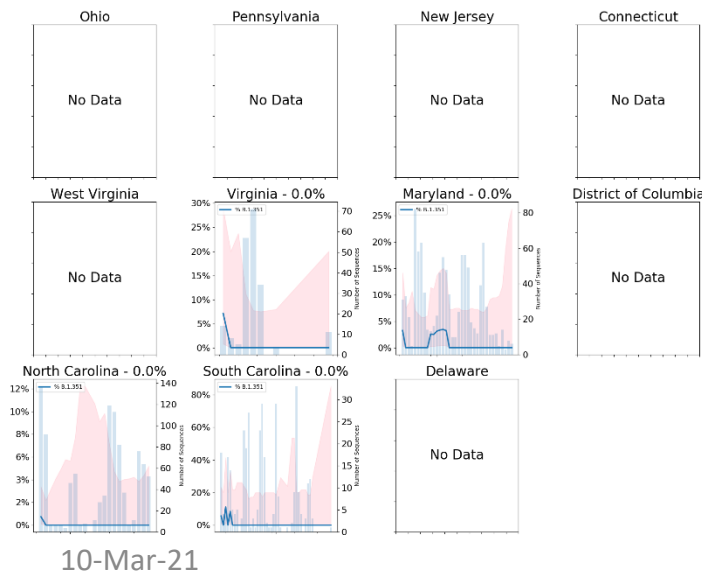
Serum Neutralization of Variant Strains of SARS-CoV-2 after the Second Dose of BNT162b2 Vaccine. Compared with neutralization of USA-WA1/2020, neutralization of B.1.1.7-spike and P.1-spike viruses was roughly equivalent, and neutralization of B.1.351-spike virus was robust but lower NEJM
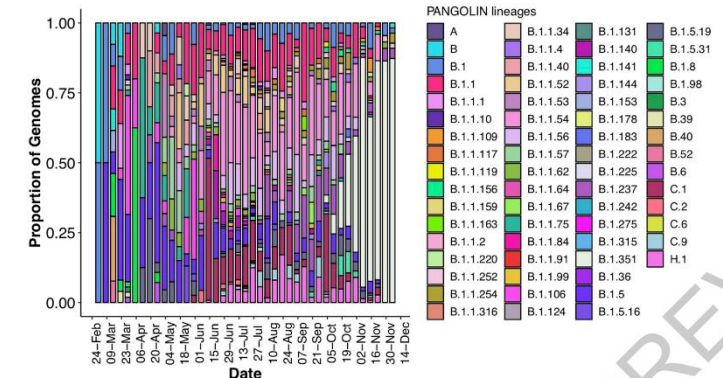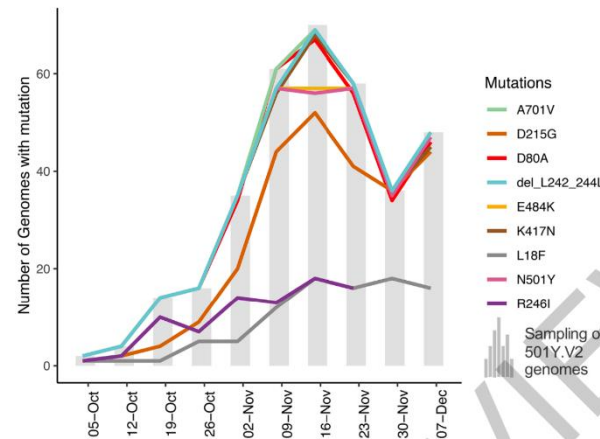
501Y.V2 could be approximately 50% more transmissible than the previously circulating variants. Three mutations at key sites in the RBD (K417N, E484K and N501Y) N501Y mutation has been shown through deep mutation scanning and in a mouse model to enhance binding affinity to ACE2
E484K mutation may also increase binding affinity to ACE2   Nature

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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

Lineage B.1.429

- 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, with an estimated frequency of 9.1%
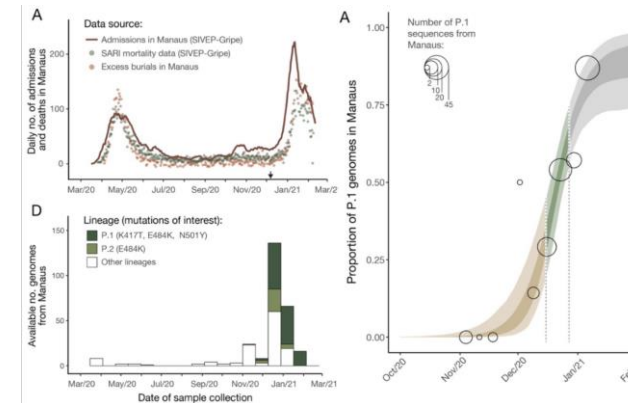
Estimate that P.1 may be 1.4–2.2 times more transmissible and able to evade 25-61% of protective immunity elicited by previous infection with non-P.1 lineages.
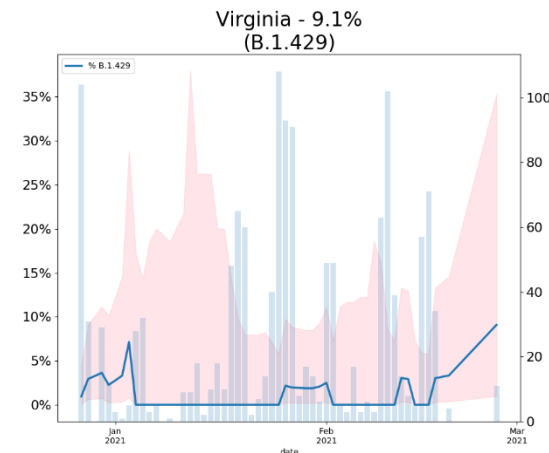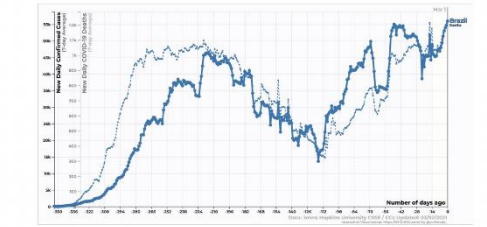
Limited neutralization from COVID-19 patient sera. BioRxiv

Virginia - 9.1% (B.1.429)

GISAID

outbreak.info

Outbreak Info

Estimating Daily Reproductive Number

March 8th Estimates

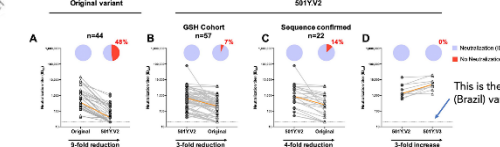| Region	Date Confirmed R_e	Date Confirmed Diff Last Week
State-wide	0.817	-0.019
Central	0.834	0.015
Eastern	0.768	-0.059
Far SW	0.927	-0.159
Near SW	0.805	-0.006
Northern	0.842	-0.101
Northwest	0.825	0.184

Methodology

- Wallinga-Teunis method (EpiEstim[1]) 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

VA state-wide RE with 7 day moving window by confirmation date 03/08/21

VA RE by VHASS region with 7 day moving window by confirmation date 03/08/21
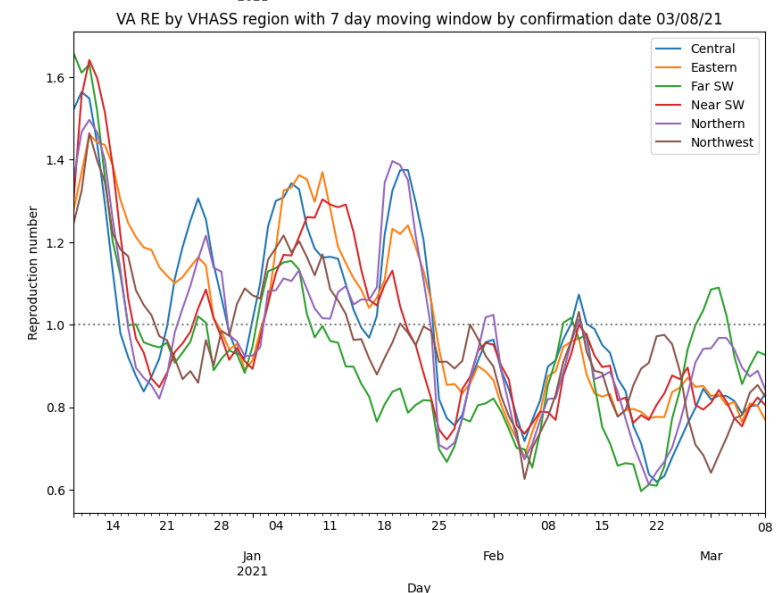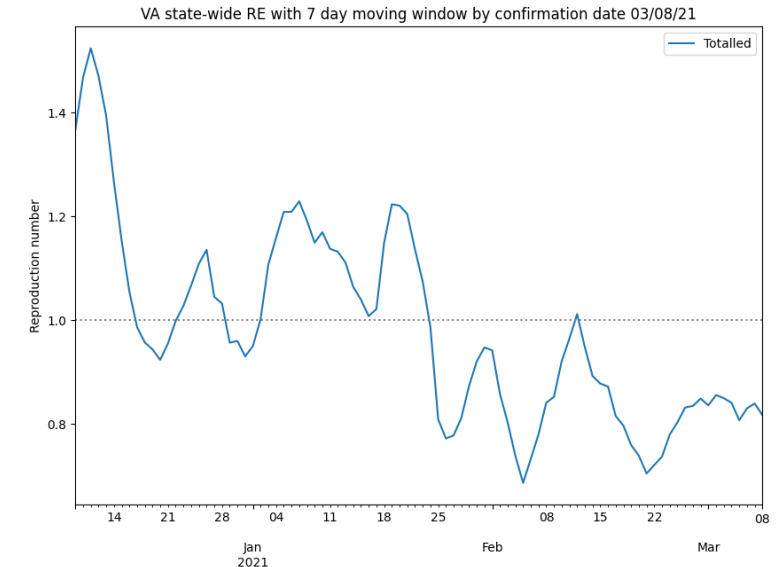
Changes in Case Detection

Timeframe (weeks)	Mean days	% difference from overall mean
July (26-30)	6.2	-9%
Aug (31-34)	4.9	-28%
Sept (35-38)	4.5	-33%
Oct (39-43)	4.5	-34%
Nov (44-47)	4.5	-34%
Dec (48-49)	4.2	-38%
Jan (00-04)	3.9	-42%
Feb (05-06)	3.4	-50%
Overall (13-05)	6.8	--

Test positivity vs. Onset to Diagnosis

Positivity continues its rapid decline

Number of Testing Encounters by Lab Report Date - All Health Districts, PCR Only
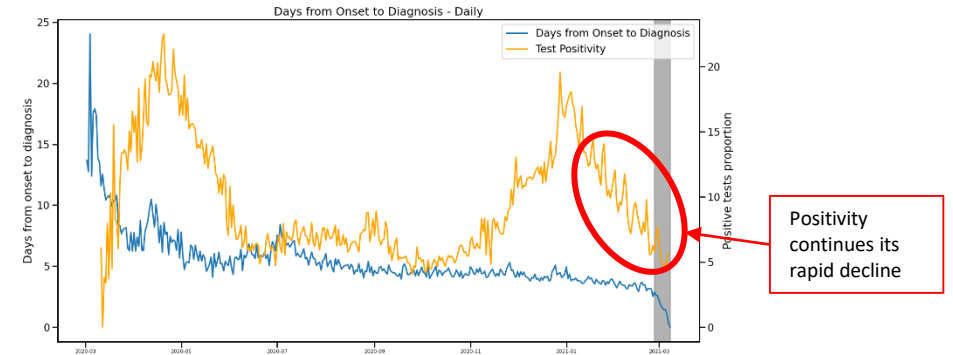
Days from Onset to Diagnosis and Test Positivity - Weekly

Accessed 9:30am March 10, 2021
https://www.vdh.virginia.gov/coronavirus/

Weeks (WW-YYYY)

Vaccine Acceptance in Virginia

Displaying [Vaccine Acceptance] for [Counties] on [March 5, 2021]

Percentage of people who would definitely or probably choose to receive a COVID vaccine if it were offered to them today, based on surveys of Facebook users ?

Rest of Virginia
Population 4,007,532
Percentage 68.60%

NA   0.00%   47.41%   54.61%   61.81%   69.02%   76.22%   83.43%   90.63%   97.83%+   12% Coverage

Acceptance remains high:

- Proportion of Virginians that would definitely or probably accept vaccination if offered today
- Nearly ¾ of Virginians are likely to choose to be vaccinated
- Down very slightly from high at end of January, but has been stable for several weeks
- Urban areas have slightly higher acceptance rates

Vaccine Acceptance in Virginia

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

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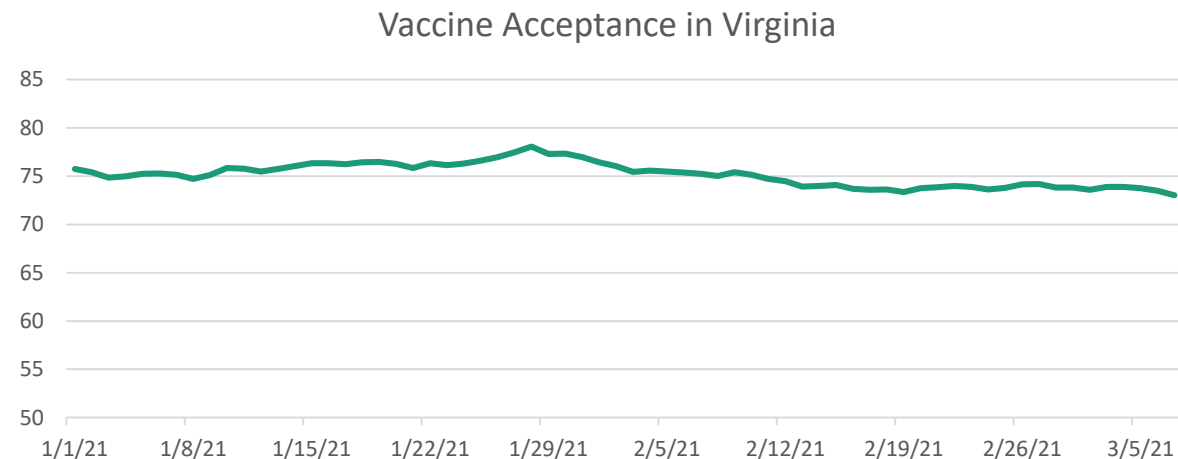
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Shifting Behaviors in Virginia

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

- Google Mobility has increased mobility to Workplaces, Transit, Other Shopping
- SafeGraph shows up tick in restaurant visits over last 2 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

Virginia - Google Mobility Report - by activity type - March 05, 2021

Restaurant Visits in Virginia
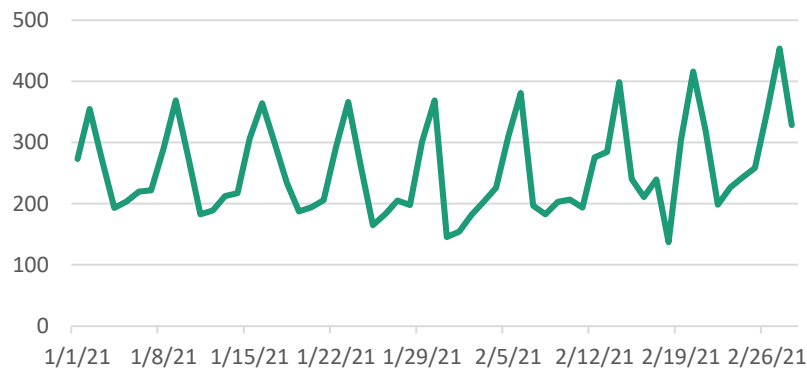
Spending more than 3 hours away from home in Virginia

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

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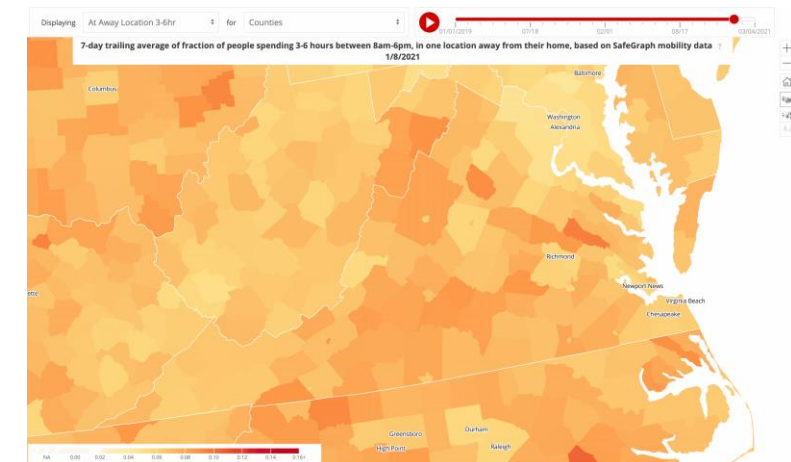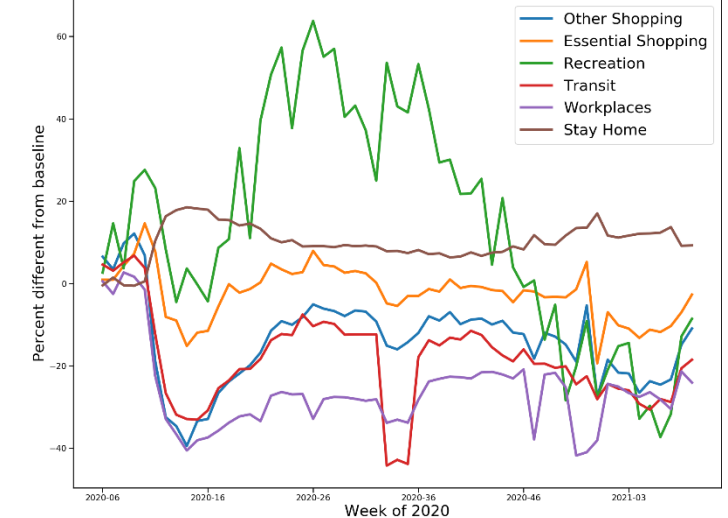
Race and Ethnicity – Recent Rate Changes (per 100K)

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

- Two week change in population level rates

- Black, Latinx and 2 or more races populations have much higher changes in rates; disparity is more pronounced in some regions than others

- Based on 2019 census race-ethnicity data by county

Case Rate
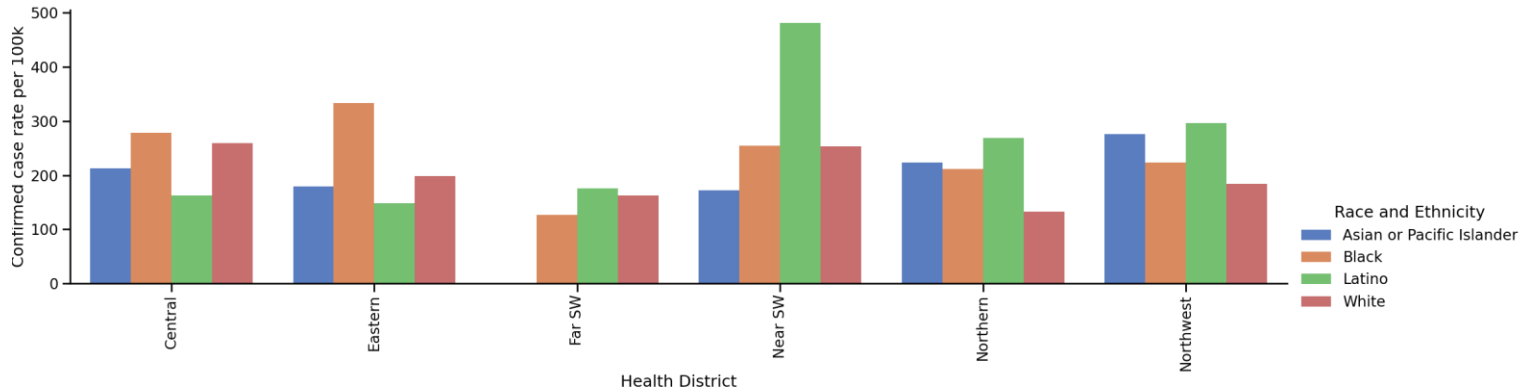
Hospitalization Rate

Death Rate

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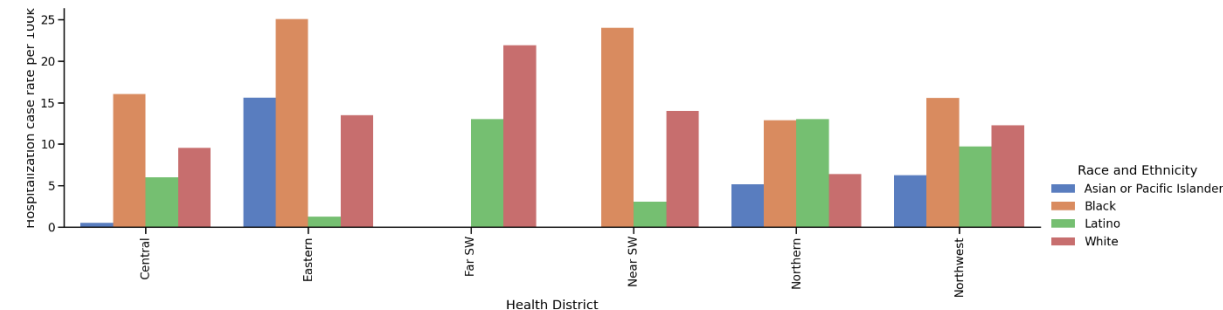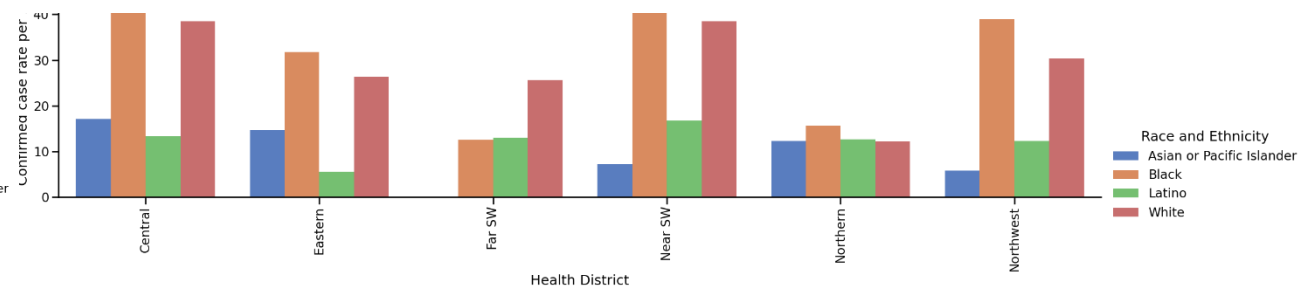
Race and Ethnicity cases per 100K
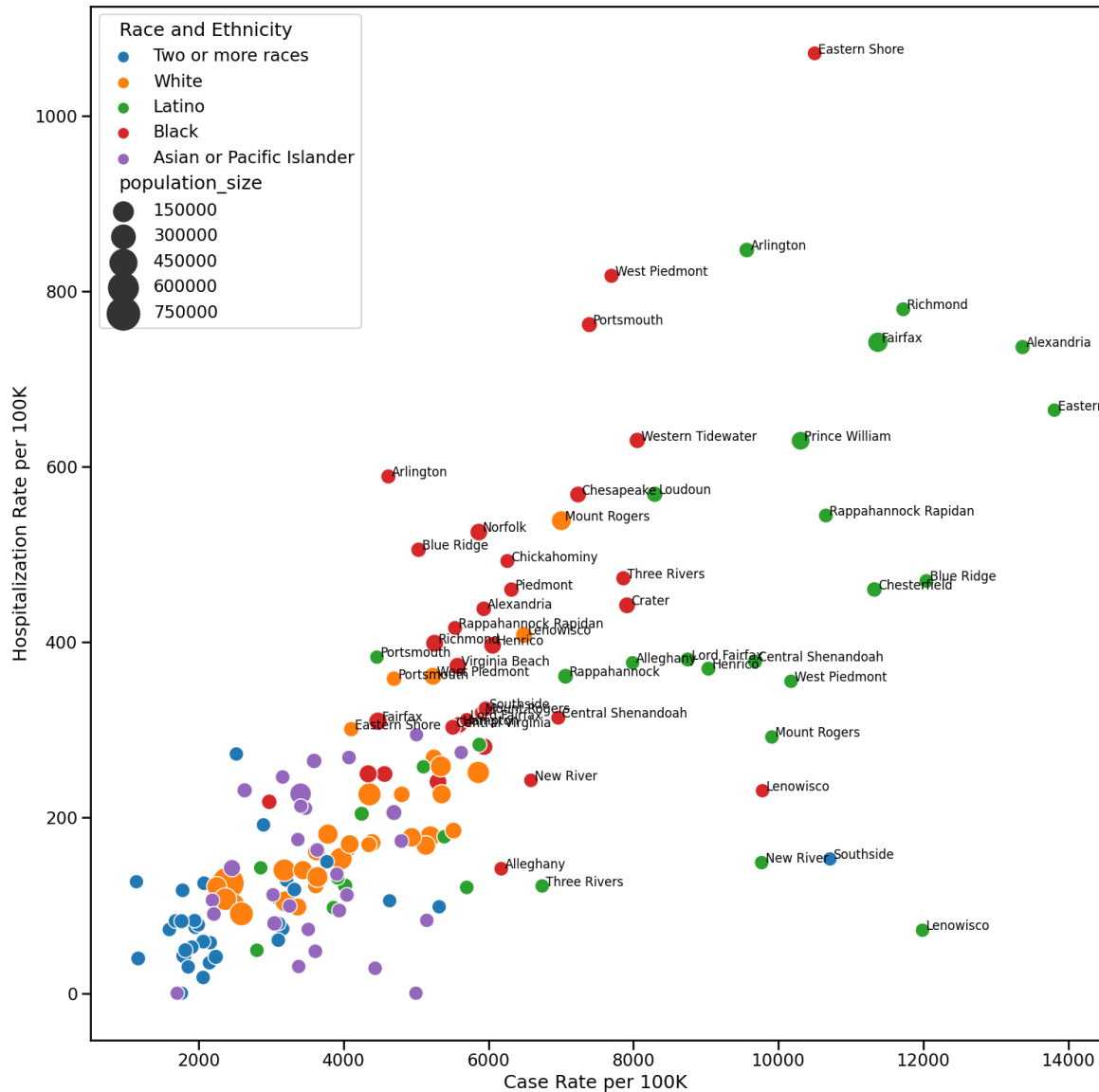
Rates per 100K of each Racial-Ethnic population by Health District

- 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)

Recent Weekly case rates by zip codes by poverty levels
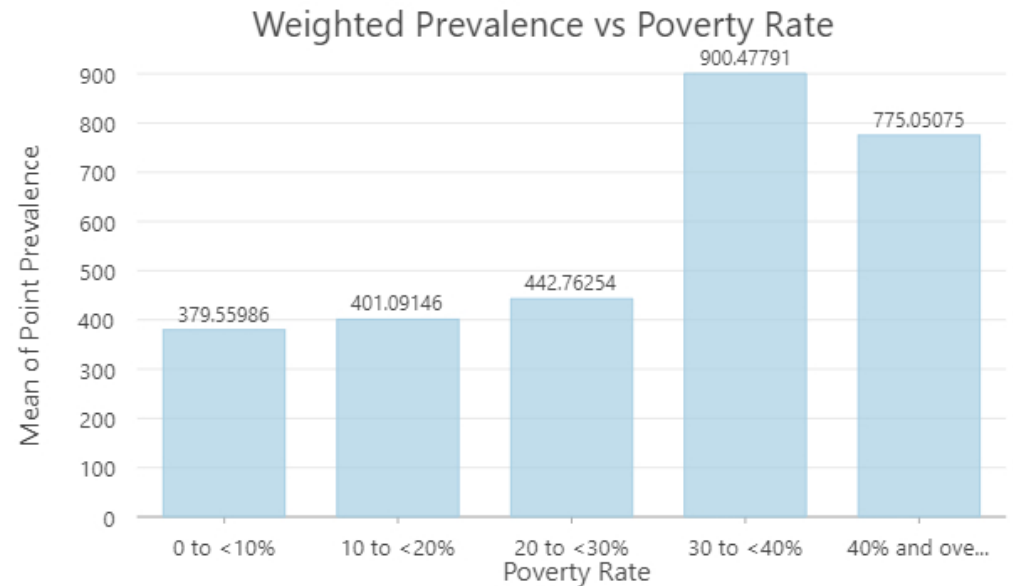
Other State Comparisons

Trajectories of States

Virginia and her neighbors
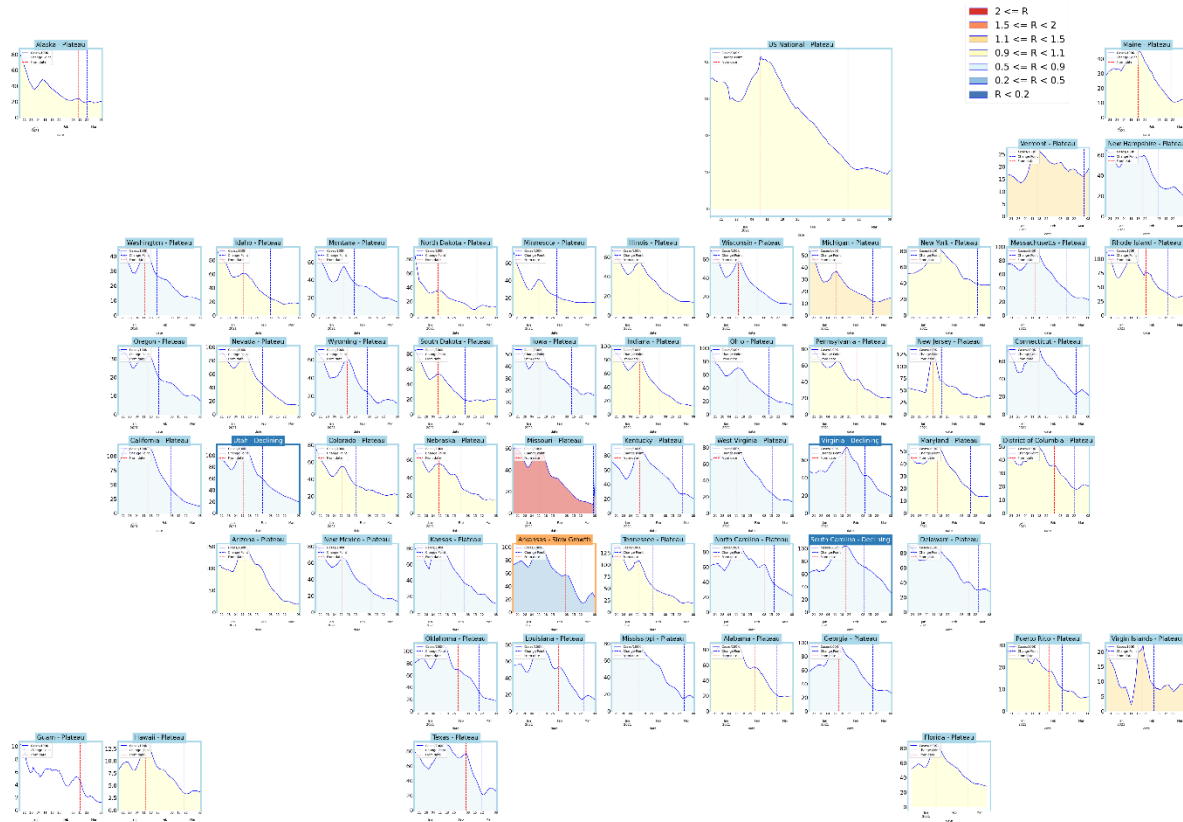
- Now nearly all states are plateaued (50) with a few declining (3) or slow growth (1)
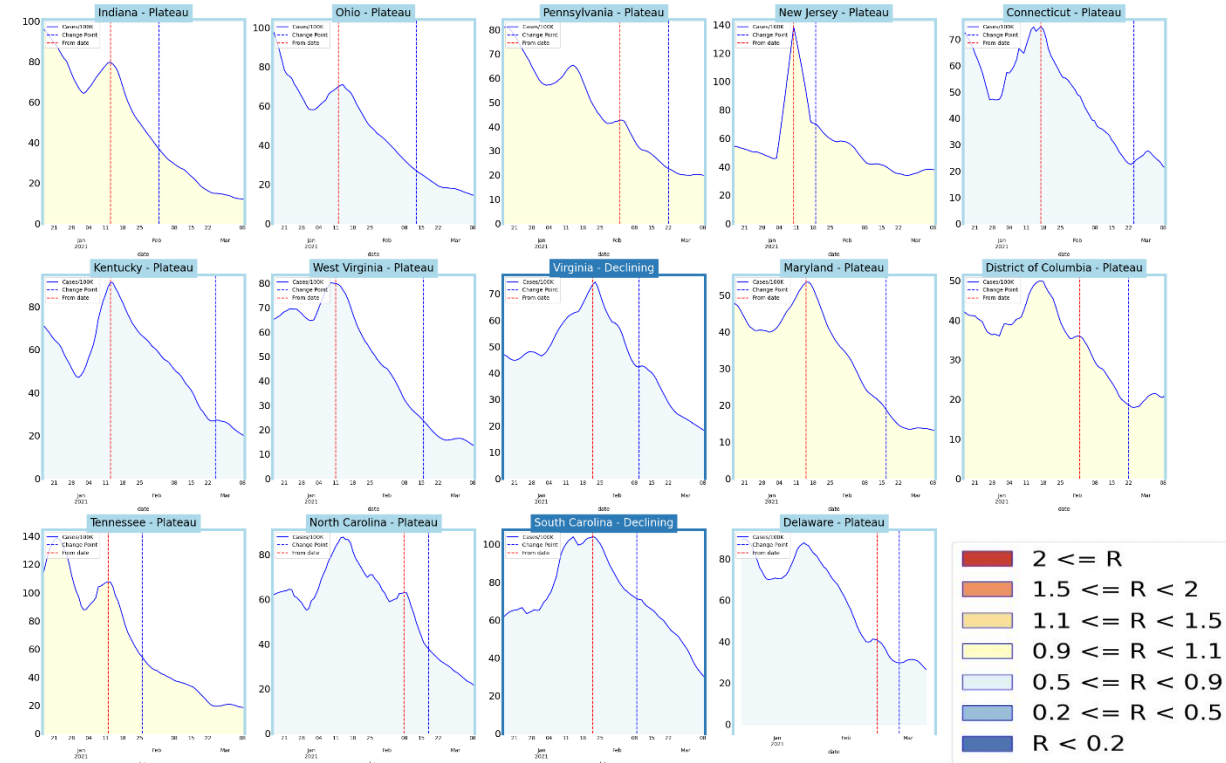
- VA remains in decline but many of her neighbors are shifting from decline to plateau, with some signs of a return to growth
- Rates remain elevated as rates of decline slow

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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: 10.19; Median: 1.46; IQR: 0.7-2.98

Proportion of Last Week's Incidence to that of Weekly Summer Mean

Recent Incidence Compared to Weekly Summer Mean by County
Mean: 2.66; Median: 1.98; IQR: 1.37-3.09

Proportion of Last Week's Incidence to that of Weekly Summer Mean
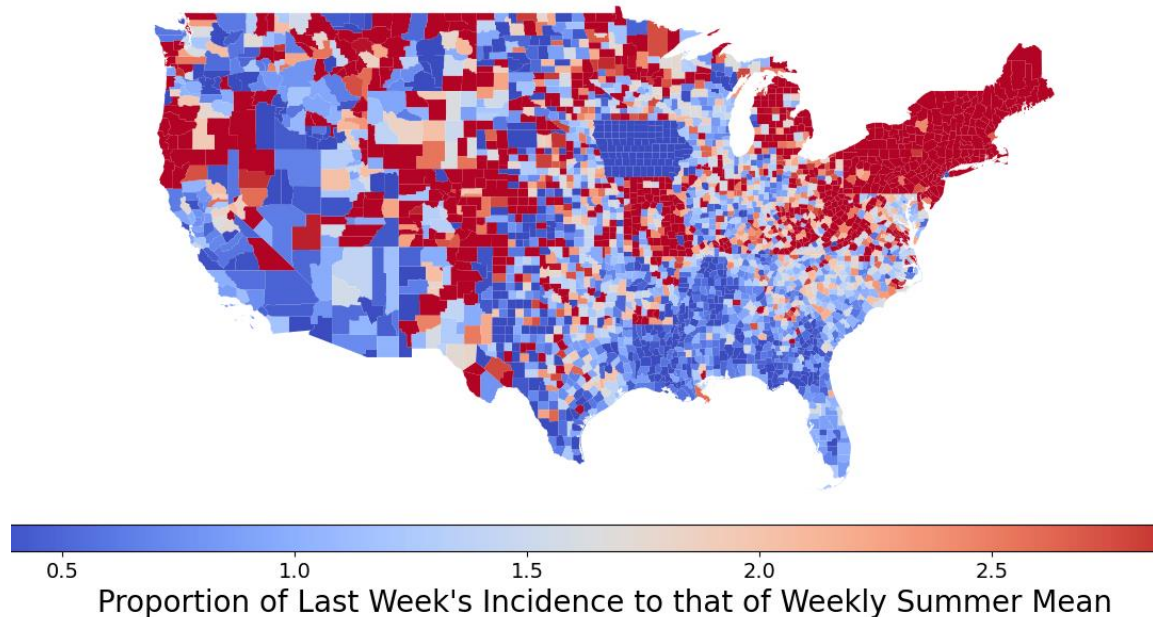
- 63% of US counties are above the summer mean case rate compared to 73% last week
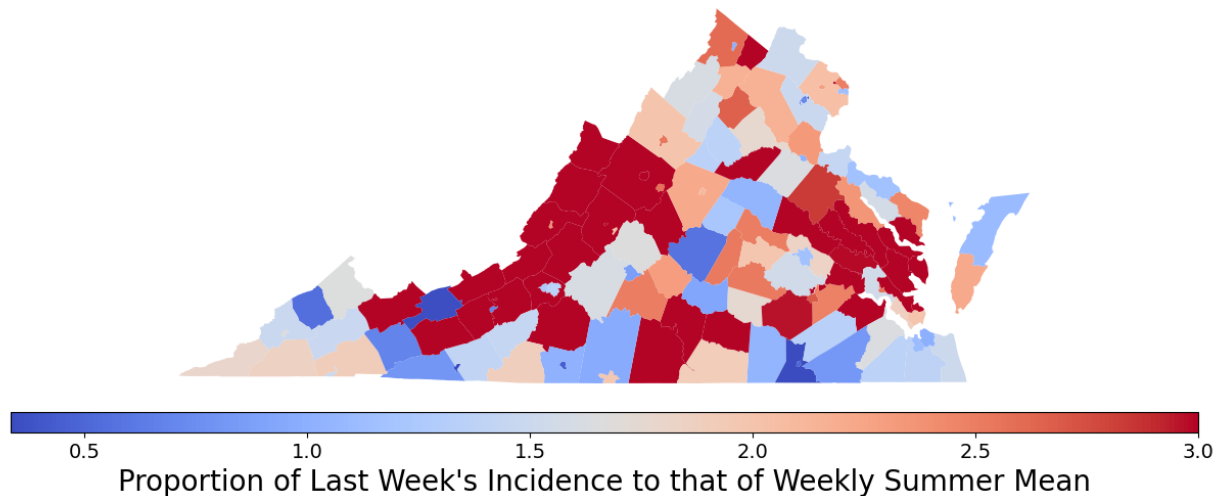
- 88% of VA counties are above the average rate for the summer compared to 88% last week

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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	Prevalence
1	22807	Harrisonburg	2,990
2	23106	Manquin	2,590
3	22967	Roseland	2,470
4	22971	Shipman	2,390
5	22904	Charlottesville	2,360
6	24060	Blacksburg	2,120
7	23156	Shacklefords	2,030
8	23882	Stony Creek	2,000
9	23885	Sutherland	1,730
10	22922	Arrington	1,460

Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.
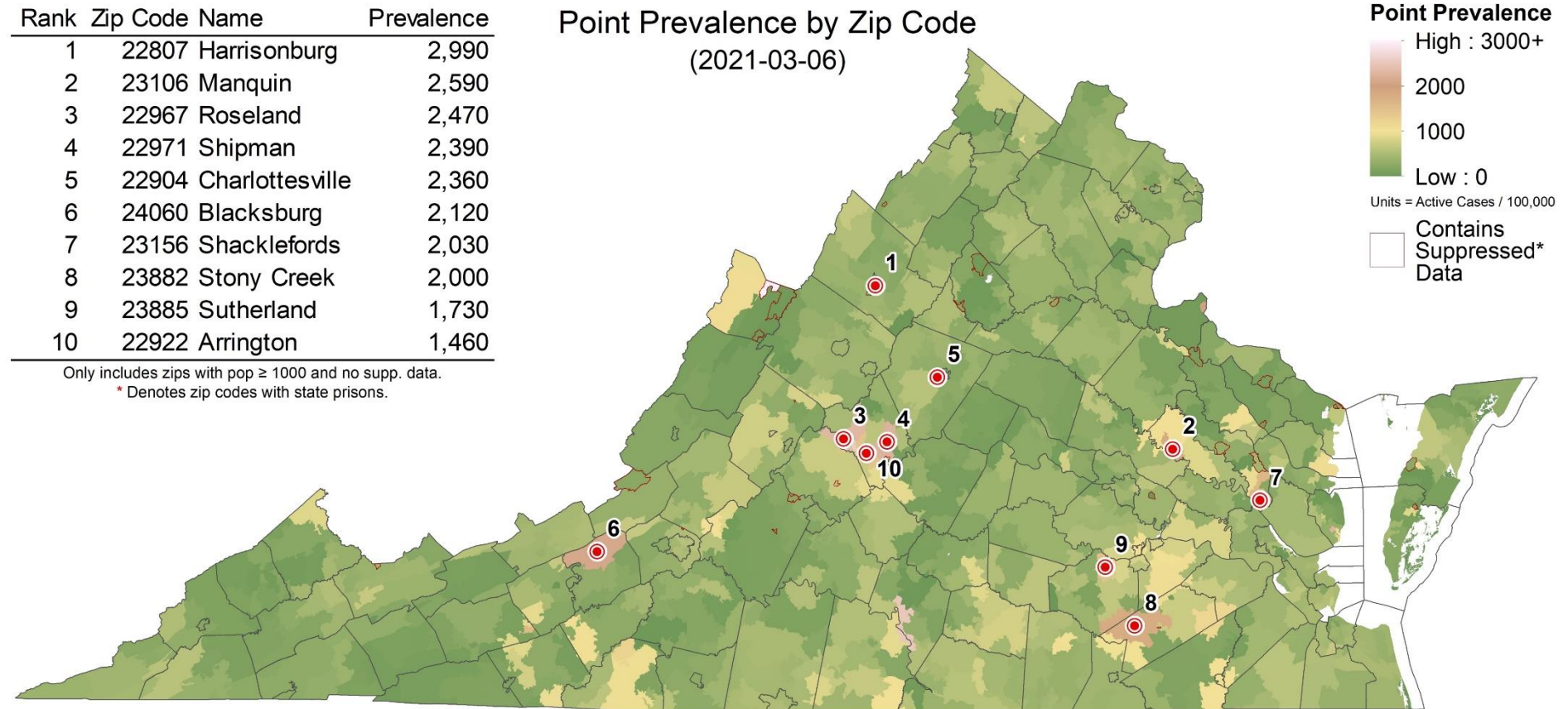
Point Prevalence by Zip Code
(2021-03-06)

Point Prevalence
High : 3000+
2000
1000
Low : 0
Units = Active Cases / 100,000

Contains Suppressed* Data

Based on spatial empirical Bayes smoothed point prevalence for week ending 2021-03-06

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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 29 in Charlottesville, 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	23106	Manquin	26
3	22967	Roseland	28
4	22971	Shipman	29
5	22904	Charlottesville	29
6	24060	Blacksburg	32
7	23156	Shacklefords	34
8	23882	Stony Creek	34
9	23885	Sutherland	40
10	22922	Arrington	47

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+
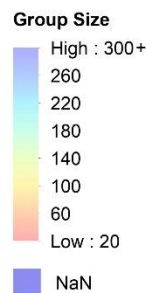260
220
180
140
100
60
Low : 20
NaN

Rank	Zip Code	Name	Likelihood
1	22807	Harrisonburg	53%
2	23106	Manquin	48%
3	22967	Roseland	46%
4	22971	Shipman	45%
5	22904	Charlottesville	45%
6	24060	Blacksburg	41%
7	23156	Shacklefords	40%
8	23882	Stony Creek	40%
9	23885	Sutherland	35%
10	22922	Arrington	31%

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

Likelihood of ≥1 Infected Members (Group of 25)
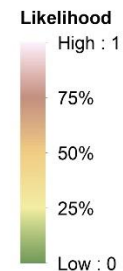
Likelihood
High : 1
75%
50%
25%
Low : 0

Based on spatial empirical Bayes smoothed point prevalence for week ending 2021-03-06

Based on spatial empirical Bayes smoothed point prevalence for week ending 2021-03-06

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Current Spatial Hot Spots

Spot	Zip Code	Name	Conf.
1	22807	Harrisonburg	99%
2	22904	Charlottesville	99%
3	24060	Blacksburg	99%
4	22967	Roseland	99%
5	22971	Shipman	99%
6	23106	Manquin	99%
7	23156	Shacklefords	99%
8	23882	Stony Creek	99%
9	23885	Sutherland	99%

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
(2021-03-06)

Getis-Ord Gi* HotSpots
- Cold Spot - 99% Confidence
- Cold Spot - 95% Confidence
- Cold Spot - 90% Confidence
- Not Significant
- Hot Spot - 90% Confidence
- Hot Spot - 95% Confidence
- Hot Spot - 99% Confidence
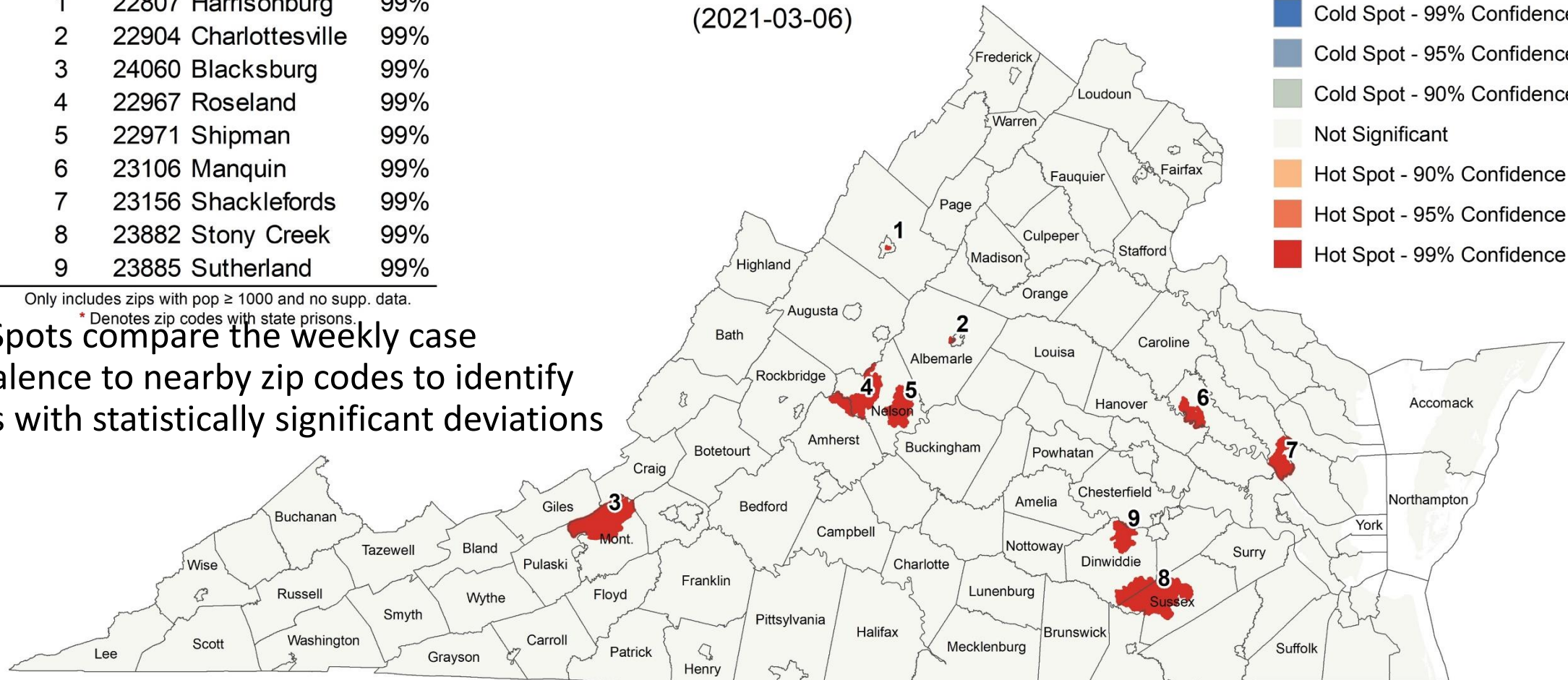
Based on global empirical Bayes smoothed point prevelence for week ending 2021-03-06

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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 23FEB Predicting
Week ending 2021-03-07
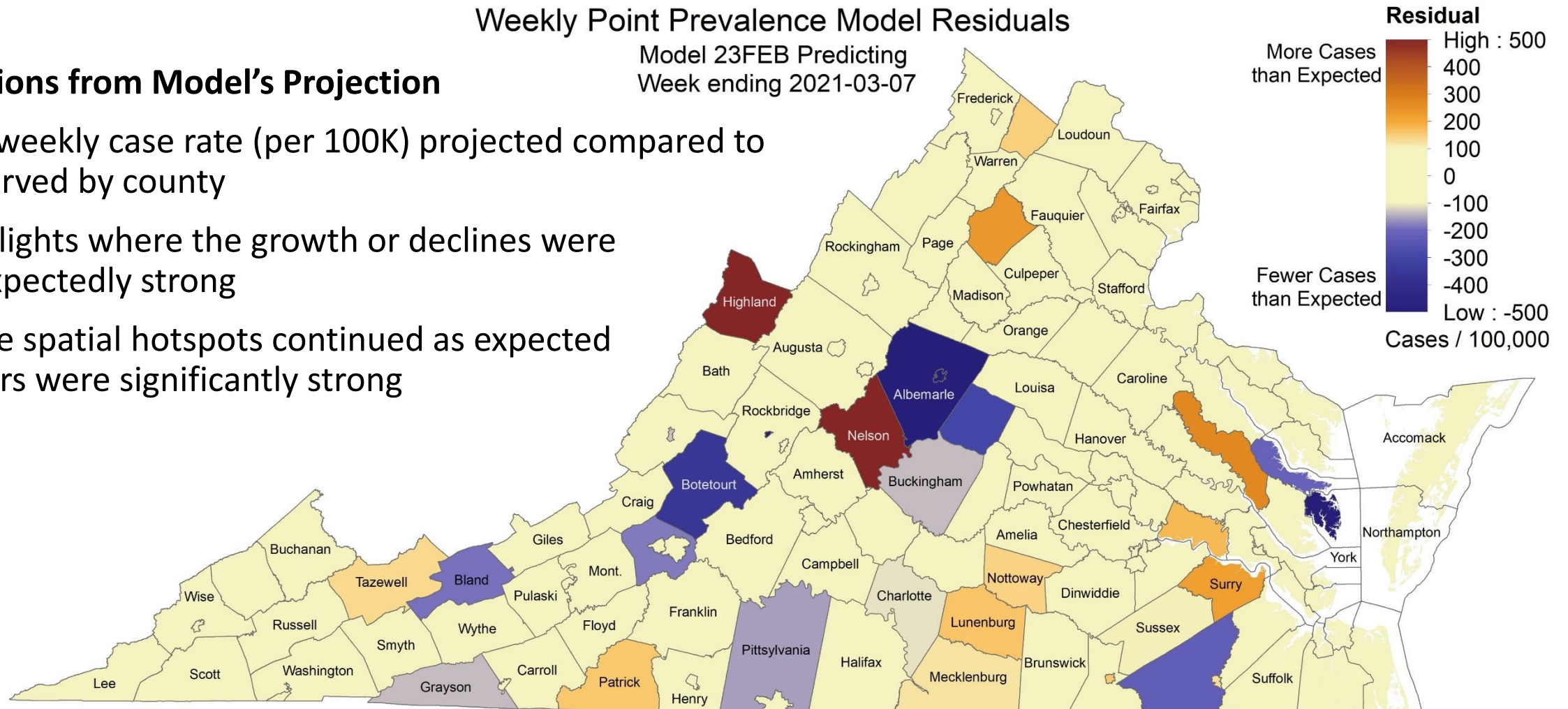
Moran's I = 0.10763, P-Value = 0.116509
No Residual Autocorrelation Detected

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Model Update – Adaptive Fitting

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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

Fairfax County

Initial State (T)   Effective population   Disease Dynamics   Updated State (T+1)

$S \rightarrow E \rightarrow I \rightarrow R$

Susceptible ➡ Exposed ➡ Infectious ➡ Removed

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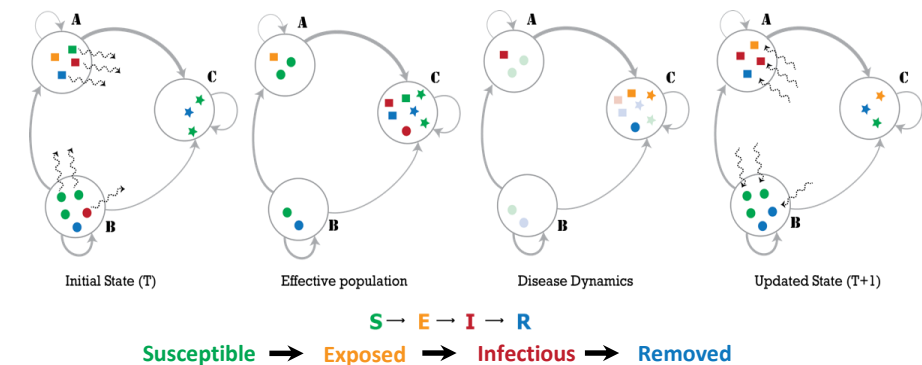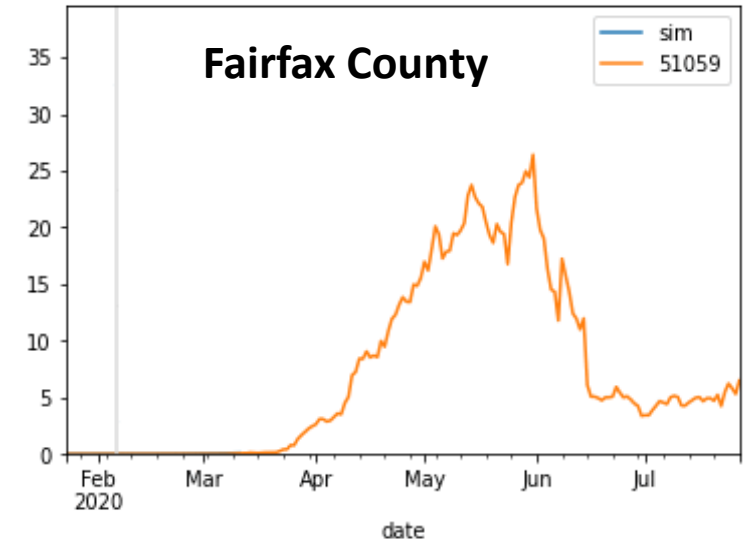
Using Ensemble Model to Guide Projections

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

- Autoregressive (AR, ARIMA)

- Neural networks (LSTM)

- Kalman filtering (EnKF)

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.

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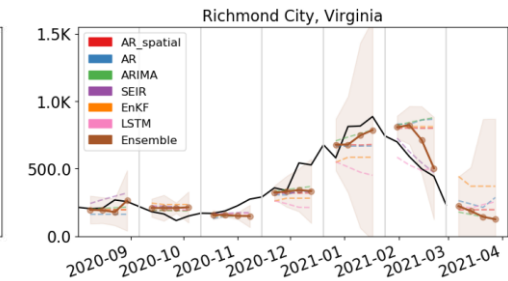
Seroprevalence updates to model design

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

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

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

- Thus for 2x there are 2 total infections in the population for every confirmed case recently

- This measure now fully tracks the estimated ascertainment over time

- Uncertainty design has been shifted to these bounds (previously higher ascertainments as was consistent earlier in the pandemic were being used)

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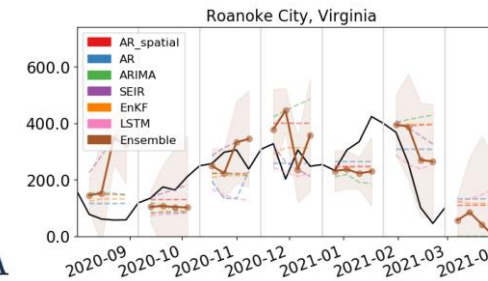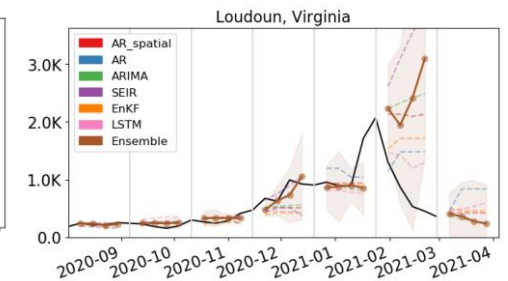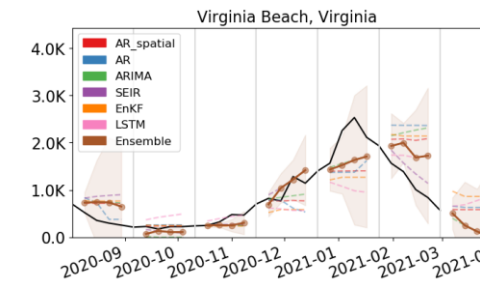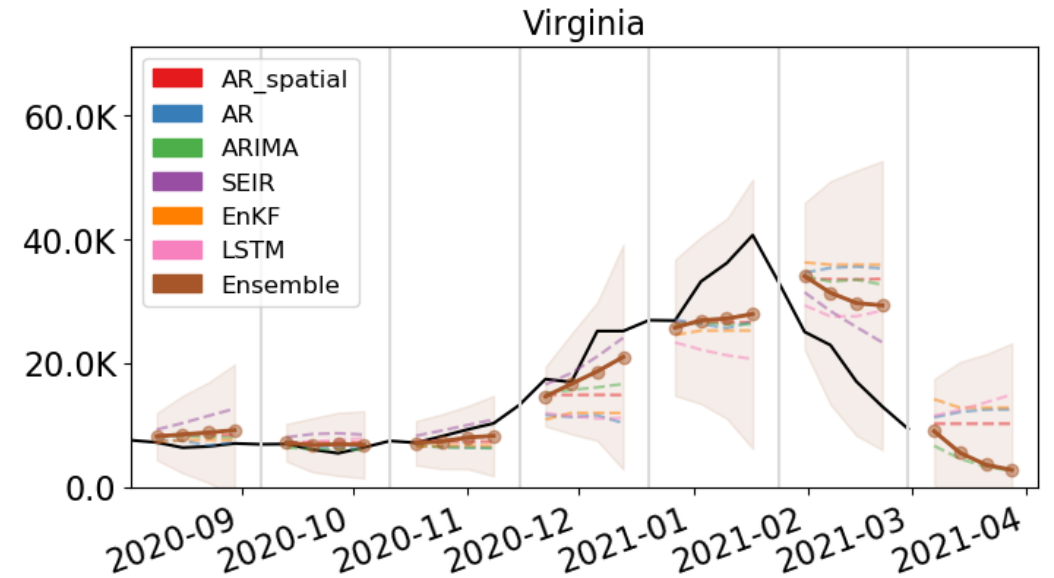

VA Seroprevalence Data

December 2020 (Second Half)

Seroprevalence Estimate
5.7%
95% Confidence Interval: 3.8%-8.5%

Number of Estimated Infections
480,000
95% Confidence Interval: 318,000-719,000

Total Number of Cases Reported by End of 12/31/2020
349,568

Catchment Area: Statewide   Number of Samples Tested: 1,217

VA 5.7%

© 2021 Mapbox © OpenStreetMap

Age Specific Seroprevalence Estimate   Samples

Age	Estimate	Samples
0-17	No Estimate	21
18-49	8.8%	429
50-64	3.8%	391
65+	3.7%	376

Sex-Specific Seroprevalence Estimate

Sex	Estimate	Samples
Male	4.6%	432
Female	6.8%	785

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Calibration Approach

- **Data:**
  - County level case counts by date of onset (from VDH)
  - Confirmed cases for model fitting
- **Calibration:** fit model to observed data and ensemble's forecast
  - Tune transmissibility across ranges of:
    - Duration of incubation (5-9 days), infectiousness (3-7 days)
    - Undocumented case rate (1x to 7x) guided by seroprevalence studies
    - Detection delay: exposure to confirmation (4-12 days)
  - Approach captures uncertainty, but allows model to precisely track the full trajectory of the outbreak
- **Project:** future cases and outcomes generated using the collection of fit models run into the future
  - **Mean trend from last 7 days of observed cases and first week of ensemble's forecast used**
  - Outliers removed based on variances in the previous 3 weeks
  - 2 week interpolation to smooth transitions in rapidly changing trajectories

COVID-19 in Virginia:

Dashboard Updated: 3/10/2021
Data entered by 5:00 PM the prior day.

Cases, Hospitalizations and Deaths		
Total Cases*	**Total Hospitalizations****	**Total Deaths**
589,375	**24,925**	**9,849**
(New Cases: 1,246)^		

Confirmed†	Probable†	Confirmed†	Probable†	Confirmed†	Probable†
464,360	125,015	23,690	1,235	8,217	1,632

* Includes both people with a positive test (Confirmed), and symptomatic with a known exposure to COVID-19 (Probable).
** Hospitalization of a case is captured at the time VDH performs case investigation. This underrepresents the total number of hospitalizations in Virginia.
^New cases represent the number of confirmed and probable cases reported to VDH in the past 24 hours.
† VDH adopted the updated CDC COVID-19 confirmed and probable surveillance case definitions on August 27, 2020. Found here: https://wwwn.cdc.gov/nndss/conditions/coronavirus-disease-2019-covid-19/case-definition/2020/08/05/

Outbreaks	
Total Outbreaks*	**Outbreak Associated Cases**
2,697	**66,166**

* 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****
6,083,095	**5.7%**

* "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**
42	**0**

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

Accessed 9:30am March 10, 2021

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

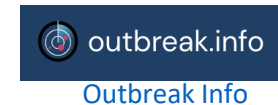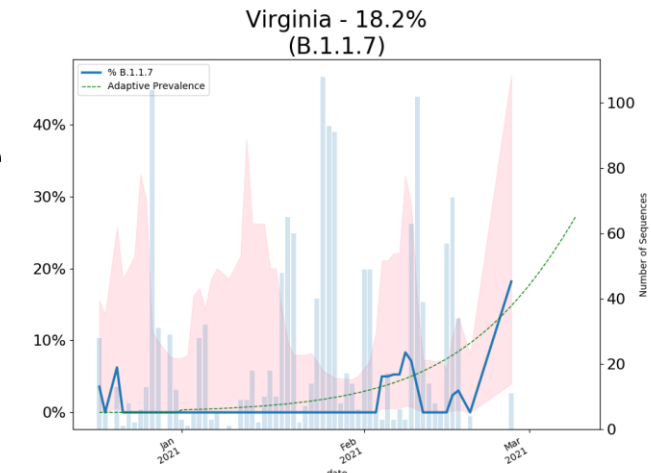UNIVERSITY of VIRGINIA

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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 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 (10th percentile)
  - **Fatigued Control**: Highest level of transmission (95th percentile) increased by additional 5%

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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 increases gradually over 4 months to level 50% more transmissible

Estimated frequency from public genome repository with added analysis: 18% Current frequency used in model: 24%

Outbreak Info

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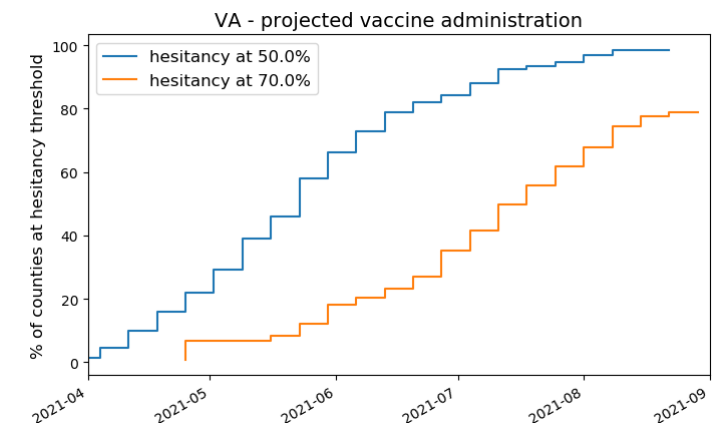
Scenarios – Vaccines

- 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 schedule not included explicitly, as administration data comes into focus will be incorporated

- 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
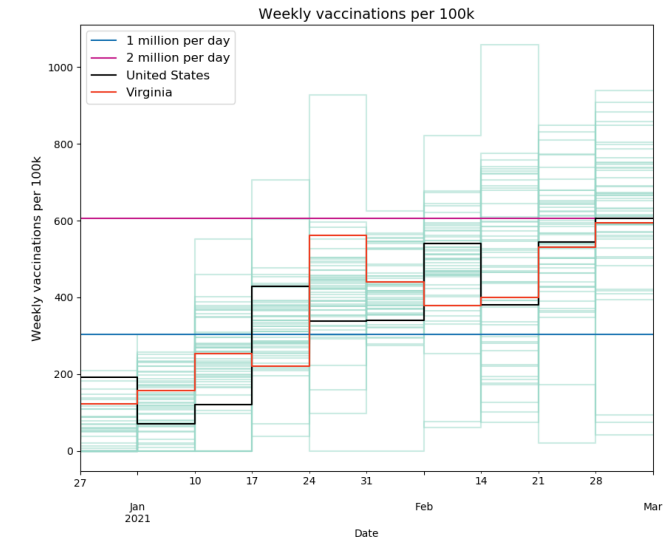
Lines represent 1M & 2M total doses administered a day (rate of 303/100K & 606/100K)

Anticipated Vax Hesitancy Impact
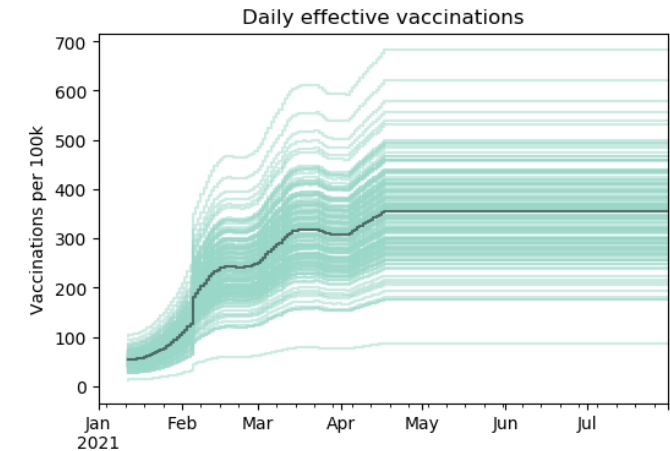
Scenarios – Vaccines

- 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**
  - **Current rate:** 275 **FIRST DOSES** per 100K per day based on median of last week
  - **Accelerated rate**: 375 **FIRST DOSES** per 100K per day
    - Total of ~32K 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

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

Weekly dose administrations
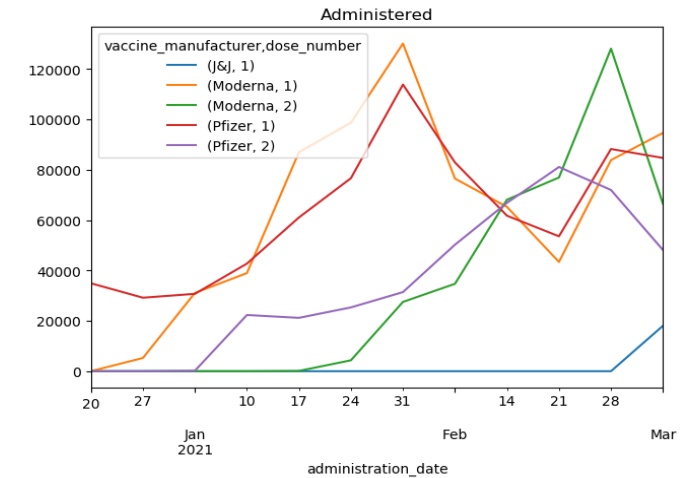
Modeled Vaccine Induced Immunity

All VA counties, state in black

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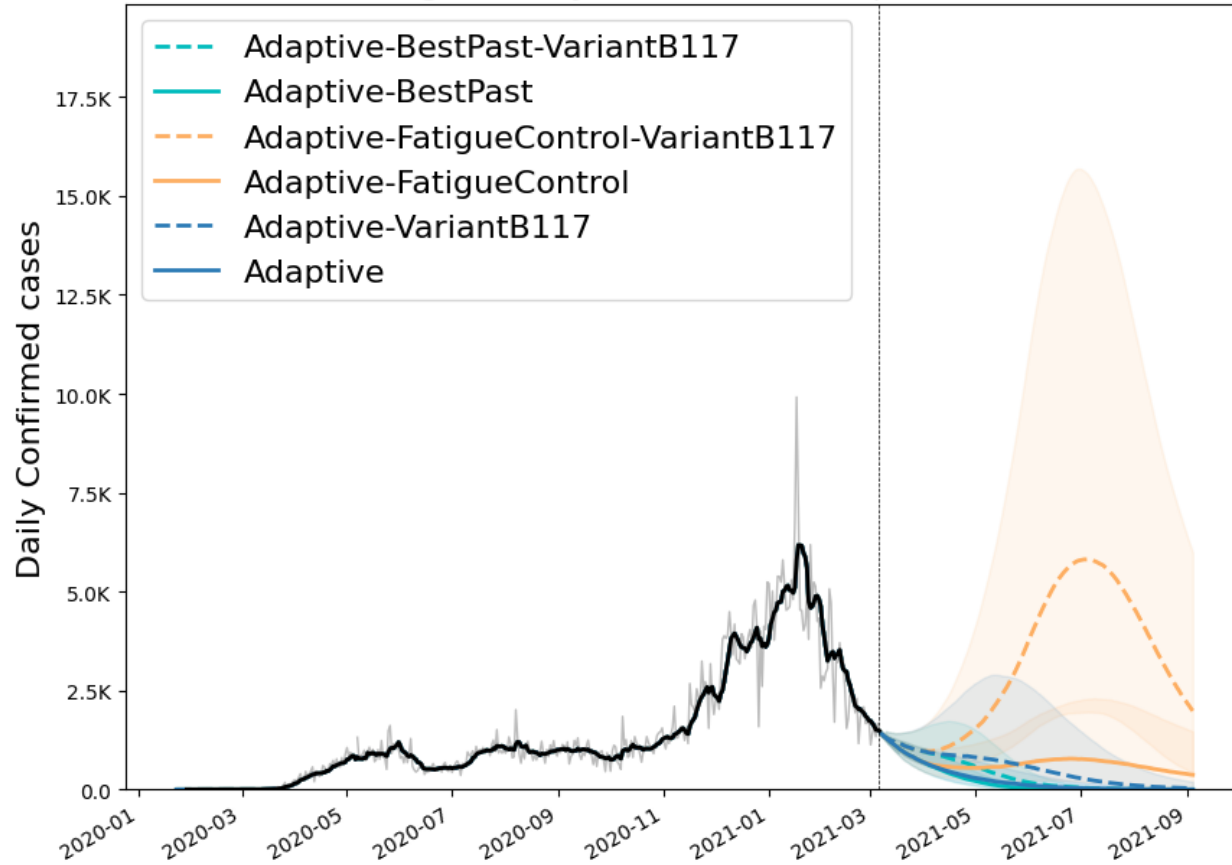
Counterfactuals with no vaccine ("NoVax") are provided for comparison purposes

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Model Results

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Outcome Projections

Estimated Hospital Occupancy

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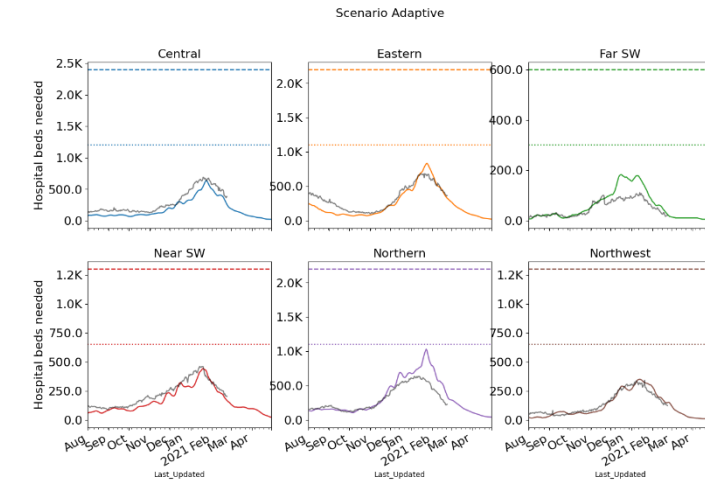
Daily Deaths
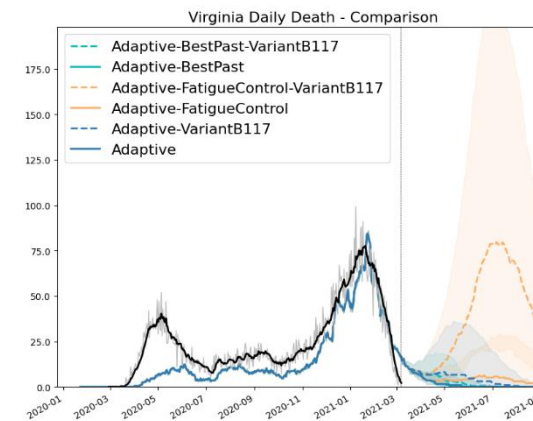
Death ground truth from VDH "Event Date" data, most recent dates are not complete

Daily Hospitalized

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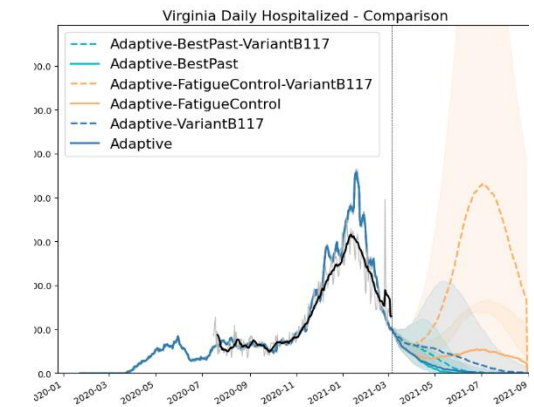
District Level Projections: Adaptive

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

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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
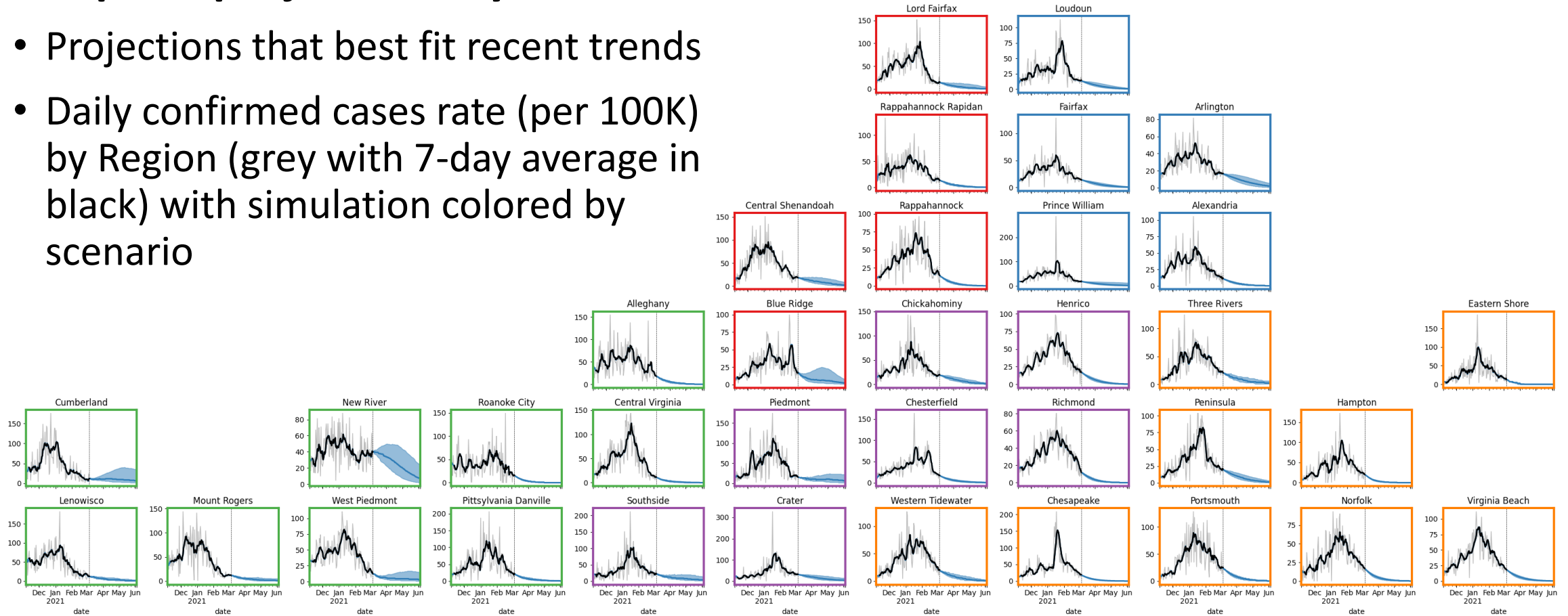
District Level Projections: Adaptive-VariantB117

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

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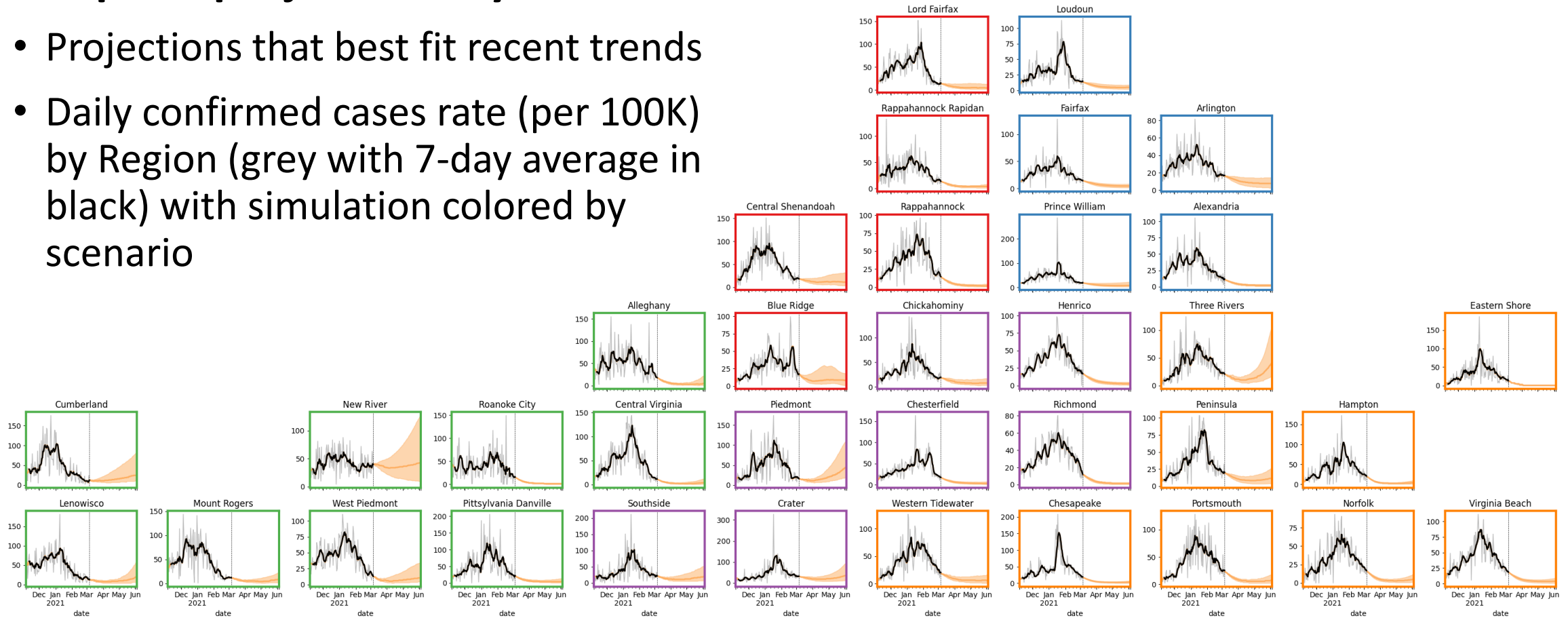
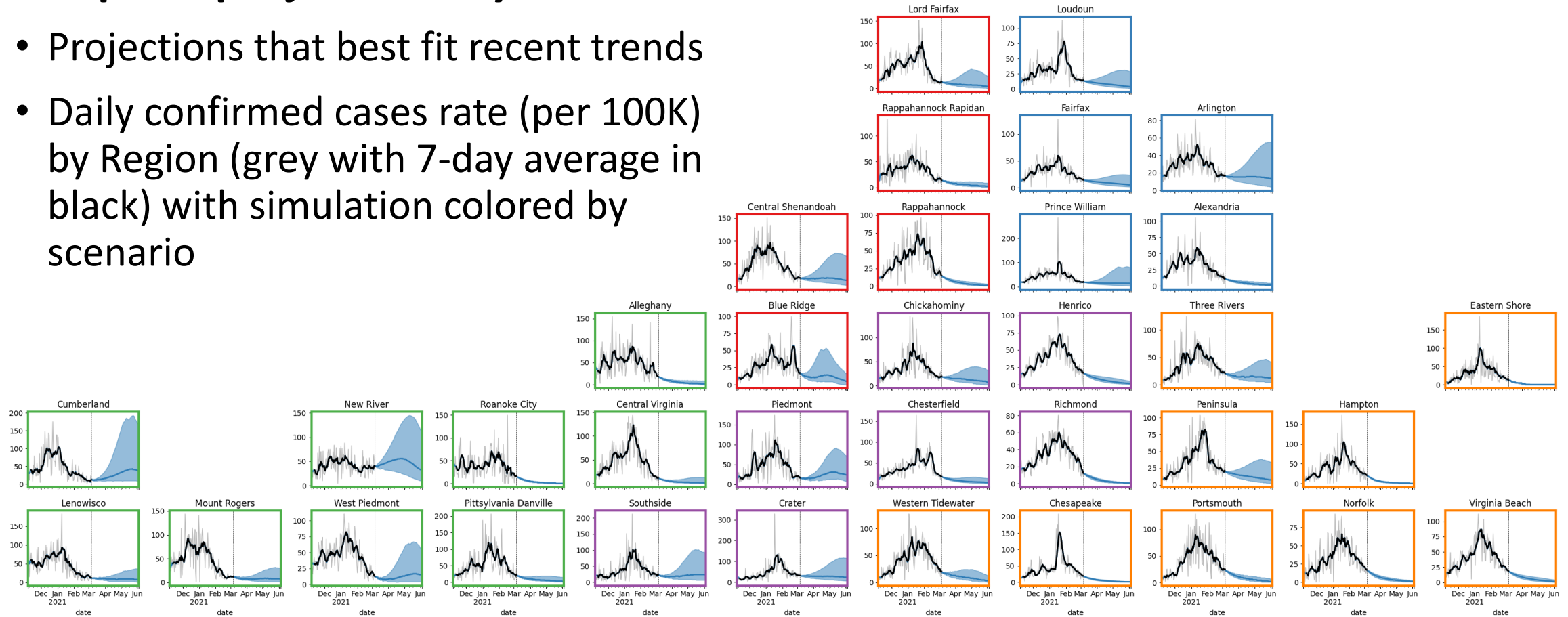## Adaptive projections by District

- 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

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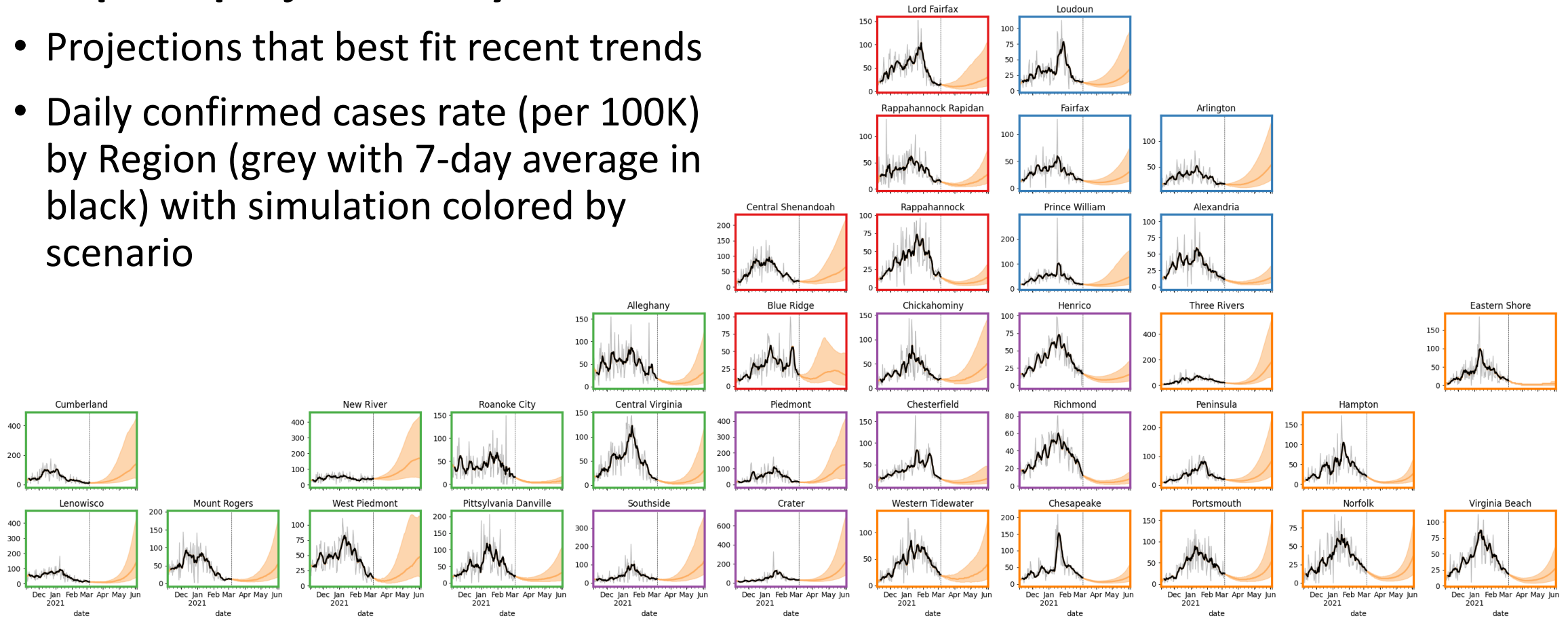
Hospital Demand and Bed Capacity by Region

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/
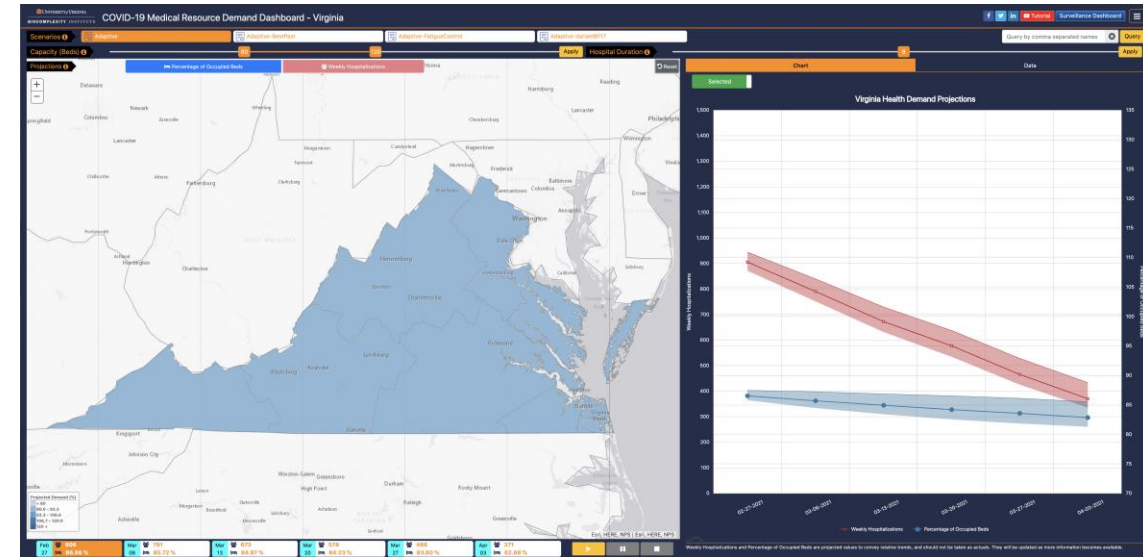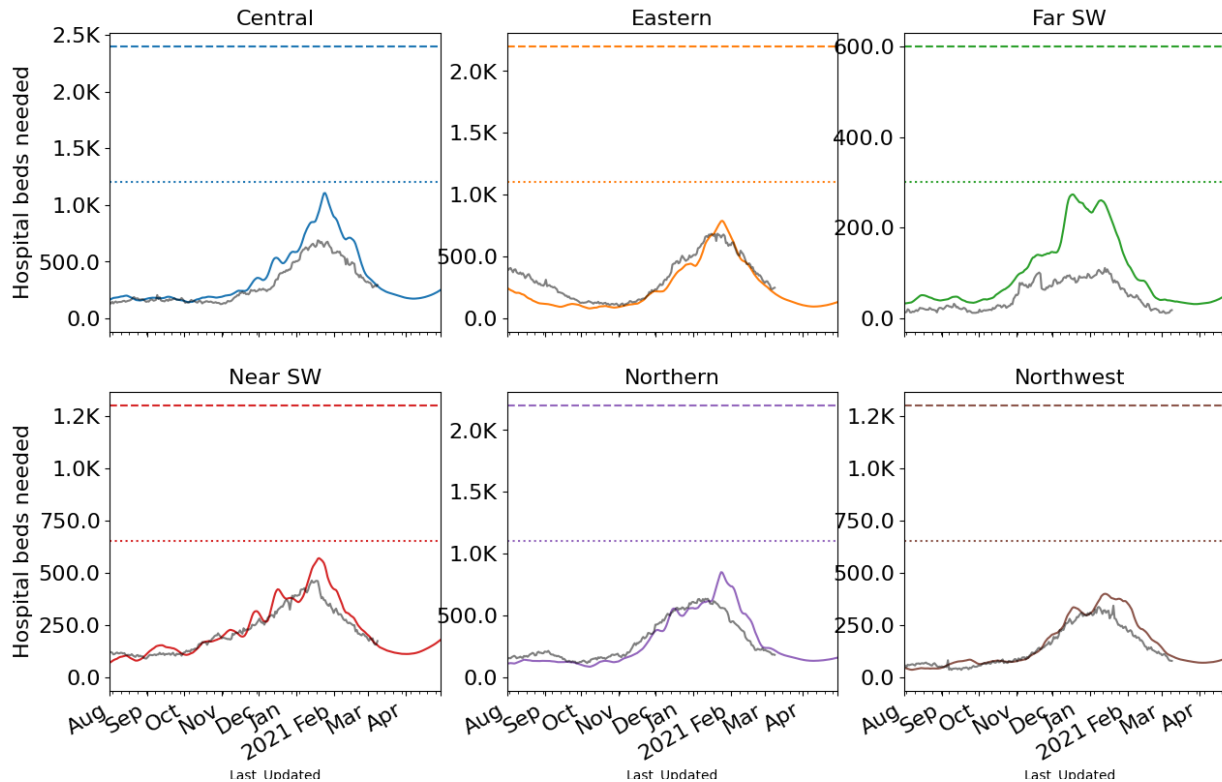
If Adaptive-FatigueControl-Variant scenario:

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

* Assumes average length of stay of 8 days

10-Mar-21

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Impact of Accelerated Vaccine on Projections

Comparison of maintaining the status quo rates (current) vs. the accelerated rate based on ramped up supplies in coming weeks

- Accelerated rate significantly diminishes size of resurgence from fatigued controls and /or variants with enhanced transmission

- Accelerated rate is 30% more than recent week

- **Current rate:** 275 **FIRST DOSES** per 100K per day based on median of last week (~23K per day)

- **Accelerated rate:** 375 **FIRST DOSES** per 100K per day (32K per day)

Confirmed cases

Legend:
- Adaptive accelerated vax
- Adaptive-VariantB117 accelerated vax
- Adaptive current vax
- Adaptive-VariantB117 current vax
- Adaptive-FatigueControl-VariantB117 current vax
- Adaptive-FatigueControl-VariantB117 accelarated vax

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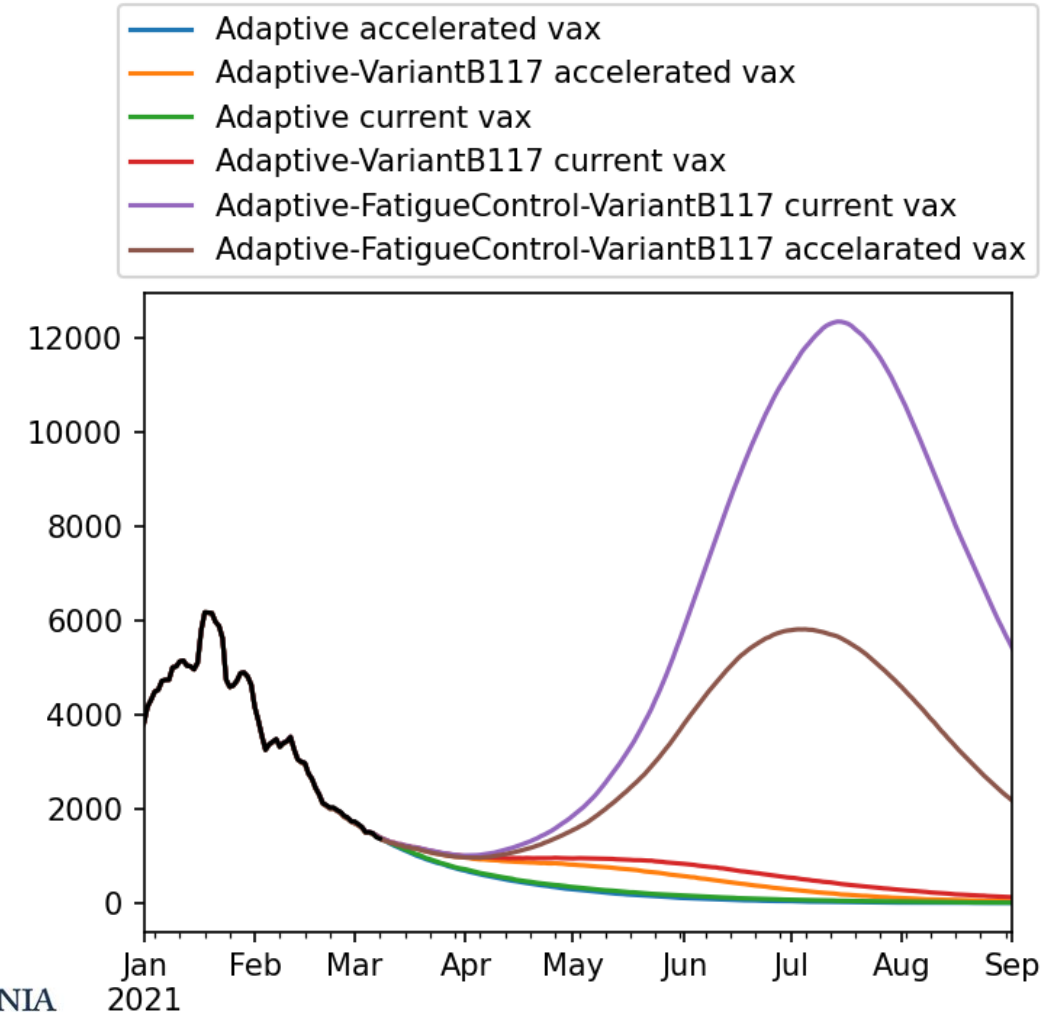
Weekly Cases and Hospitalizations

Weekly confirmed cases

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-BestPast	Adaptive-VariantB117	Adaptive-Fatigued Control-VariantB117
3/7/21	10,802	10,801	10,801	10,802	10,801
3/14/21	8,814	8,812	8,813	9,024	9,020
3/21/21	7,138	7,138	7,141	8,061	8,044
3/28/21	5,826	5,826	5,820	7,245	7,219
4/4/21	4,770	4,823	4,760	6,730	6,785
4/11/21	3,926	4,272	3,813	6,378	6,916
4/18/21	3,226	4,017	2,946	6,129	7,614
4/25/21	2,654	3,888	2,226	5,951	8,738
5/2/21	2,148	3,846	1,629	5,780	10,331
5/9/21	1,766	3,883	1,129	5,497	12,403
5/16/21	1,406	3,990	744	5,184	15,256
5/23/21	1,144	4,222	482	4,790	18,658

Weekly Hospitalizations

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-BestPast	Adaptive-VariantB117	Adaptive-Fatigued Control-VariantB117
3/7/21	743	743	743	743	743
3/14/21	615	615	614	628	628
3/21/21	472	473	473	552	551
3/28/21	382	383	382	480	478
4/4/21	318	321	317	457	459
4/11/21	258	282	251	440	475
4/18/21	193	252	181	427	525
4/25/21	160	240	126	408	602
5/2/21	126	238	85	398	730
5/9/21	98	252	50	375	882
5/16/21	71	264	27	332	1,110
5/23/21	57	276	18	311	1,367

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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 down to 16/100K from 19/100K, US levels plateau (to 19 from 18 per 100K)

- Significant progress made in last month, however 88% of VA counties above mean rate of Summer 2020

- Projections continue to be down but are flattening out across Commonwealth

- Recent updates:
  - Accelerated vaccine schedule 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
  - Ascertainment rate adjusted to better capture total infections to date

- The situation is changing rapidly. Models continue to be updated regularly.

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

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

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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/

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Questions?

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Biocomplexity COVID-19 Response Team

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Supplemental Slides

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Date of Onset Reproductive Number

Feb 27th Estimates

Region	Date of Onset R_e	Date Onset Diff Last Week
State-wide	0.810	-0.002
Central	0.838	0.069
Eastern	0.746	-0.072
Far SW	0.877	0.014
Near SW	0.831	0.089
Northern	0.945	0.158
Northwest	0.628	-0.374

Methodology

- Wallinga-Teunis method (EpiEstim[1]) 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

VA state-wide RE with 7 day moving window by date of onset 03/08/21

VA RE by VHASS region with 7 day moving window by date of onset 03/08/21
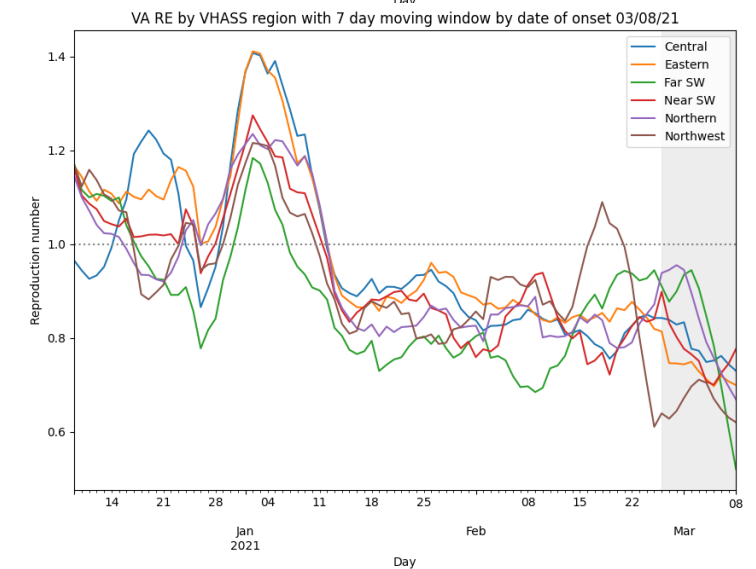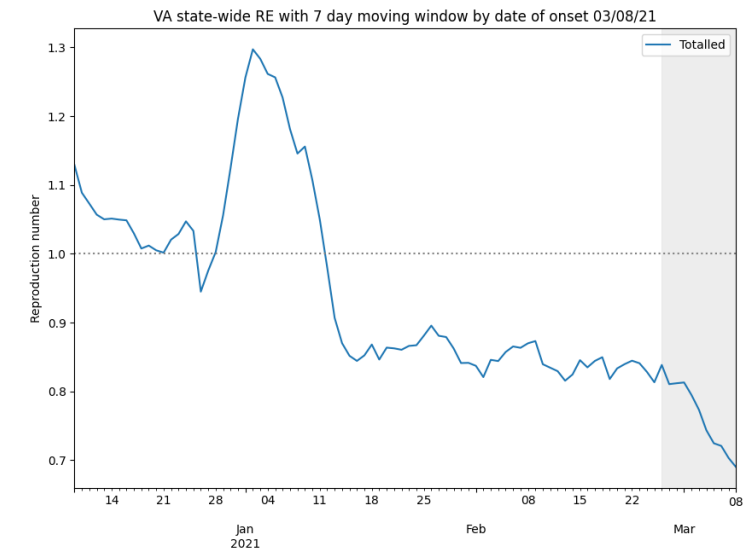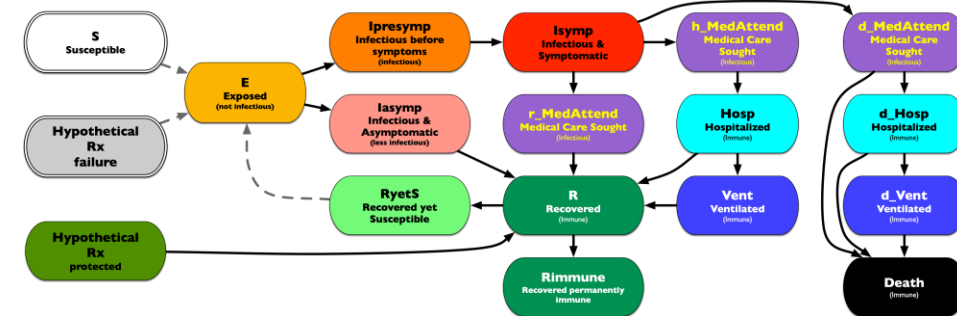
Agent-based Model (ABM)

EpiHiper: Distributed network-based stochastic disease transmission simulations

- Assess the impact on transmission under different conditions

- Assess the impacts of contact tracing
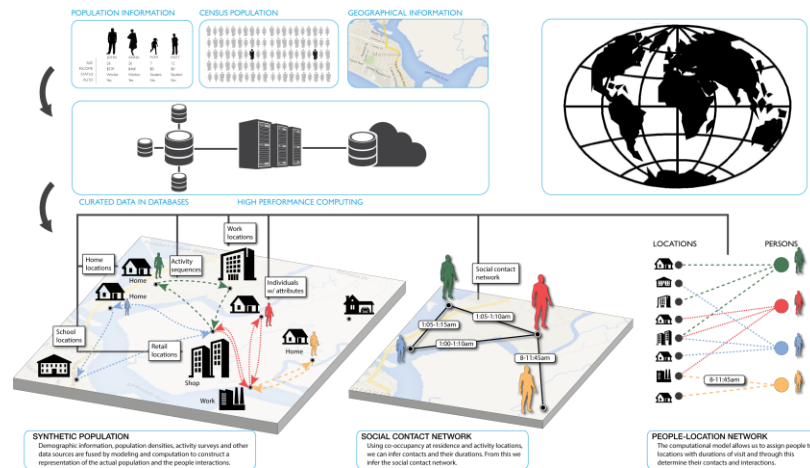
Synthetic Population
- Census derived age and household structure
- Time-Use survey driven activities at appropriate locations


Detailed Disease Course of COVID-19
- Literature based probabilities of outcomes with appropriate delays
- Varying levels of infectiousness
- Hypothetical treatments for future developments

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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"
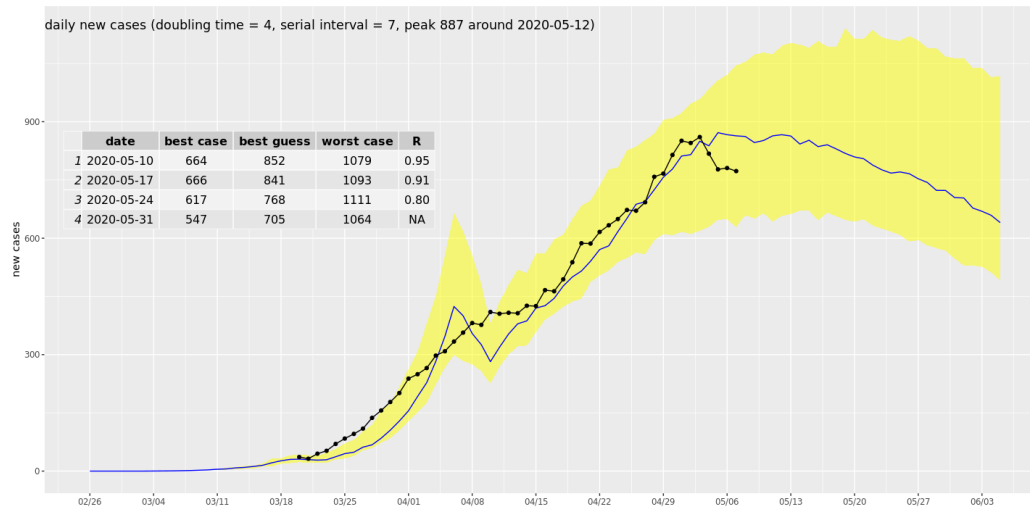
Calibration to Current State
- Adjust transmission and adherence to current policies to current observations
- For Virginia, with same seeding approach as PatchSim
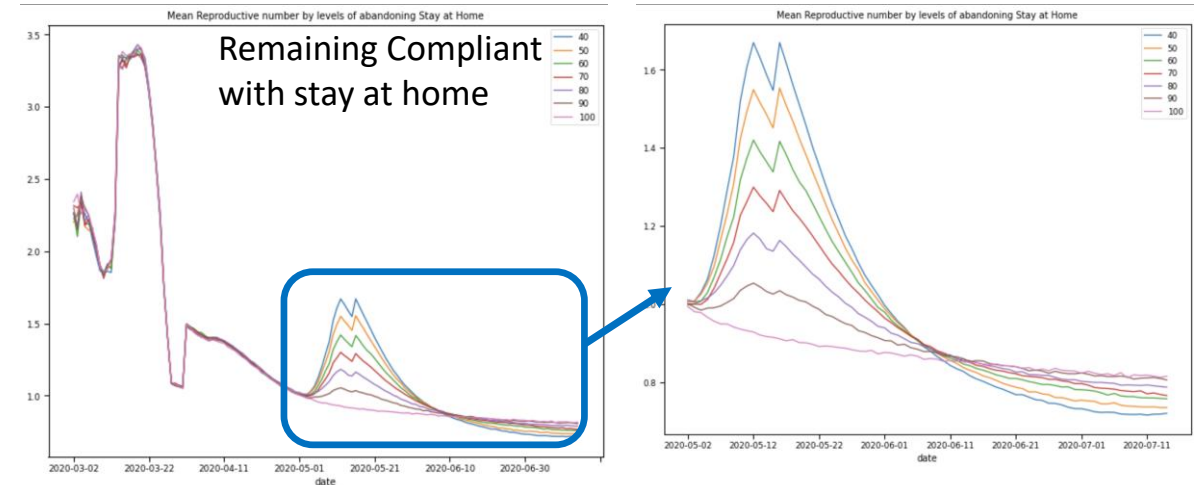
Impacts on Reproductive number with release
- After release, spike in transmission driven by additional interactions at work, retail, and other
- At 25% release (70-80% remain compliant)
- Translates to 15% increase in transmission, which represents a 1/6th return to pre-pandemic levels

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