Network Systems Science & Advanced Computing

Biocomplexity Institute & Initiative

University of Virginia

Estimation of COVID-19 Impact in Virginia

February 10th, 2021

(data current to February 8th – 9th)

Biocomplexity Institute Technical report: TR 2021-018

UNIVERSITY of VIRGINIA

BIOCOMPLEXITY INSTITUTE

biocomplexity.virginia.edu

About Us

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

Points of Contact

Bryan Lewis
brylew@virginia.edu

Srini Venkatramanan
srini@virginia.edu

Madhav Marathe
marathe@virginia.edu

Chris Barrett
ChrisBarrett@virginia.edu

Biocomplexity COVID-19 Response Team

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

UNIVERSITY of VIRGINIA

BIOCOMPLEXITY INSTITUTE

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:

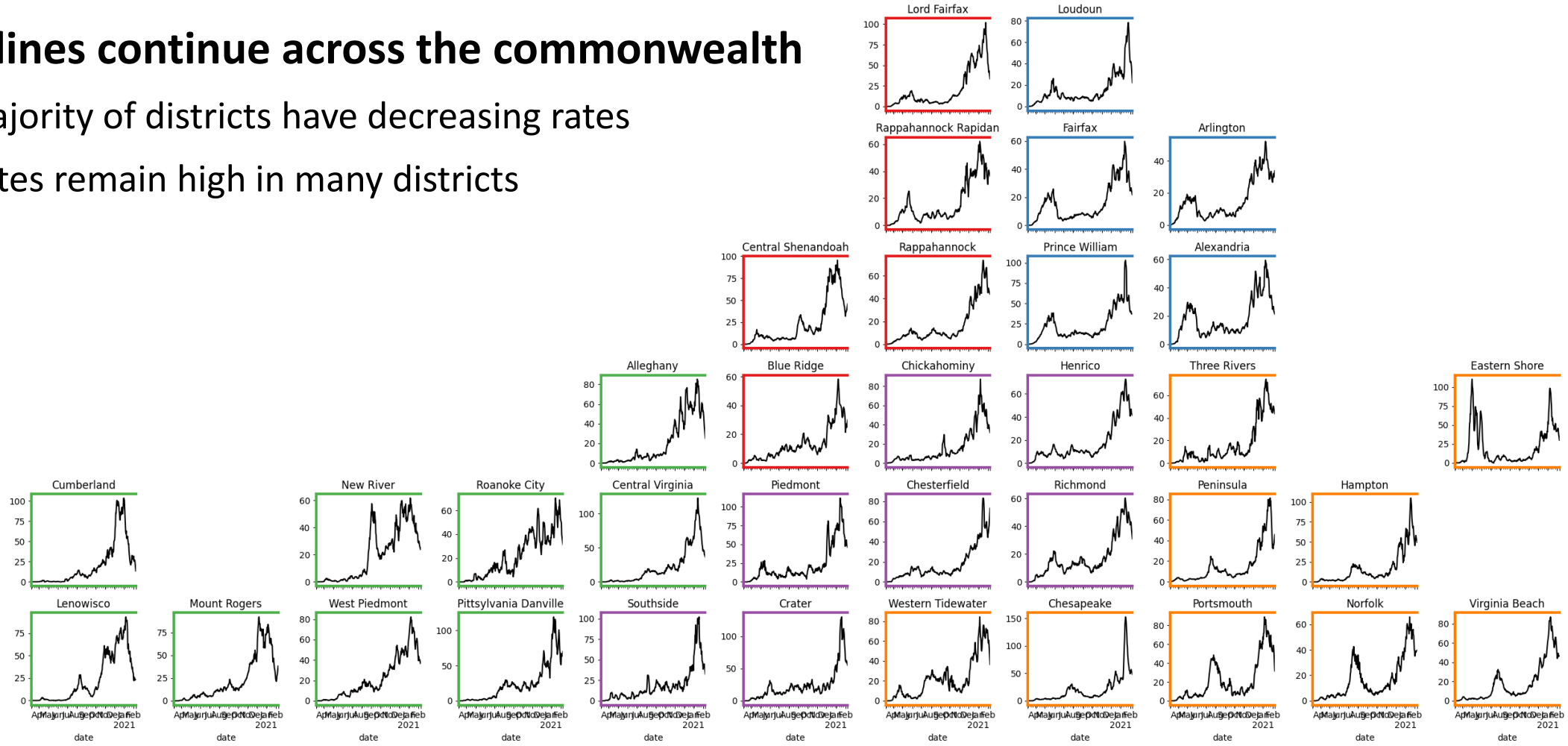
- **Case rate growth in Virginia continues to decline**
- VA mean weekly incidence down to 39/100K from 45/100K, US levels decline (to 29 from 37 per 100K)
- Case rates are still high, 46% of VA counties still report weekly incidence above half of their peak
- Projections are down across commonwealth
- Recent updates:
  - Further refinement to Variant B.1.1.7 scenarios to incorporate recent data
  - Impact of transmission boosting from Variant B.1.1.7 added to control-based scenarios
  - Further updates to vaccination schedules, with fitting now down on 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

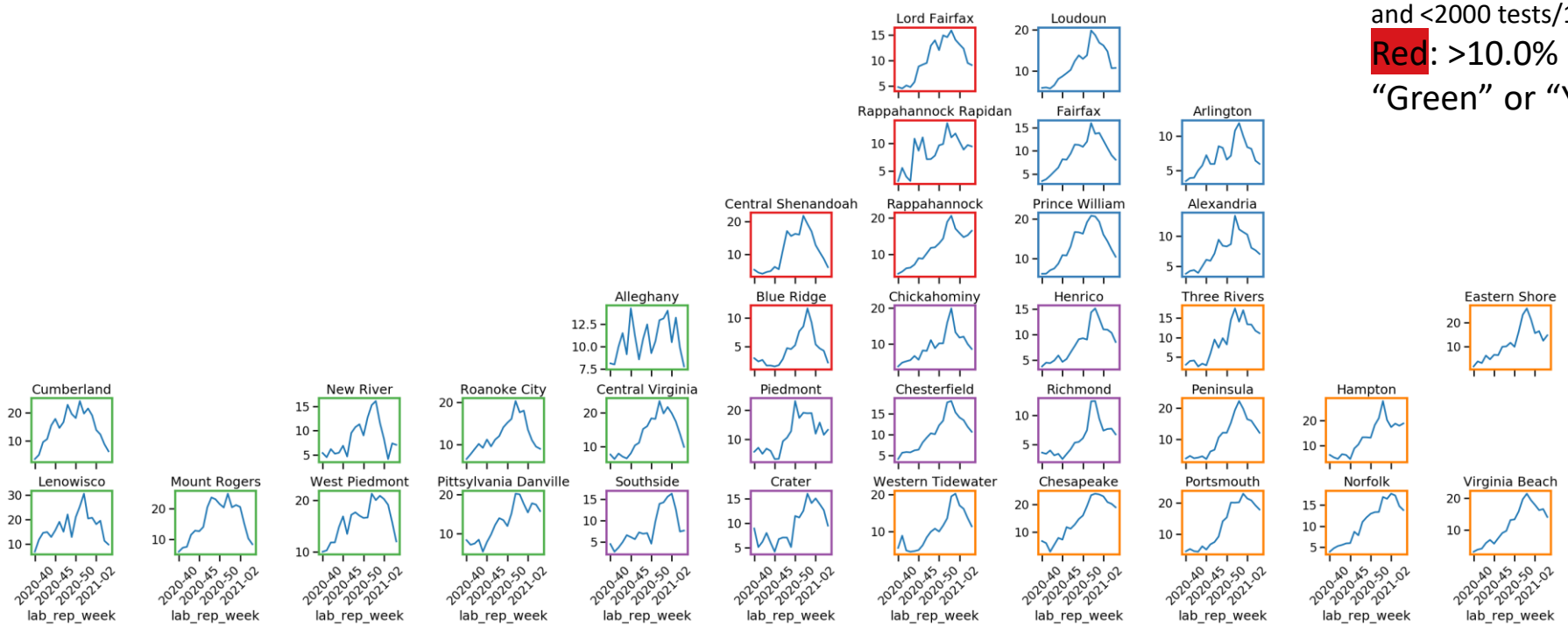


UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

Test Positivity by VDH District

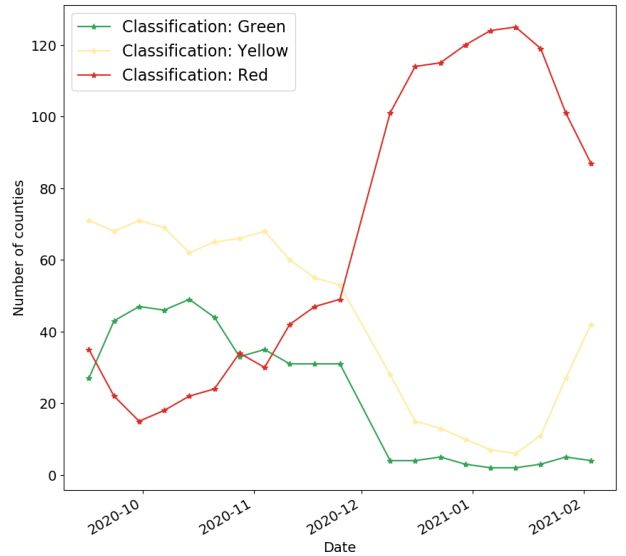
Weekly changes in test positivity by district

- Rates continue to decline
- Many fewer counties (85) over 10% (as of Feb 3rd)



County level test positivity rates for RT-PCR tests.

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



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

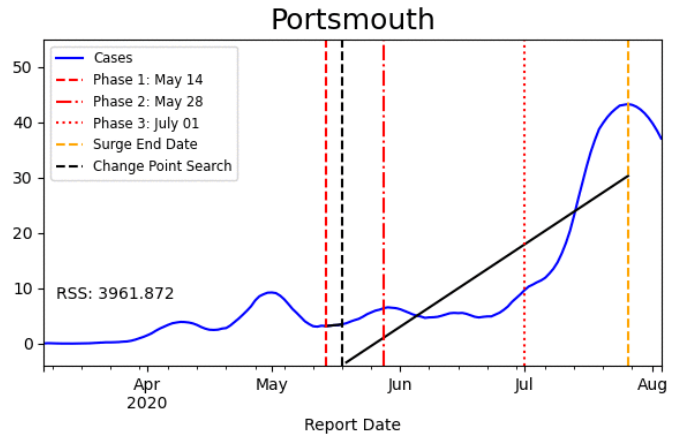
UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

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

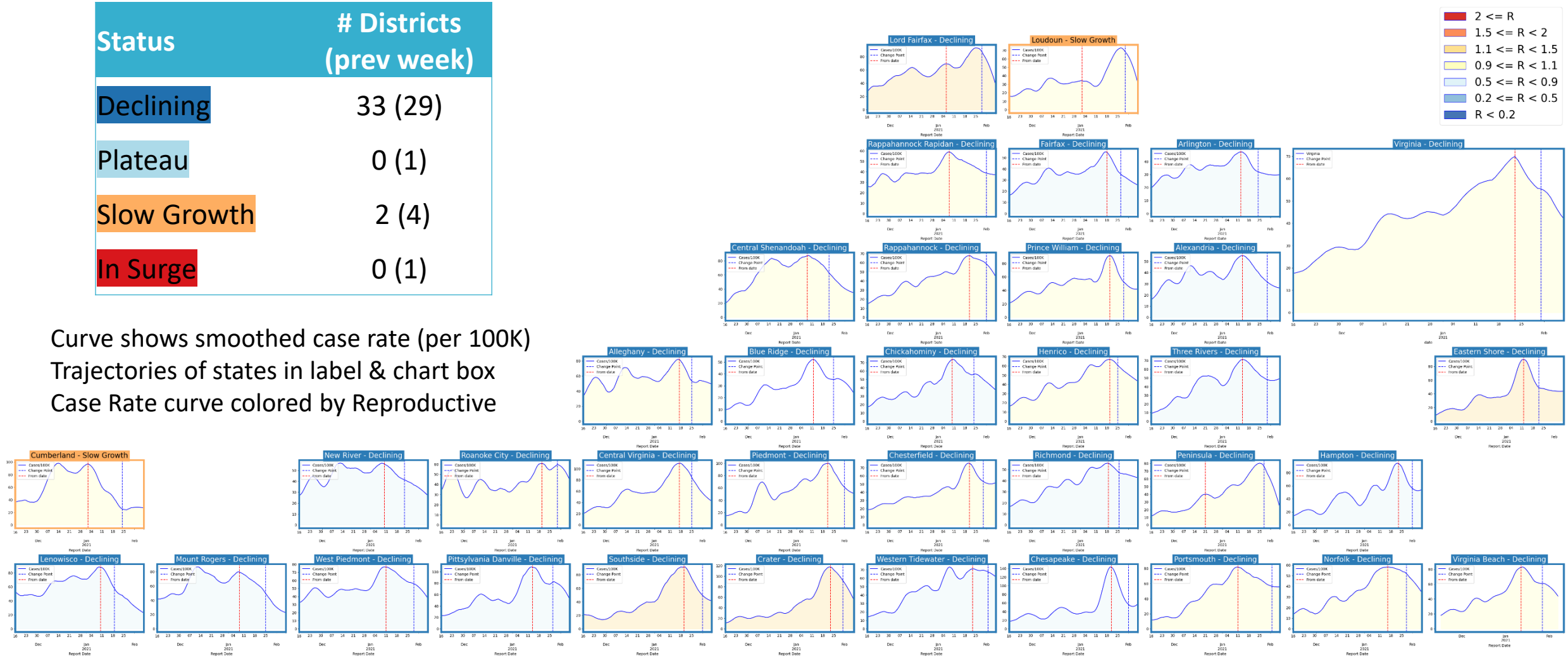


Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	33 (29)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	0 (1)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	2 (4)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	0 (1)

District Trajectories – last 10 weeks

Status	# Districts (prev week)
Declining	33 (29)
Plateau	0 (1)
Slow Growth	2 (4)
In Surge	0 (1)

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



UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

Estimating Daily Reproductive Number

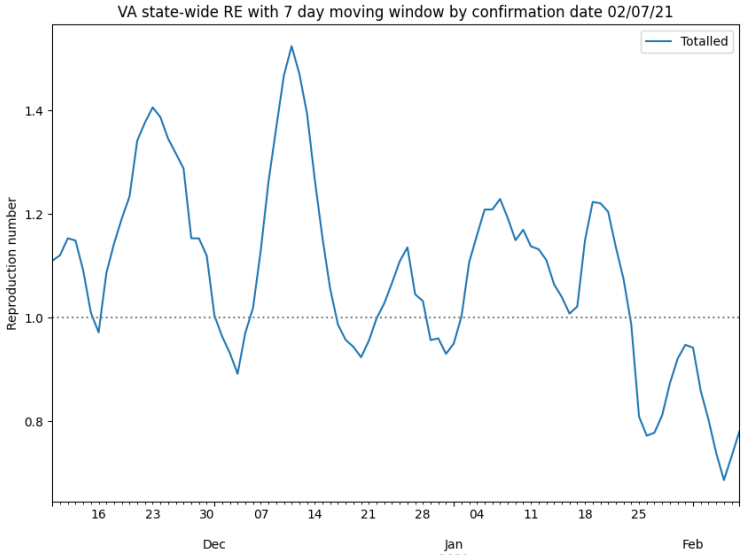
Feb 7th Estimates

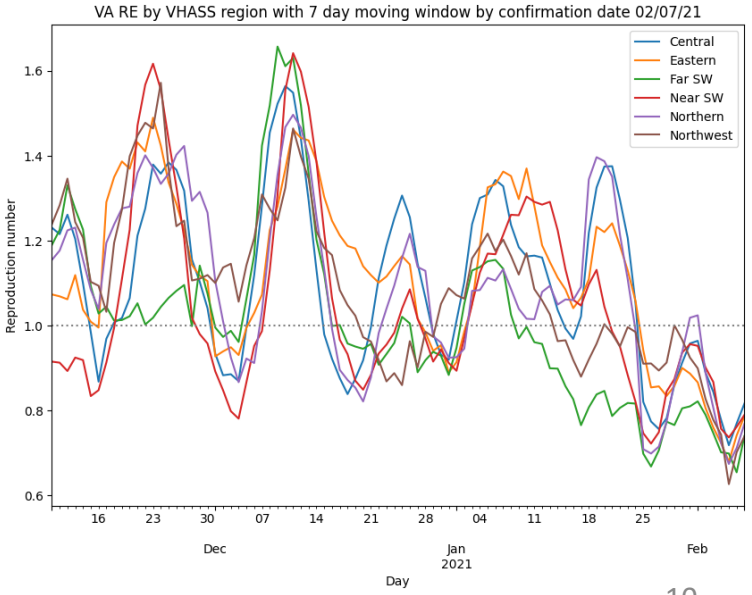
Region	Date Confirmed R_e	Date Confirmed Diff Last Week
State-wide	0.780	-0.162
Central	0.816	-0.148
Eastern	0.786	-0.080
Far SW	0.739	-0.082
Near SW	0.789	-0.163
Northern	0.768	-0.256
Northwest	0.738	-0.161

Methodology

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

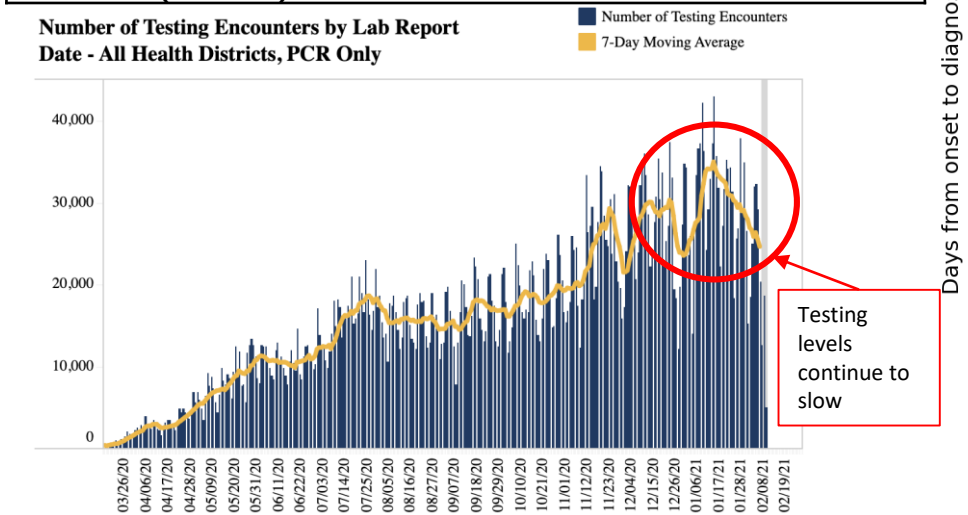
1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, https://doi.org/10.1093/aje/kwt133





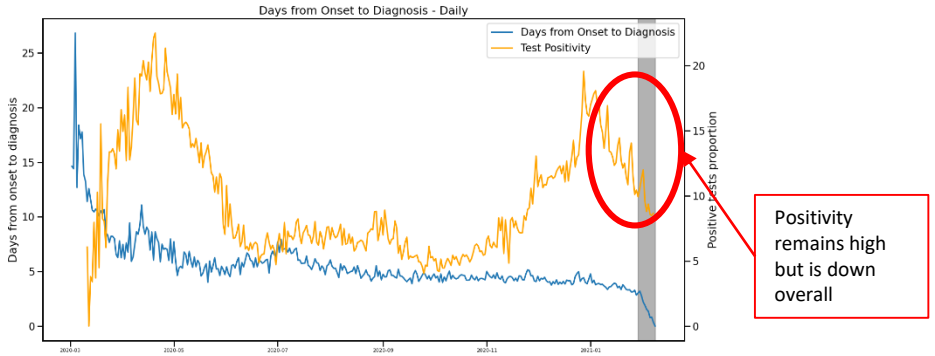
Changes in Case Detection

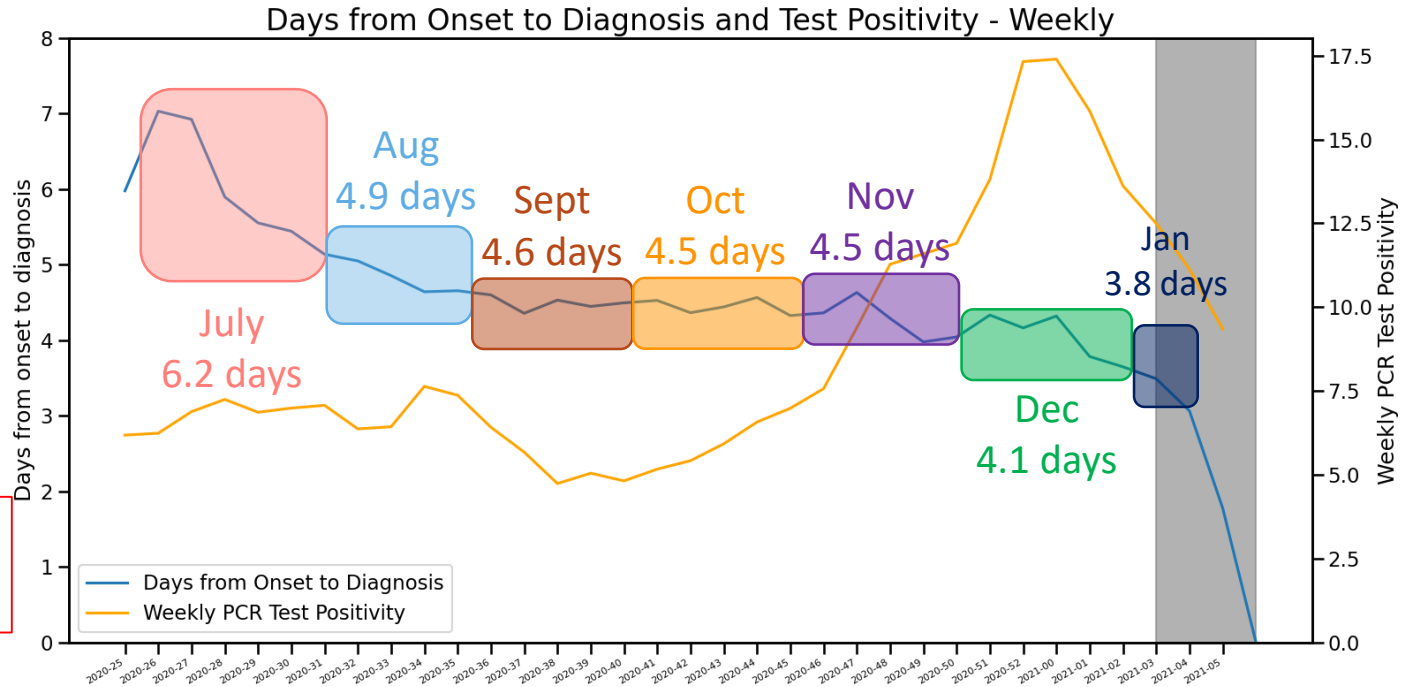
Timeframe (weeks)	Mean days	% difference from overall mean
May (17-21)	5.7	-19%
June (22-25)	5.8	-19%
July (26-30)	6.2	-13%
Aug (31-34)	4.9	-30%
Sept (35-38)	4.5	-36%
Oct (39-43)	4.5	-37%
Nov (44-47)	4.5	-37%
Dec (48-49)	4.2	-41%
Jan (00-02)	3.8	-46%
Overall (13-03)	7.1	--



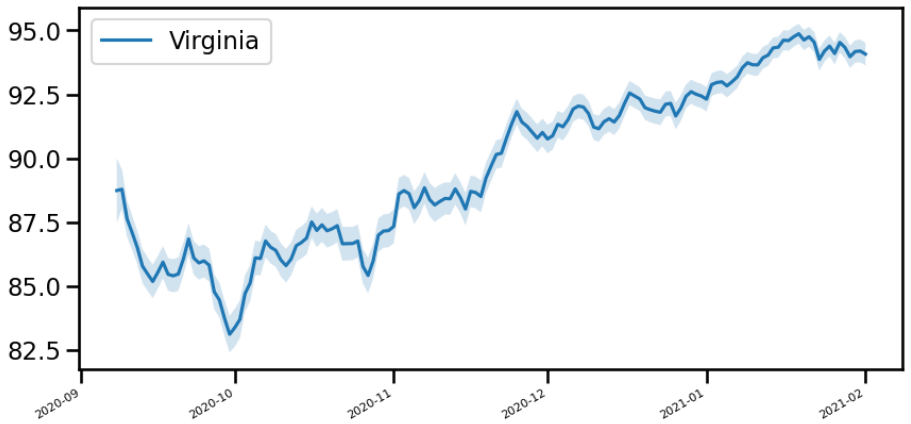
Accessed 8:30am February 10, 2021
https://www.vdh.virginia.gov/coronavirus/

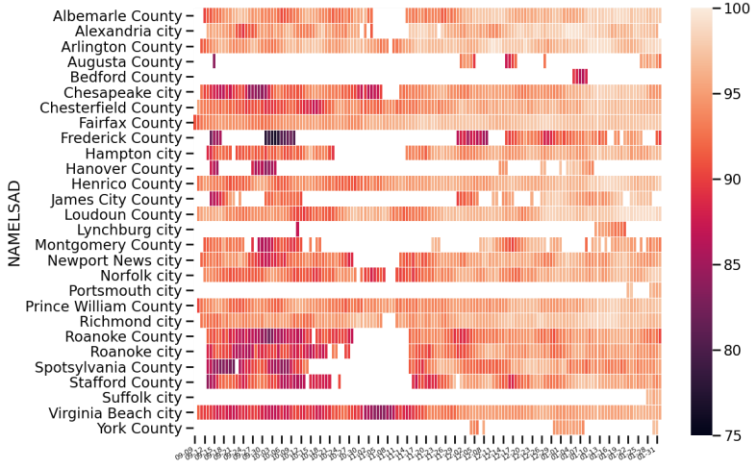
Test positivity vs. Onset to Diagnosis





Mask usage in Virginia



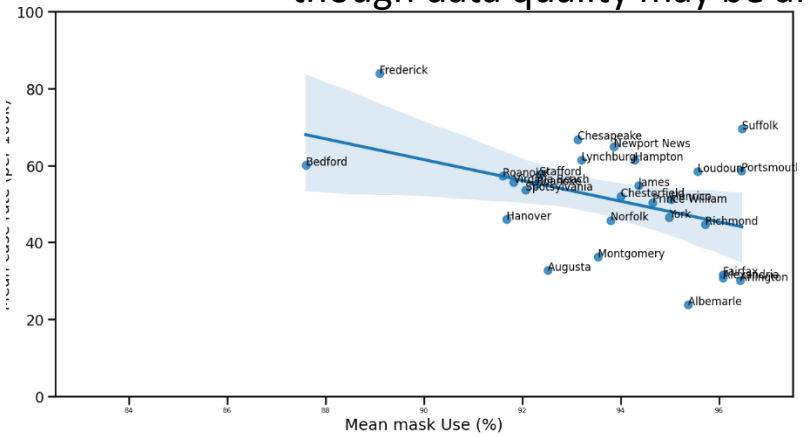


State level mask usage as reported via Facebook surveys has shown steady increase over past three months

- ~88% (early Nov) to ~94% (mid Jan)
- 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



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

Slope: - 2.7; for every % we see a ~3/100K case rate difference

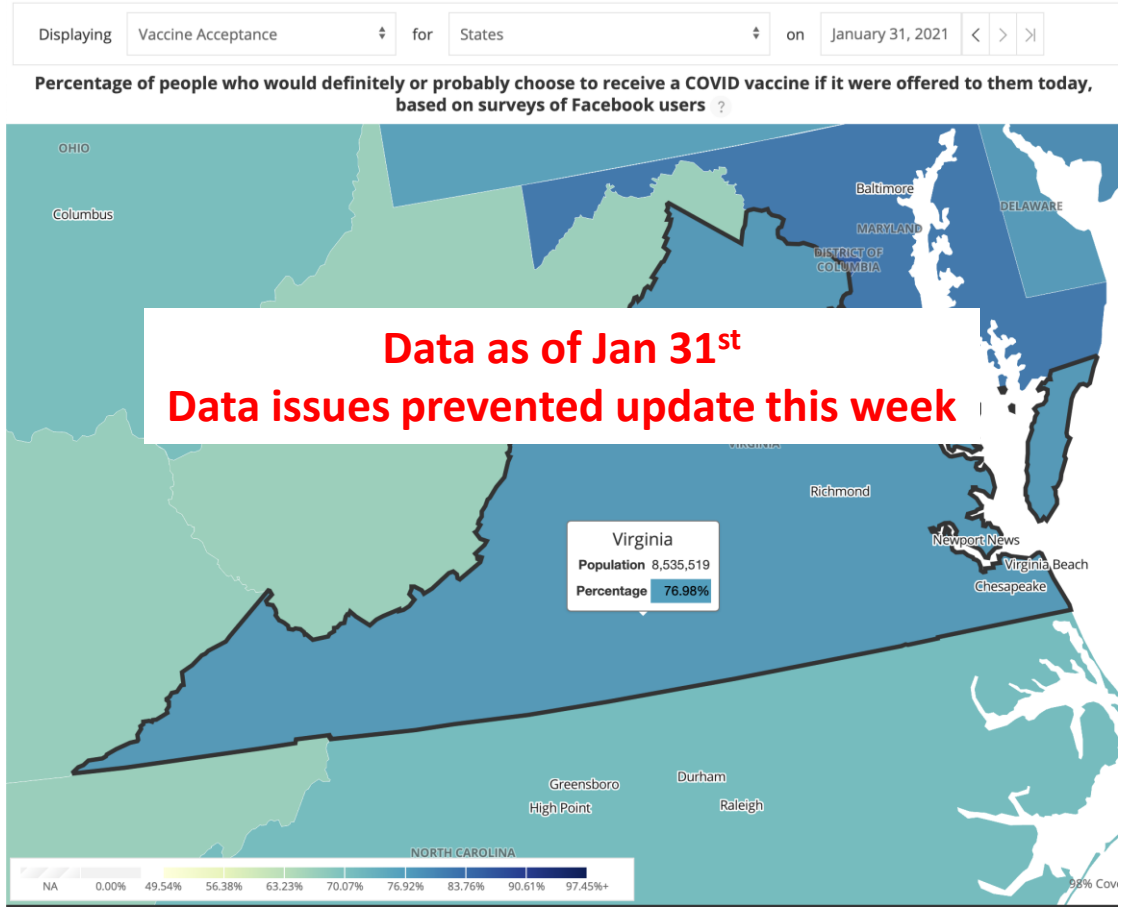
UNIVERSITY of VIRGINIA

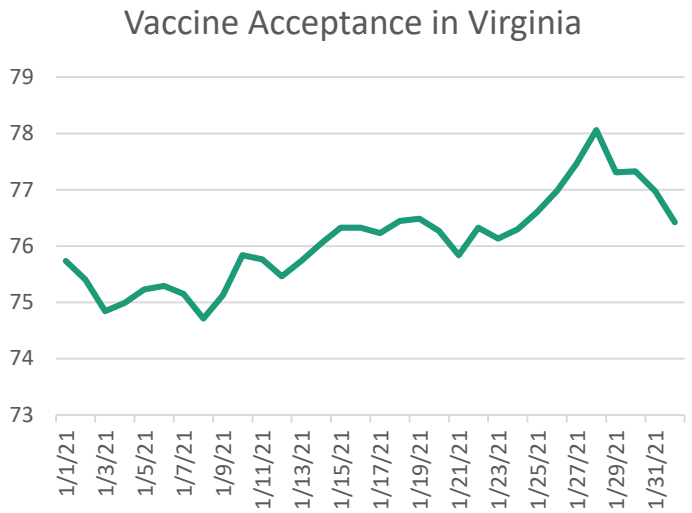
BIOCOMPLEXITY INSTITUTE

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)





Acceptance slightly up over the course of January: Over ¾ of Virginians are likely to choose to be vaccinated

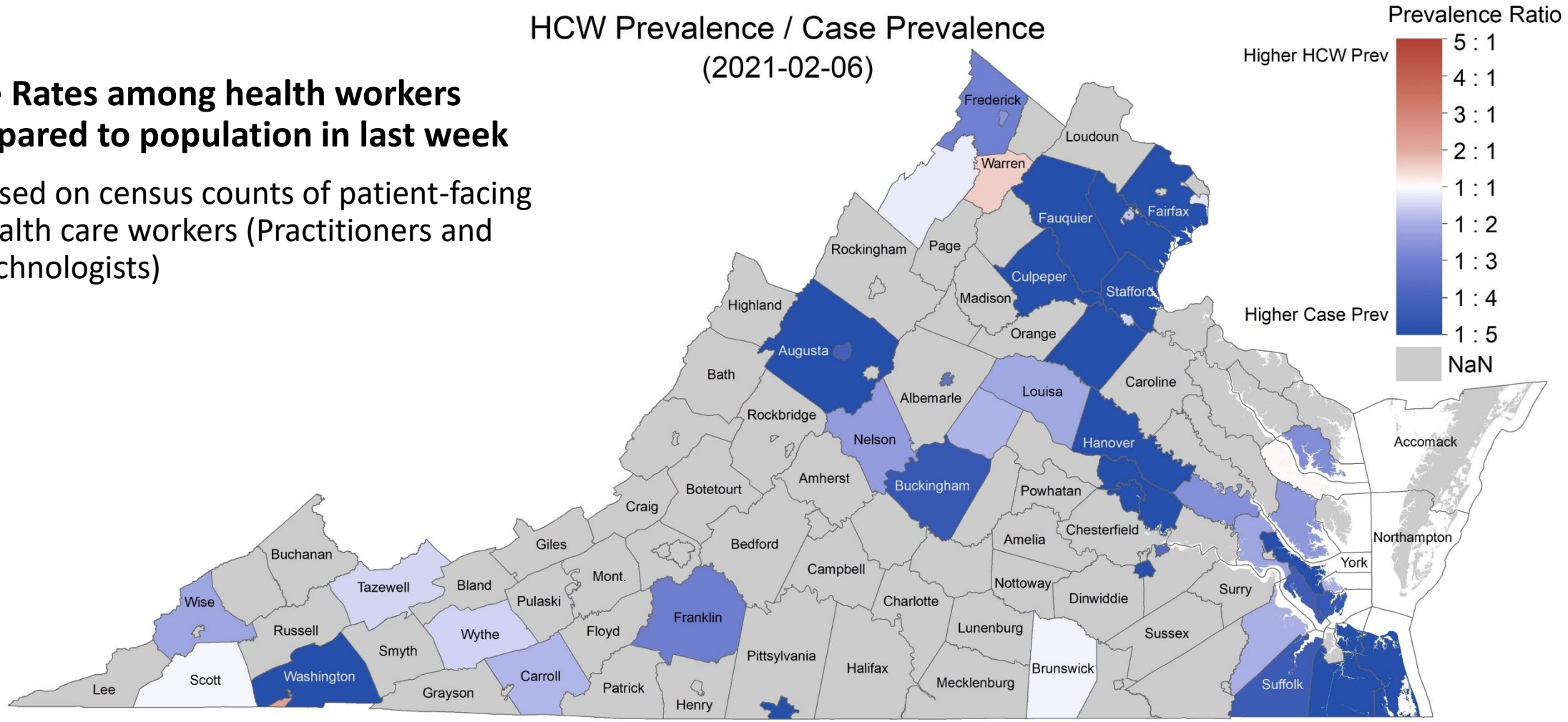
[COVIDcast Data Explorer](https://covidcast.cmu.edu)

Source: https://covidcast.cmu.edu

Health Care Worker Prevalence (per 100K)

Case Rates among health workers compared to population in last week

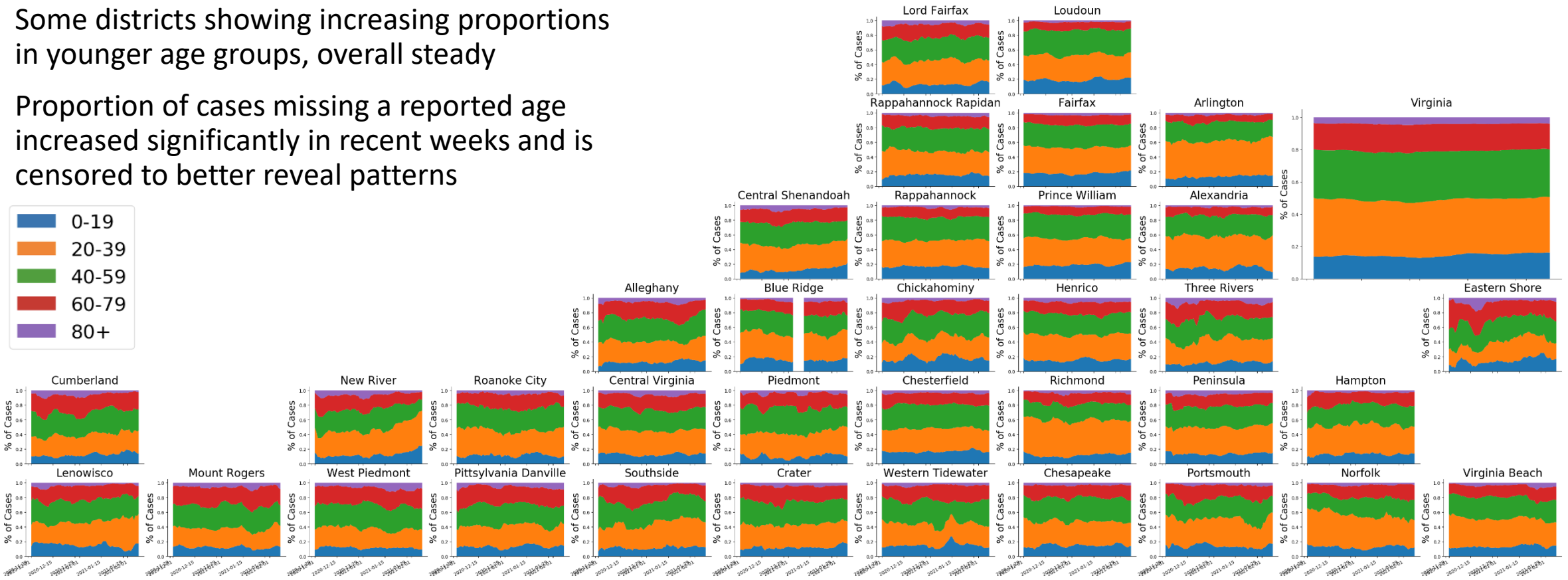
- Based on census counts of patient-facing health care workers (Practitioners and Technologists)



Age-Specific Case Rates

Proportion of cases by age-group for last 10 weeks

- Some districts showing increasing proportions in younger age groups, overall steady
- Proportion of cases missing a reported age increased significantly in recent weeks and is censored to better reveal patterns

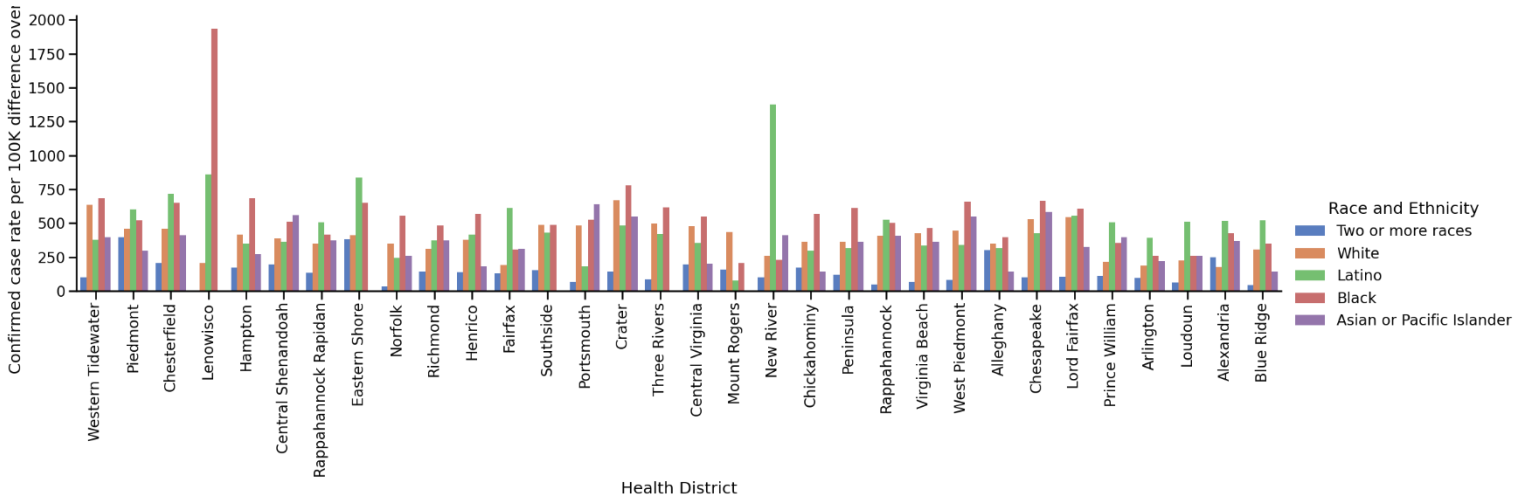


Race and Ethnicity – Recent Rate Changes (per 100K)

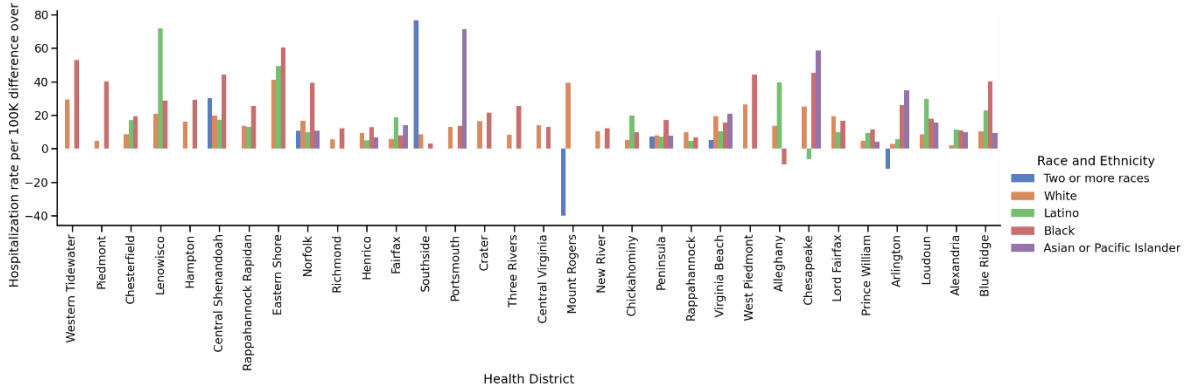
Recent Changes in Race and Ethnicity Rates (per 100k)

- 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

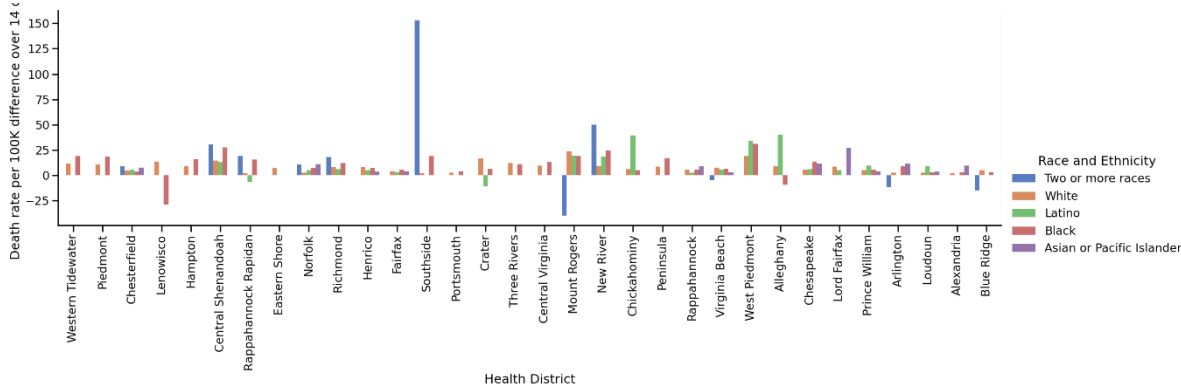
Case Rate



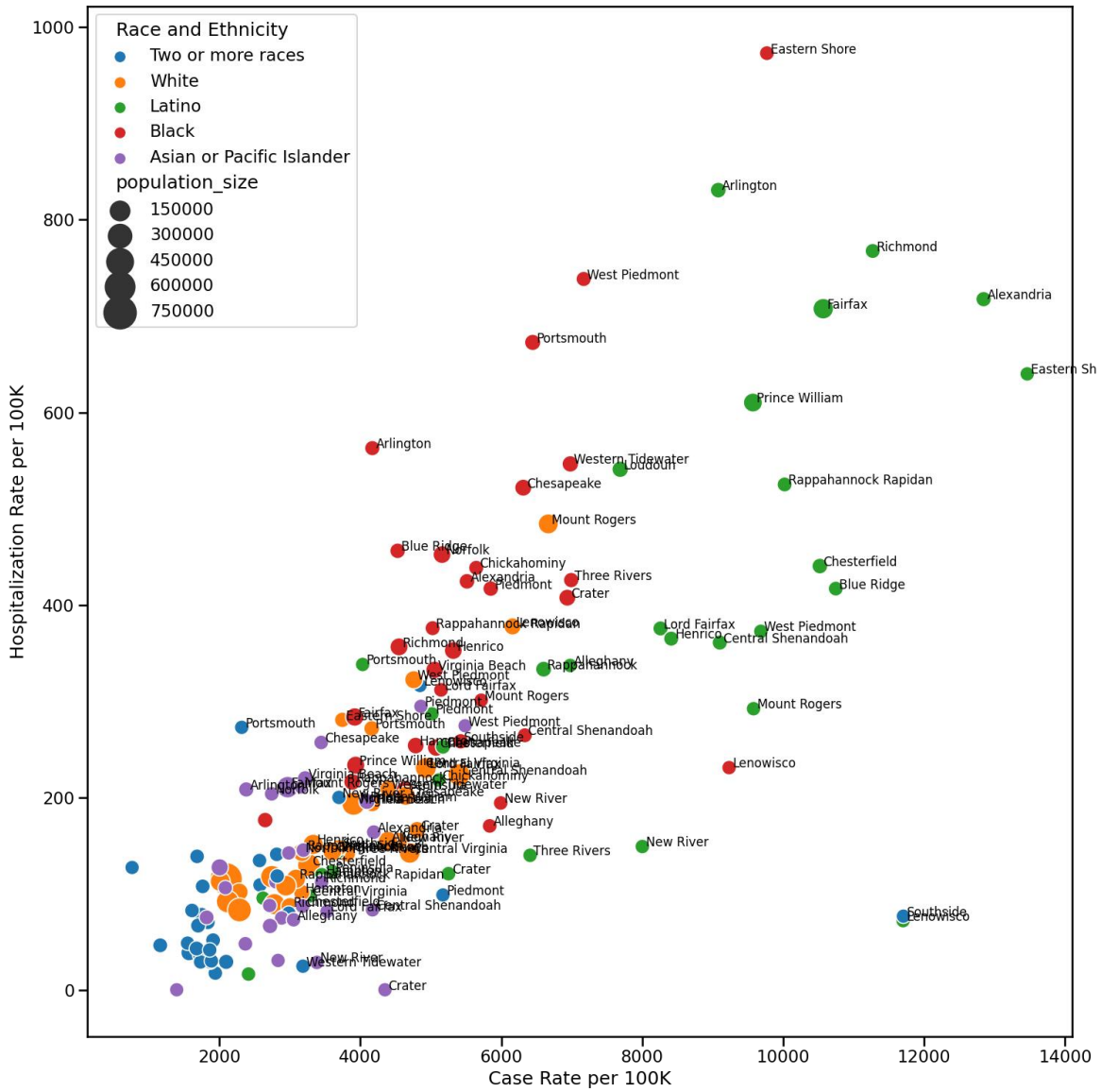
Hospitalization Rate



Death Rate



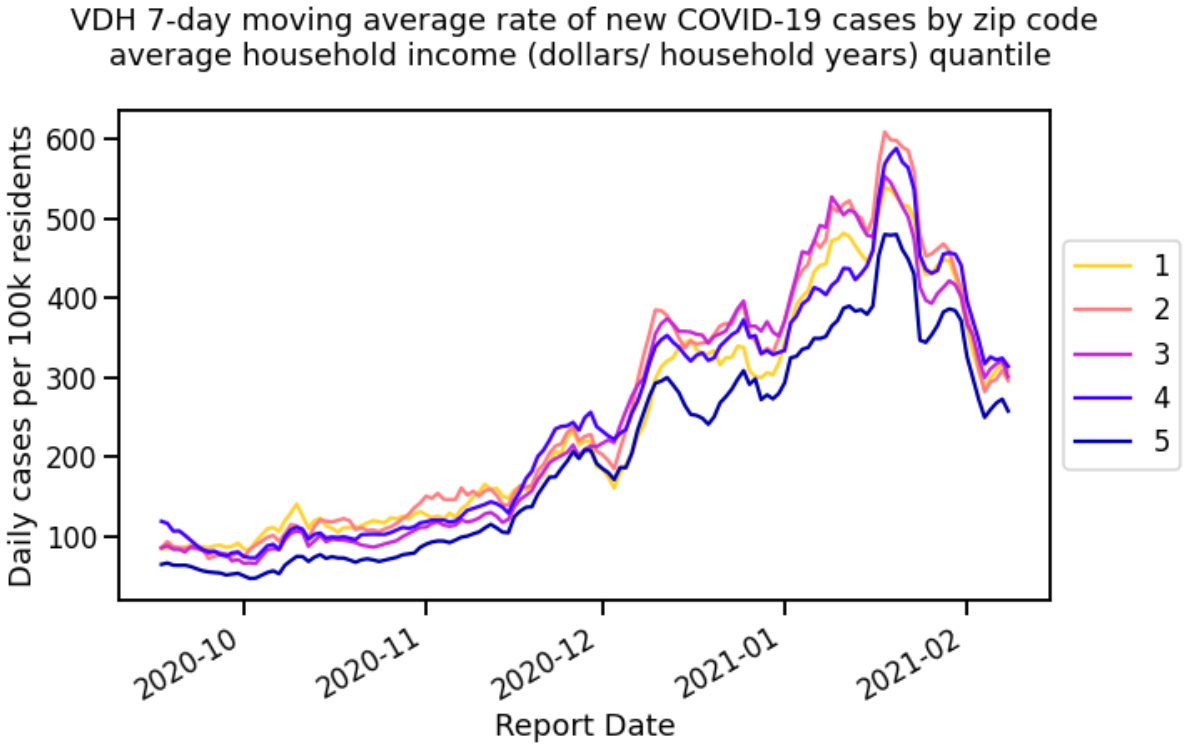
Race and Ethnicity cases per 100K



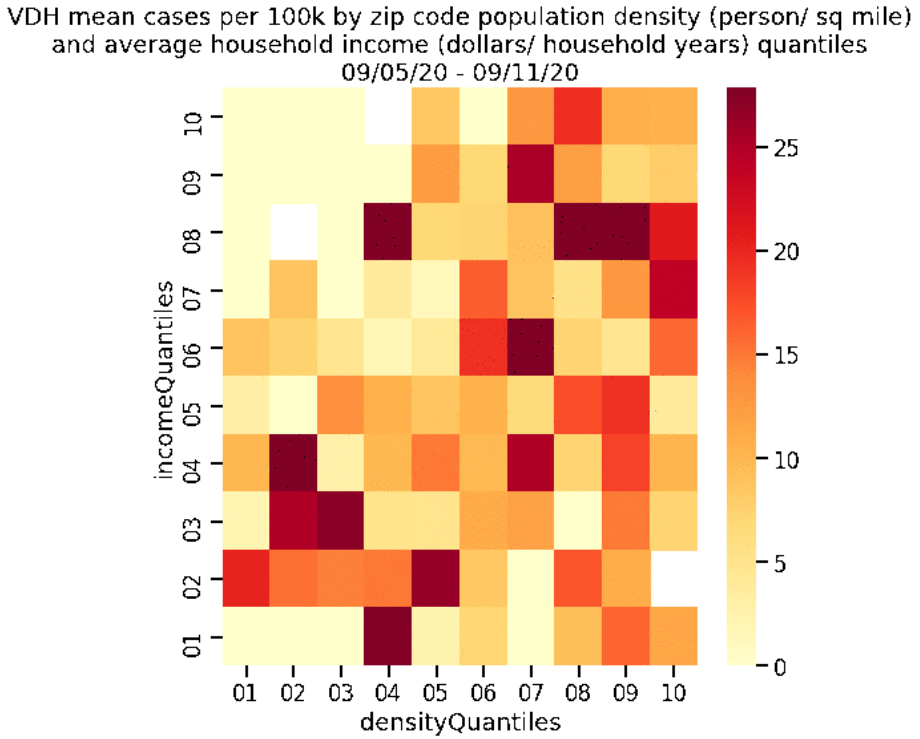
Rates per 100K of each Racial-Ethnic population by Health District

- 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 for clarity

Impact across Density and Income



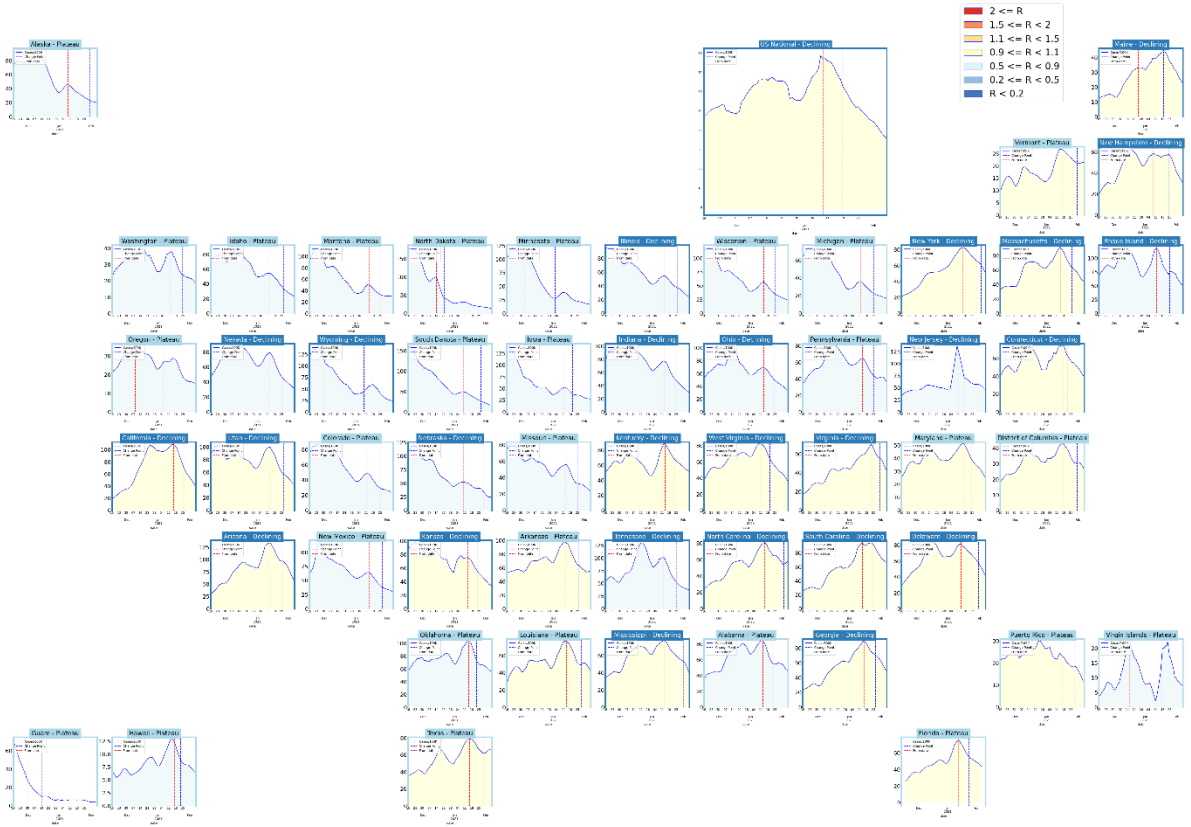
All zip codes show back into growth, wealthiest zip code now lags the rest significantly



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

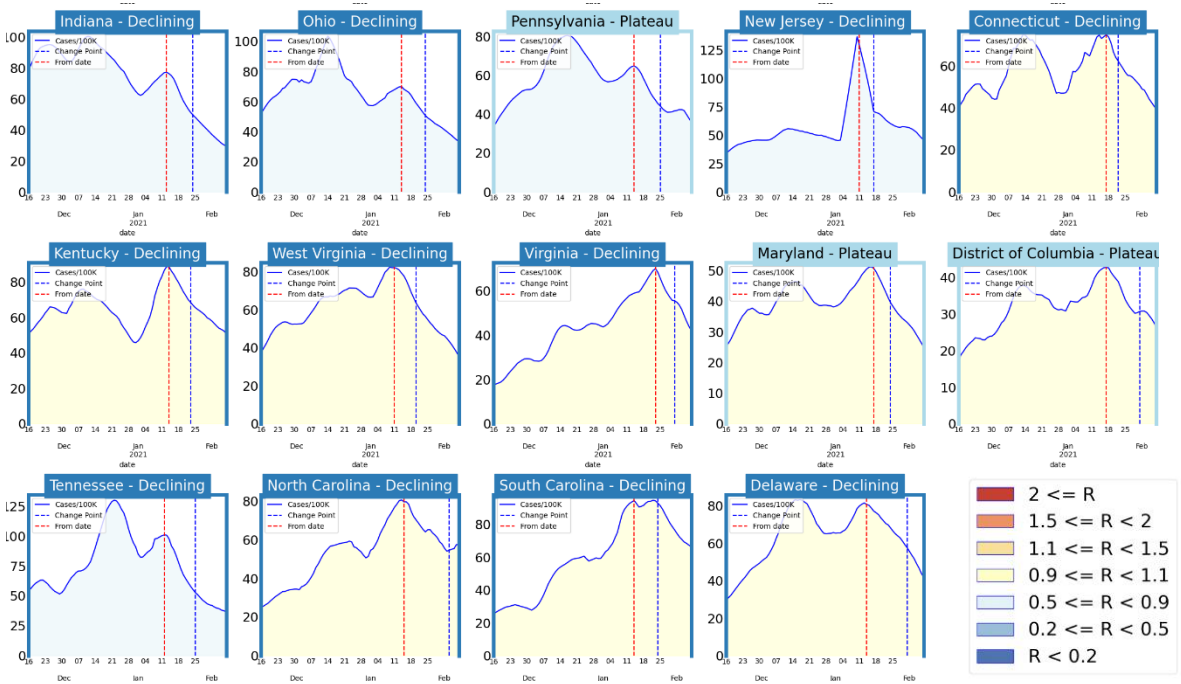
Other State Comparisons

Trajectories of States



- All states are declining (26) or plateaued (28)
- Rates still remain relatively high

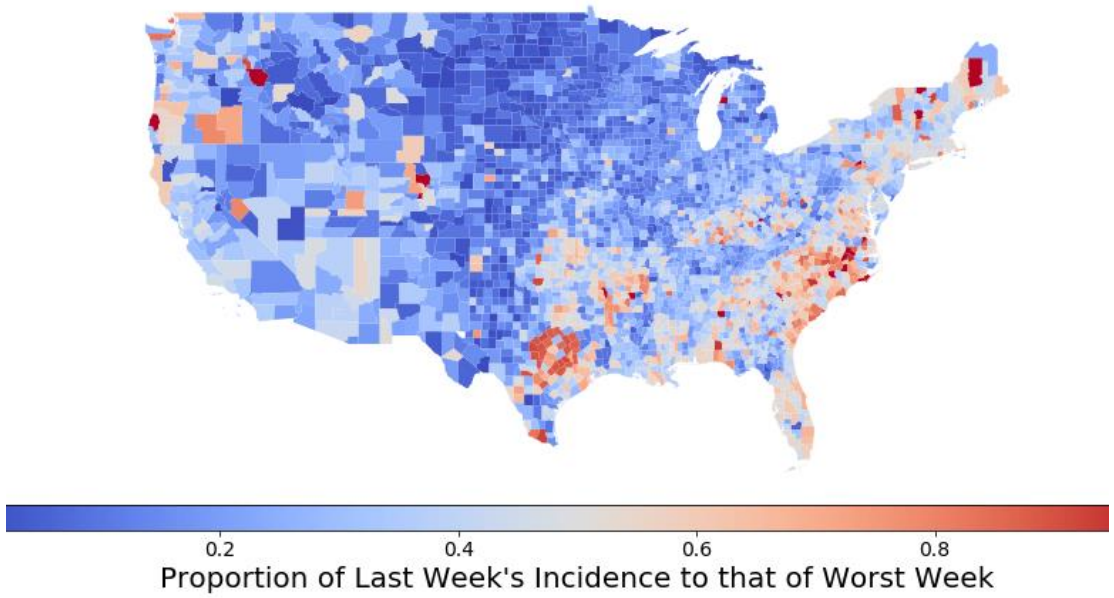
Virginia and her neighbors



- VA and her neighbors are all declining or plateaued
- Rates remain high in most states however

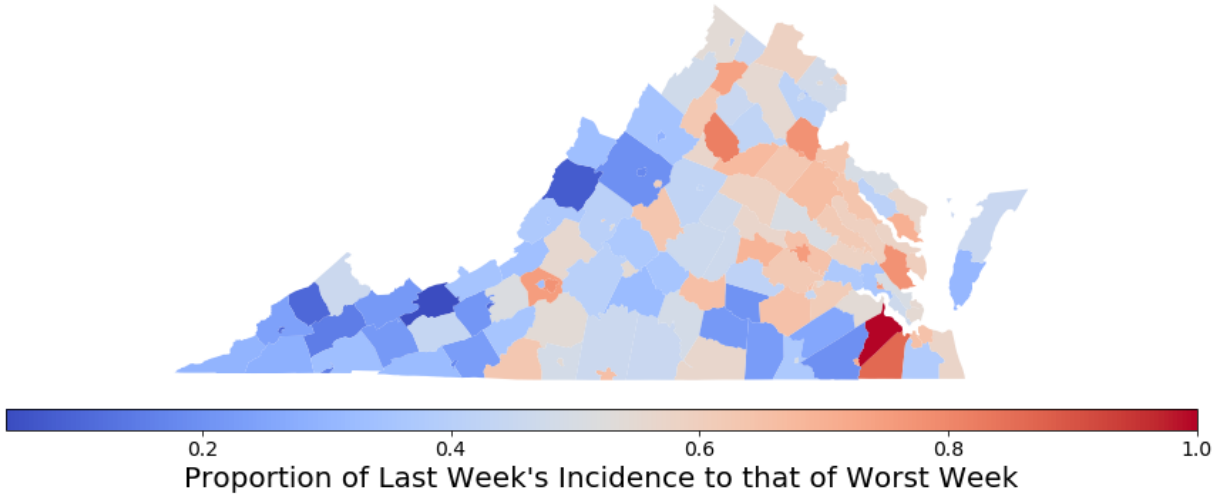
Current Week vs. Highest Week

For all counties in the US



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

Virginia's counties



- 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)

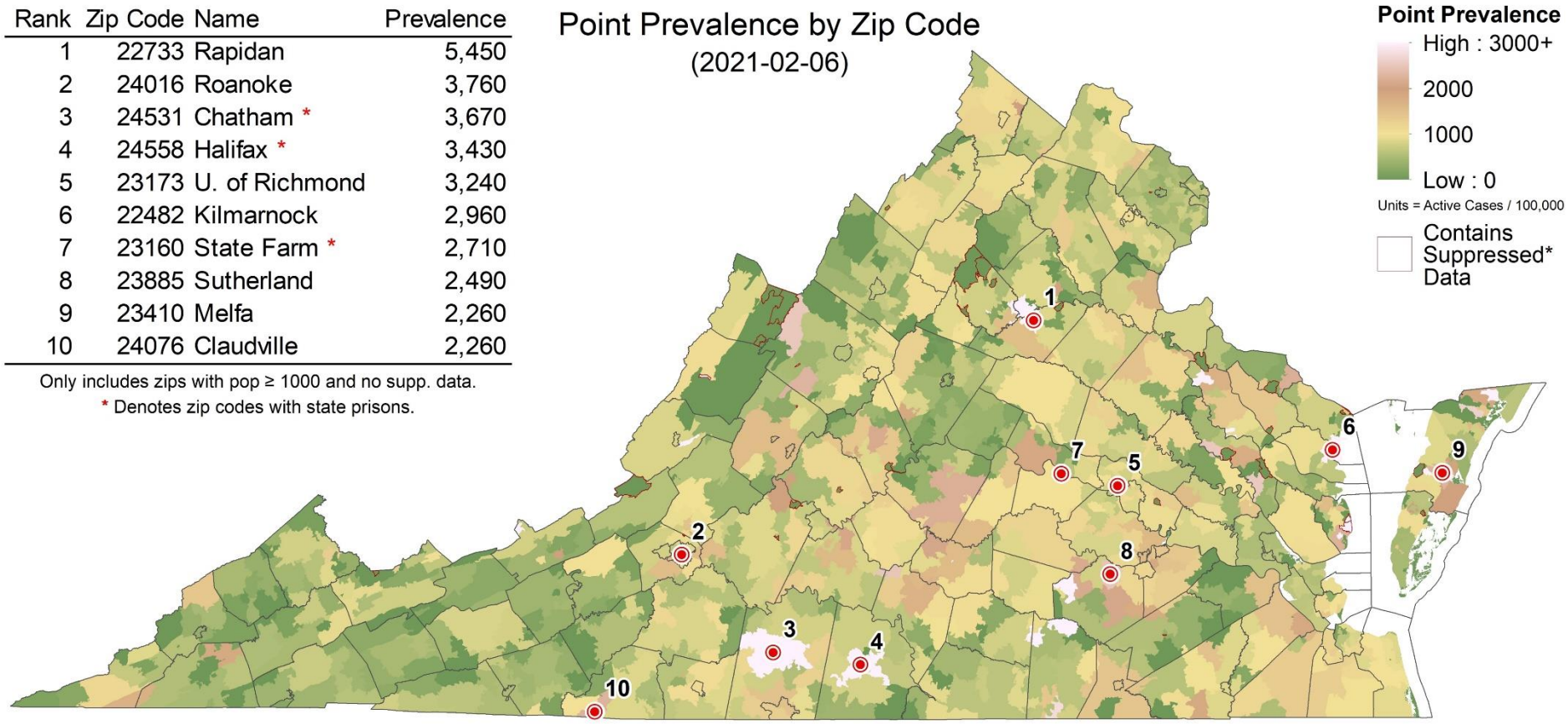
Case Rates in the last week by zip code

- Fewer prisons are in the top ten, most prisons seem to have intense rates for 2 to 3 weeks
- Concentrations of high rates in central and northwest regions
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code	Name	Prevalence
1	22733	Rapidan	5,450
2	24016	Roanoke	3,760
3	24531	Chatham *	3,670
4	24558	Halifax *	3,430
5	23173	U. of Richmond	3,240
6	22482	Kilmarnock	2,960
7	23160	State Farm *	2,710
8	23885	Sutherland	2,490
9	23410	Melfa	2,260
10	24076	Claudville	2,260

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

* Denotes zip codes with state prisons.



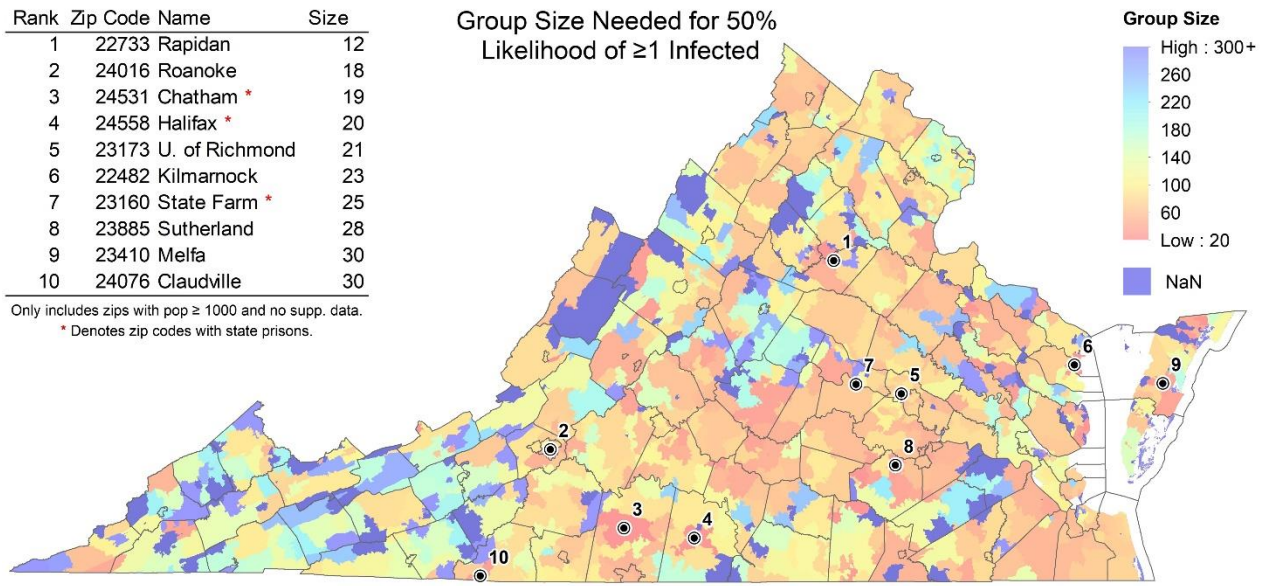
Risk of Exposure by Group Size

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	22733	Rapidan	12
2	24016	Roanoke	18
3	24531	Chatham *	19
4	24558	Halifax *	20
5	23173	U. of Richmond	21
6	22482	Kilmarnock	23
7	23160	State Farm *	25
8	23885	Sutherland	28
9	23410	Melfa	30
10	24076	Claudville	30

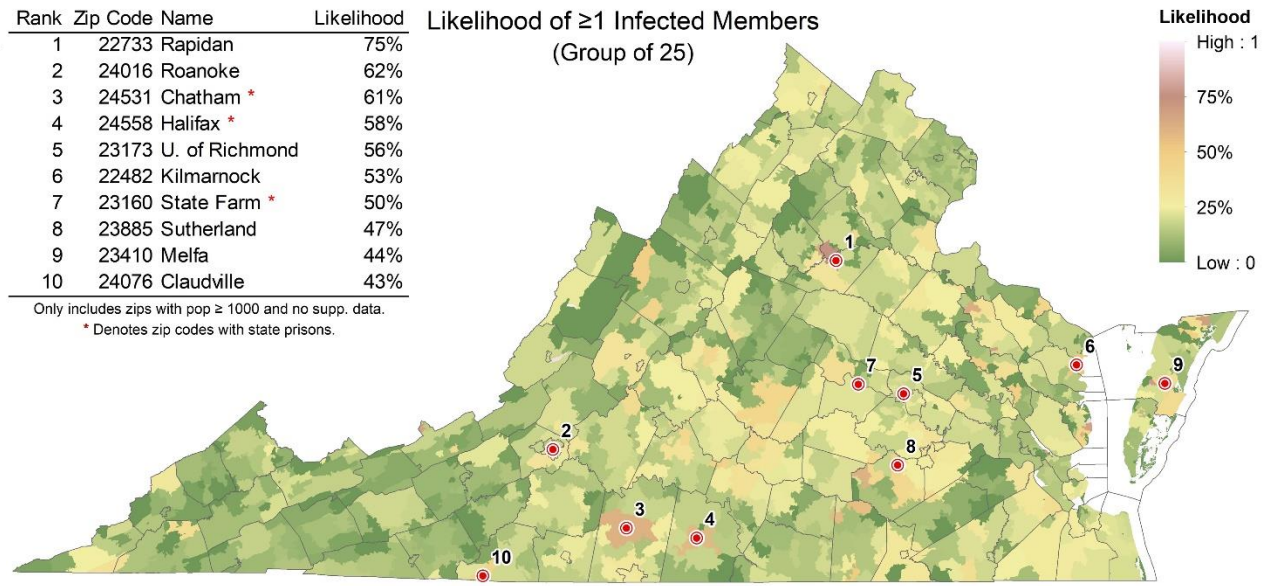
Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.



Based on zip code point prevelence for week ending 2021-01-30

Rank	Zip Code	Name	Likelihood
1	22733	Rapidan	75%
2	24016	Roanoke	62%
3	24531	Chatham *	61%
4	24558	Halifax *	58%
5	23173	U. of Richmond	56%
6	22482	Kilmarnock	53%
7	23160	State Farm *	50%
8	23885	Sutherland	47%
9	23410	Melfa	44%
10	24076	Claudville	43%

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



Based on zip code point prevelence for week ending 2021-02-06

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

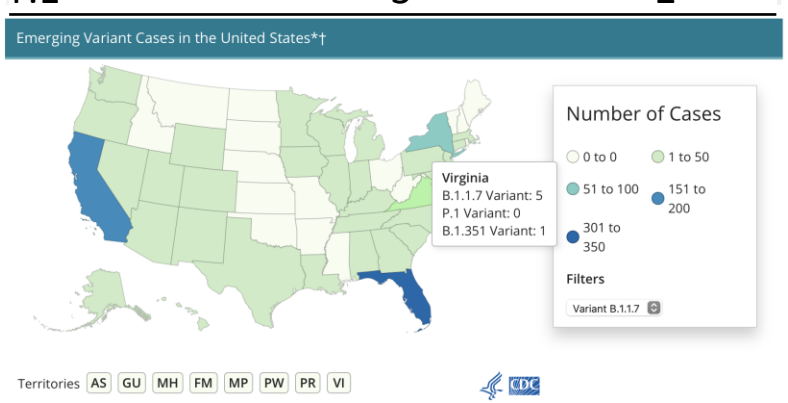
- B.1.1.7 has been detected in Virginia as well as in at least 932 cases across 34 states as of Feb 9th (avg delay of 10-20 days from isolation to reporting), will continue to grow rapidly
- Updated estimates based on US growth rates estimate it will predominate (eg reach 50% frequency) by mid to late March and is 35%-45% more transmissible.
- A recent study suggests this variant may have higher mortality
- Bioinformatic study by PHE shows E484K mutation as is found in B.1.351 has arisen multiple times in UK based B.1.1.7, also in this report household secondary attack rate is 25% greater

Lineages Of Concern

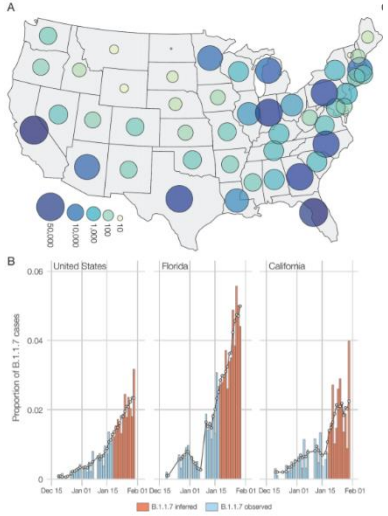
LoC name	PANGO lineage	NextStrain lineage	Other synonyms	Emergence date	Emergence location	Key AA substitutions in spike protein	Impact
B.1.1.7	B.1.1.7	20I/501Y.V1	VOC 202012/01, UK variant	September 2020	Southeast England	H69-, V70-, N501Y, D614G, P681H	Increased transmissibility; S gene target failure (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 States Reporting
B.1.1.7	932	34
B.1.351	9	3
P.1	3	2



CDC Variant Tracking



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 predominantly South Africa shows signs of vaccine escape, currently 9 reported cases in 3 states as of Feb 9th
- Some Experiments have demonstrated reduced potency of convalescent sera, while a recent study showed a strong response to spike proteins engineered with similar mutations
- Moderna and Pfizer vaccine demonstrated to have robust response to this variant, and thus likely to remain highly effective
- Another study demonstrated that while natural immunity may be limited, a single boosting dose of Pfizer or Moderna vaccine provided a robust neutralizing response
- Novovax and Johnson & Johnson vaccine demonstrated reduced efficacy in arm conducted in South Africa when this strain was circulating

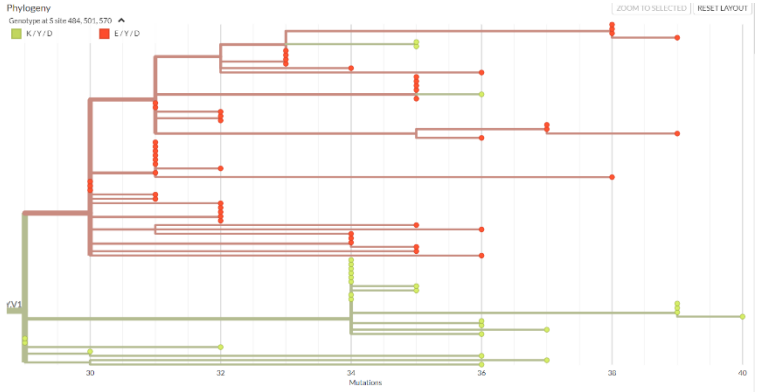
Lineage P.1 (similar mutations as in B.1.1.7 and B.1.351)

- First case reported in Minnesota on Monday Jan 25th, now 3 cases in 2 states
- Resurgence of hospitalizations in Manaus, Brazil continues this despite estimated ¾ of the population infected

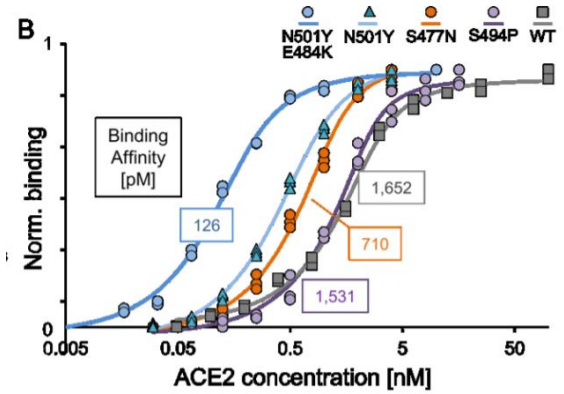
Lineage B.1.429 (similar mutations as in B.1.1.7 and B.1.351)

- Initially found in Southern California, conincided with surge in Nov and Dec
- Found in over half of sequenced samples in LA

Immune escaping mutations have arisen independently



E484K mutation found in South African (B.1.351) and Brazilian (B.1.1.28) variants has arisen 3 times independently in the B.1.1.7 strain.
Nextstrain.org – Phylogeny of 484,501, 570



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”

UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

Model Update – Adaptive Fitting

Adaptive Fitting Approach

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

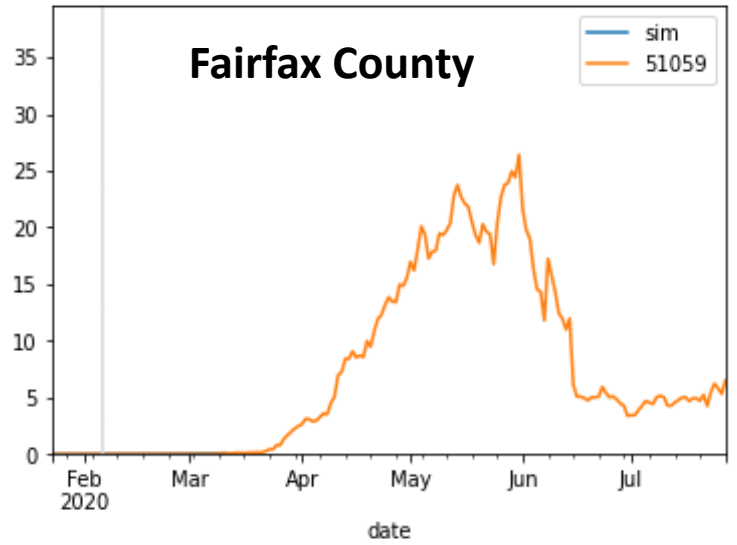
- Allows history to be precisely captured, and used to guide bounds on projections

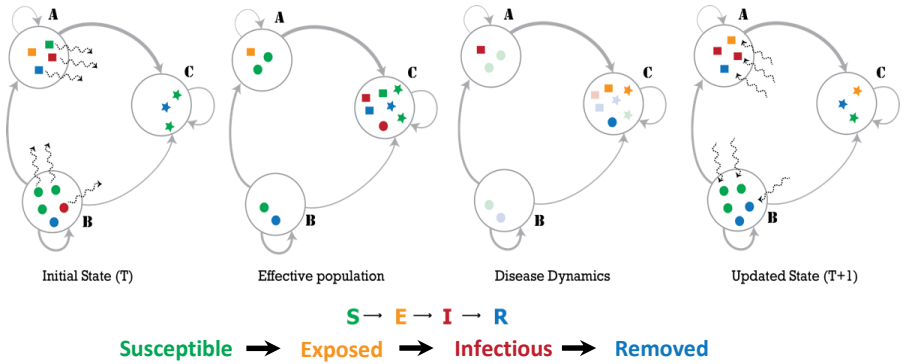
Model: An alternative use of the same meta-population model, PatchSim

- 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





UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

Using Ensemble Model to Guide Projections

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

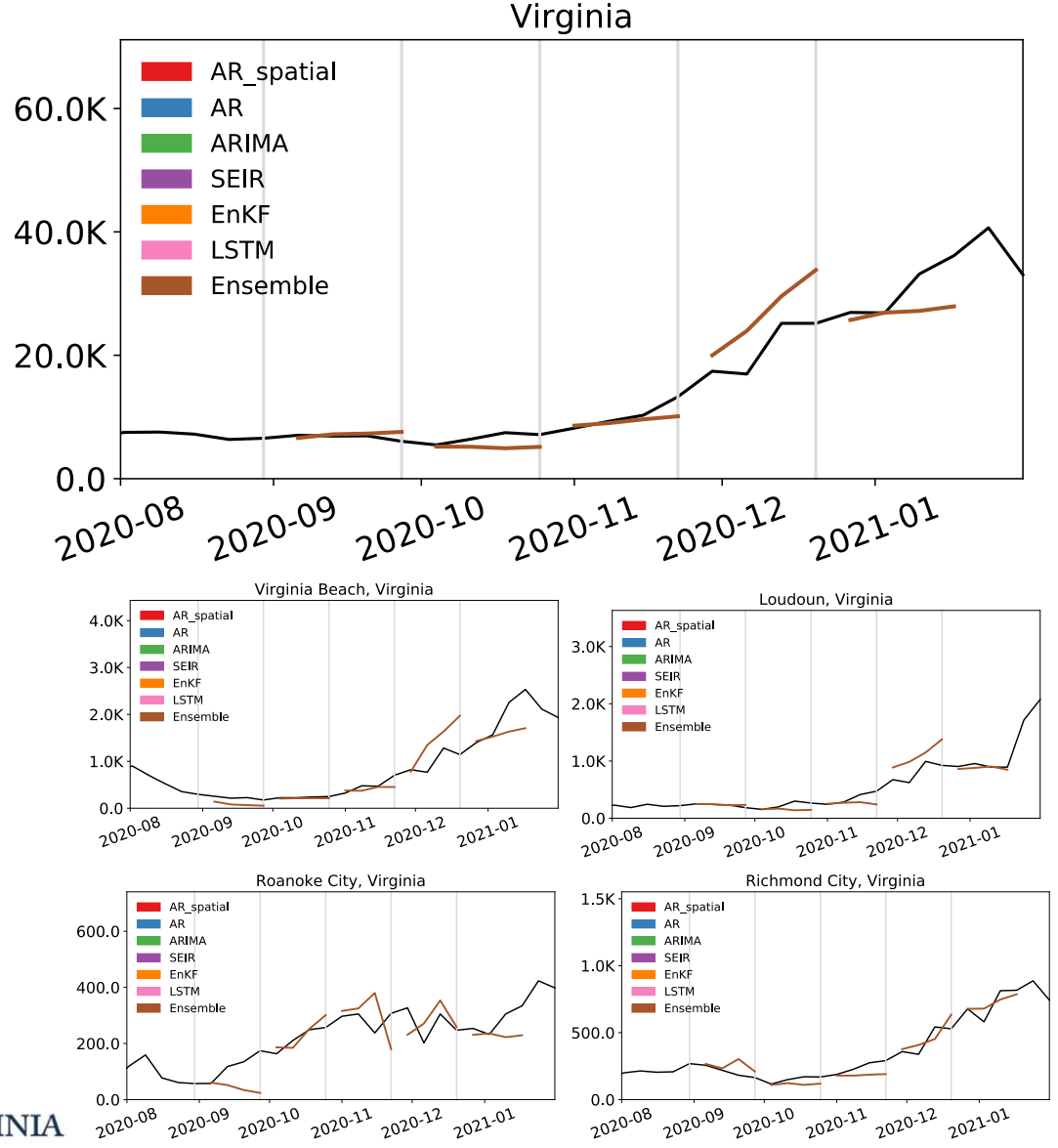
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

<u>Weekly forecasts</u> done at county level.

Models chosen because of their track record in disease forecasting and to increase diversity and robustness.

Ensemble forecast provides additional 'surveillance' for making scenario-based projections.

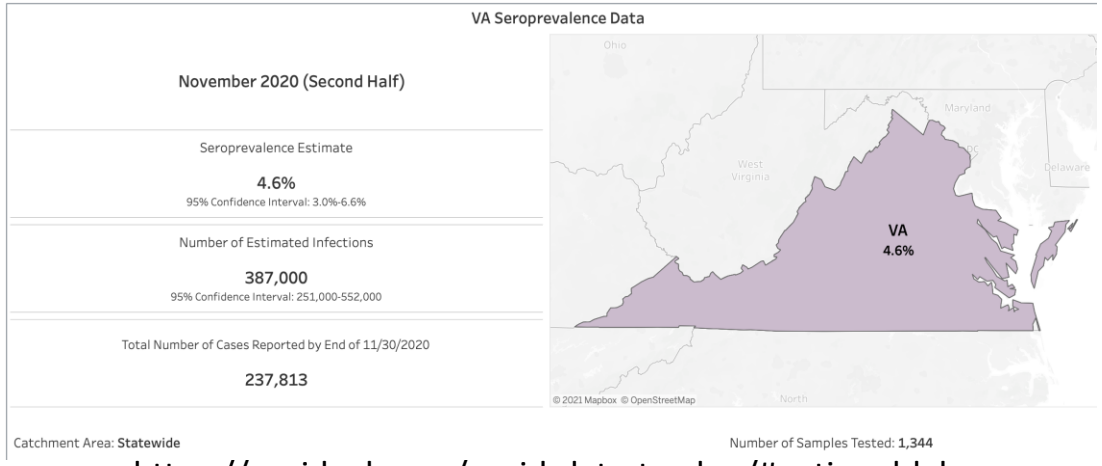
Also submitted to CDC Forecast Hub.



Seroprevalence updates to model design

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

- Virginia Serology Study estimated 2.4% of Virginians estimated infected (as of Aug 15th)
- CDC Nationwide Commercial Laboratory Seroprevalence Survey estimated 4.6% [3.0% – 6.6%] seroprevalence as of Nov 12th – 26th up from 4.1% a month earlier



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

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 ascertainments as was consistent earlier in the pandemic were being used)

Virginia Coronavirus Serology Project

Interim findings by region and statewide - July 22, 2020

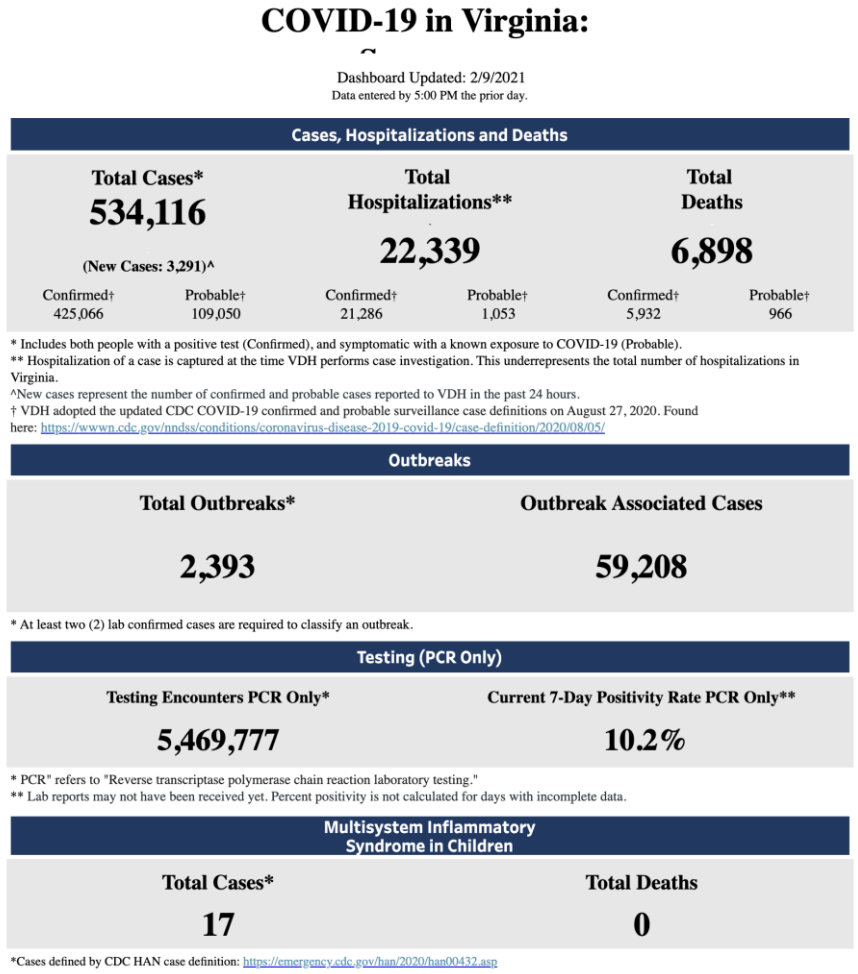
Region	Number of participants	Number antibody positive	Crude prevalence per 100 participants	Weighted prevalence*	
				per 100 population	(95% CI)
Central	400	8	2.0	3.0	(0.5, 5.5)
East	707	9	1.3	1.5	(-0.2, 3.2)
Northern	819	36	4.4	4.2	(2.5, 5.9)
Northwest	756	11	1.5	0.9	(0.2, 1.6)
Southwest	431	3	0.7	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 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: 2/9/2021
Data entered by 5:00 PM the prior day.

Cases, Hospitalizations and Deaths

Total Cases*	Total Hospitalizations**	Total Deaths
534,116	22,339	6,898
(New Cases: 3,291)^		

Confirmed†	Probable†	Confirmed†	Probable†	Confirmed†	Probable†
425,066	109,050	21,286	1,053	5,932	966

* 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
2,393	59,208

* 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**
5,469,777	10.2%

* 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
17	0

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

Accessed 8:30am February 10, 2021

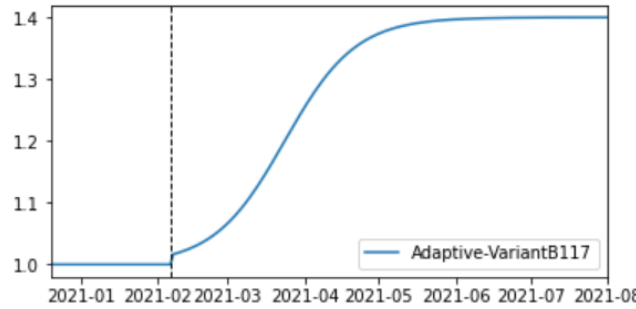
https://www.vdh.virginia.gov/coronavirus/

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^{th} percentile)
  - **Fatigued Control**: Highest level of transmission (95^{th} 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

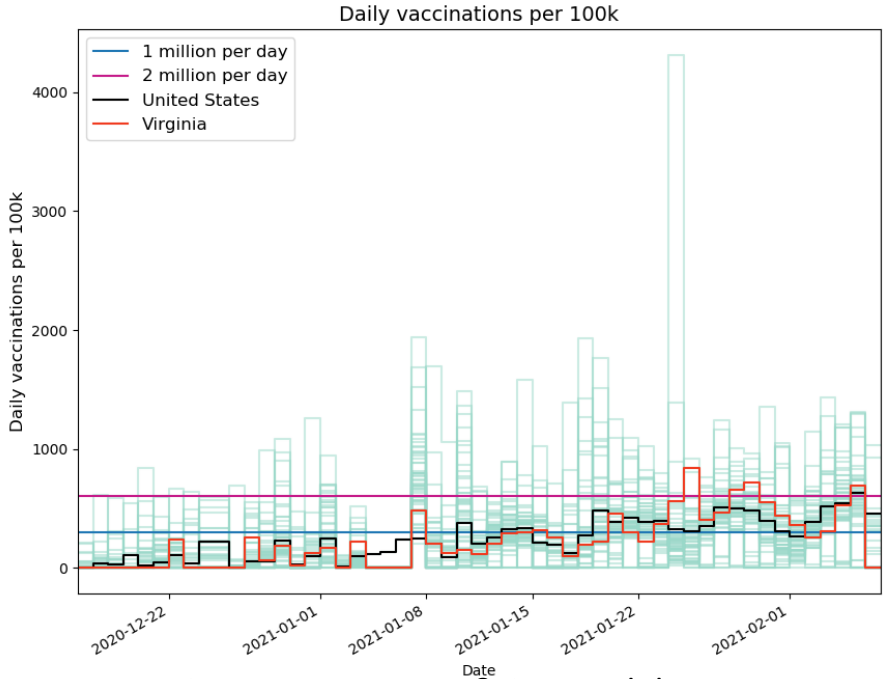


Scenarios – Vaccines

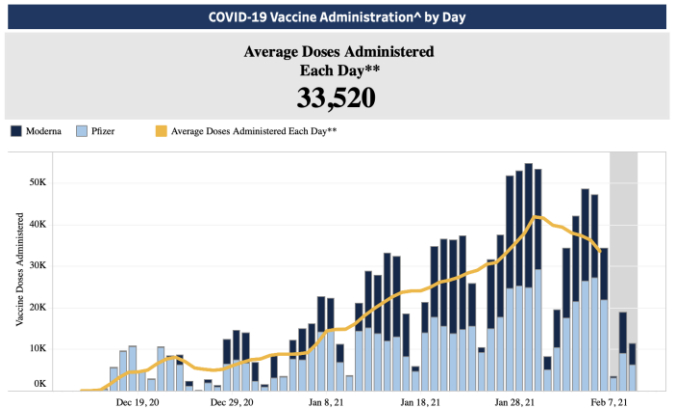
- Vaccination has started, and efforts are underway to increase its pace
  - Exact achievable rollouts and level of coverage are unknown, though coming into focus
- Vaccine efficacy varies over course of vaccine
  - FDA EUAs show 50% efficacy achieved 2 weeks after 1st dose, and 95% 2 weeks after 2nd 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

VA Vaccination Rates



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



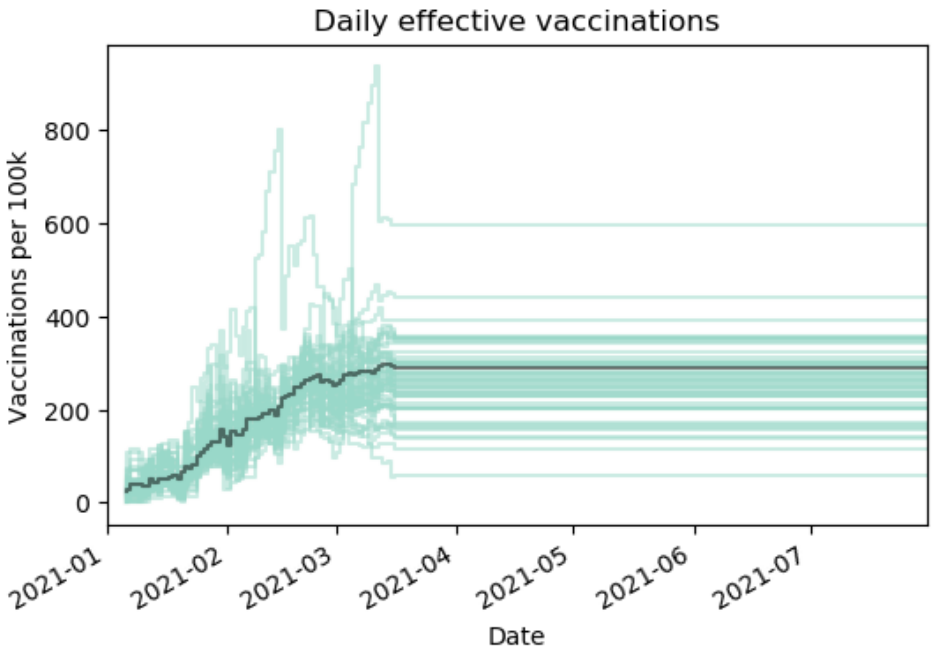
Accessed 8:30am February 10, 2021
https://www.vdh.virginia.gov/coronavirus/covid-19-vaccine-summary/

UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

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 19th) and CDC (Jan 20th 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**: 354 doses per 100K per day (~30K total per day)
    - **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

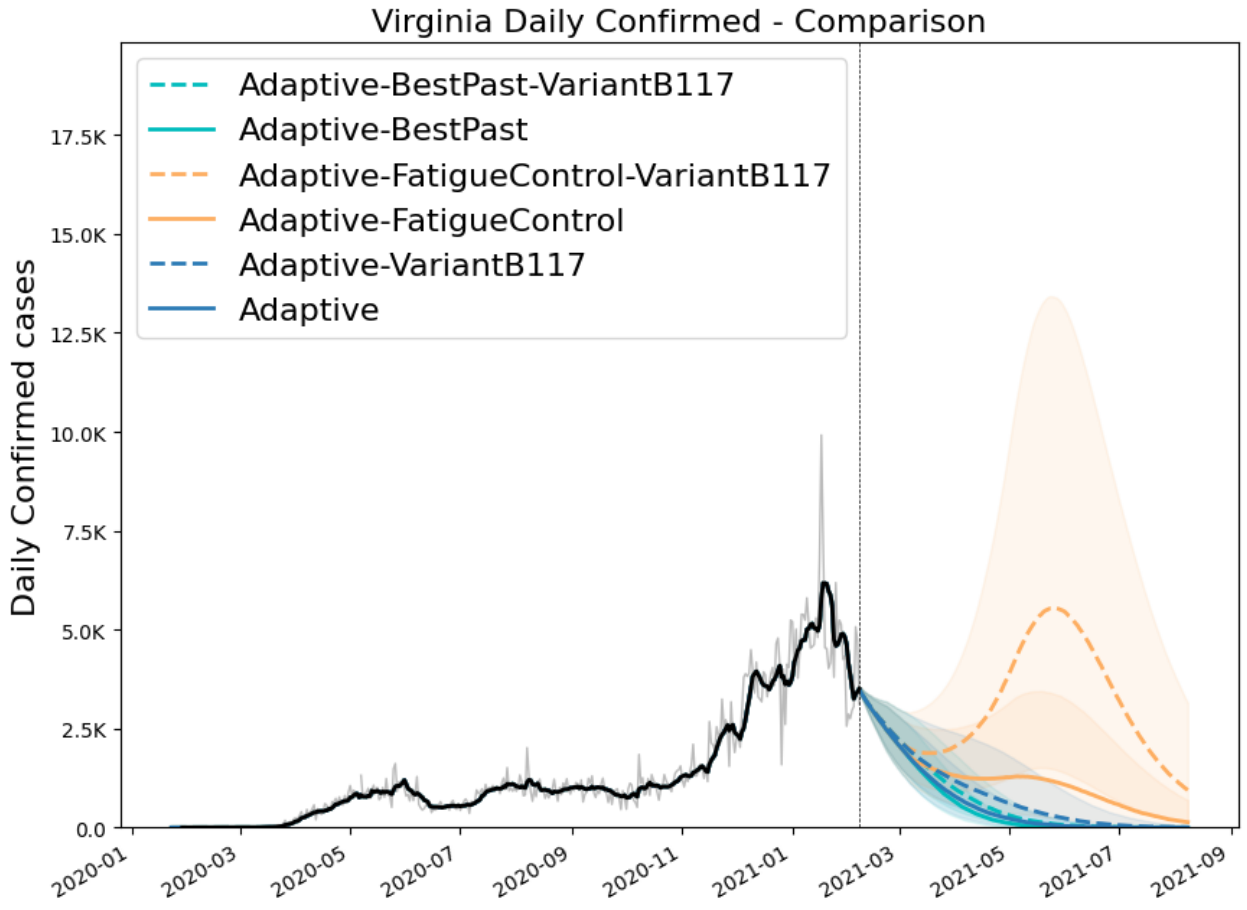
- **Adaptive**: No seasonal effects from base projection
  - If things continue as they are
- **Adaptive-FatigueControl**: Fatigued control seasonal effects
  - If we revert to slightly worst transmission experienced in last 6 months
- **Adaptive-BestPast**: Best of the past control seasonal effects
  - 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

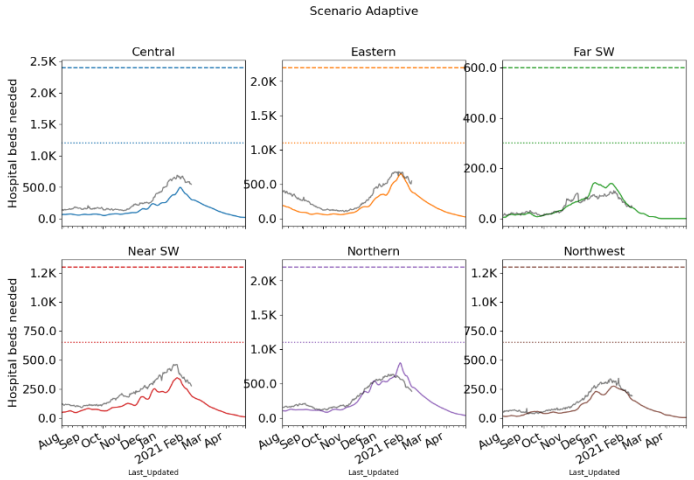
Model Results

Outcome Projections

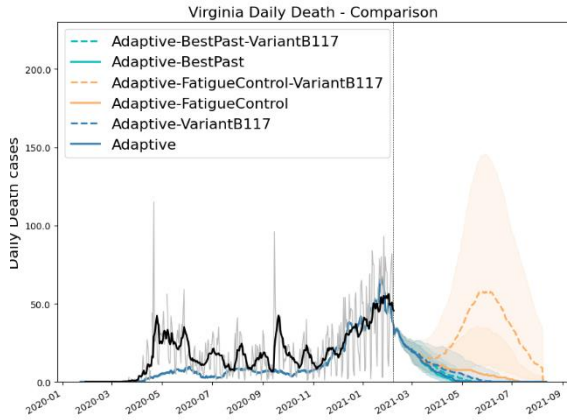
Confirmed cases



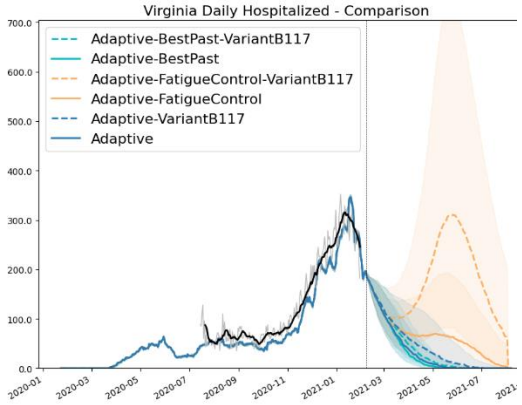
Estimated Hospital Occupancy



Daily Deaths



Daily Hospitalized

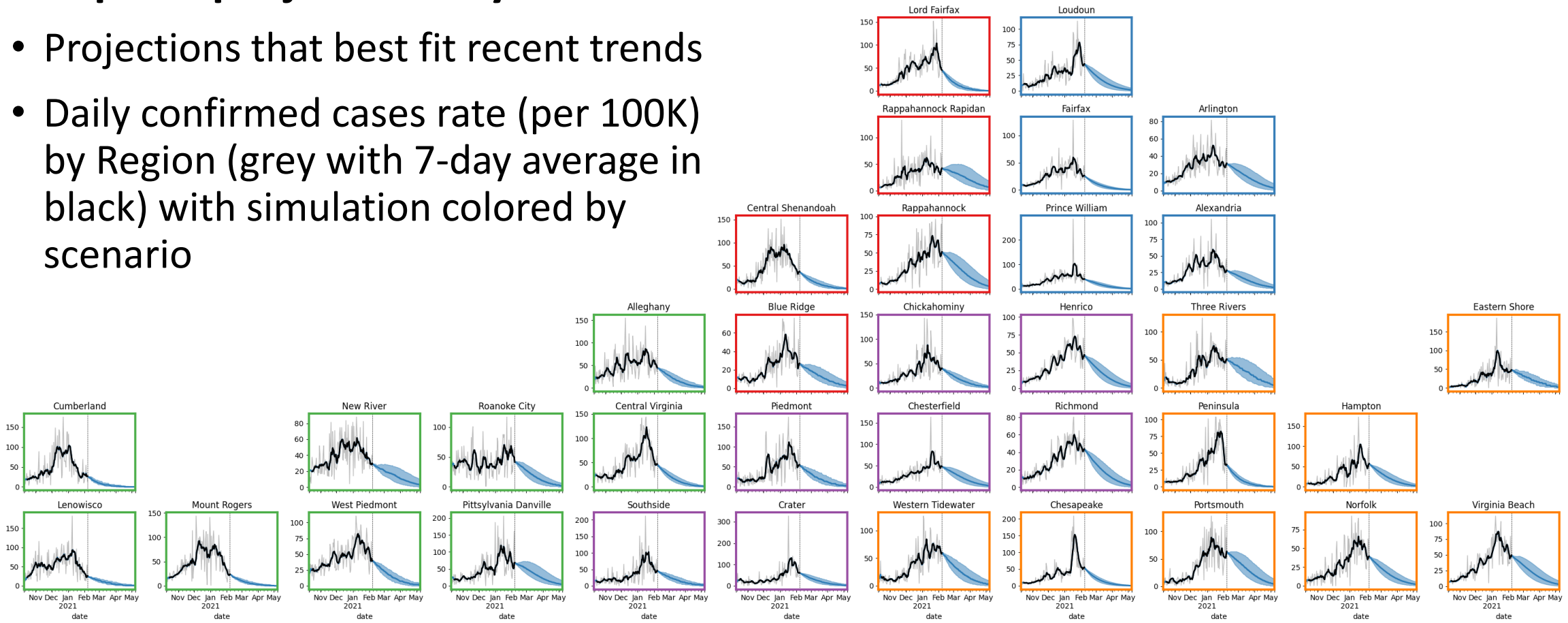


UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

District Level Projections: Adaptive

Adaptive projections by District

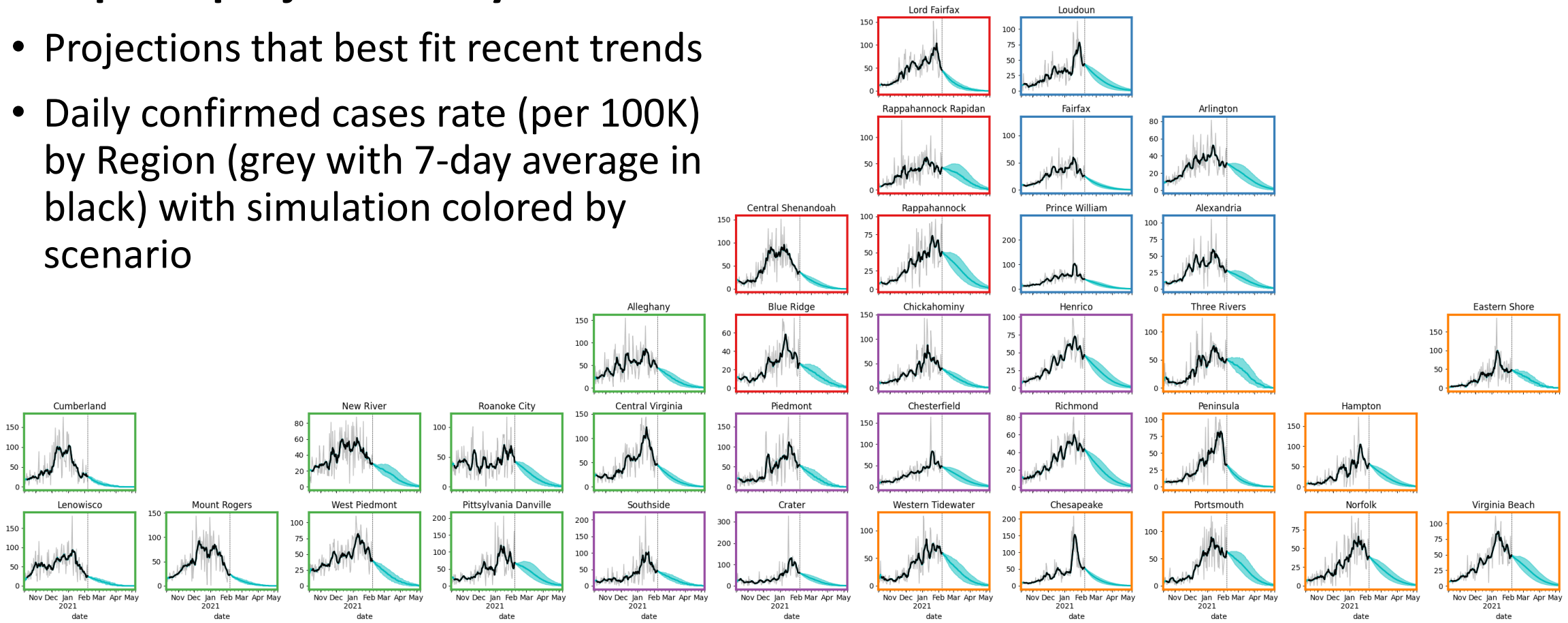
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



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

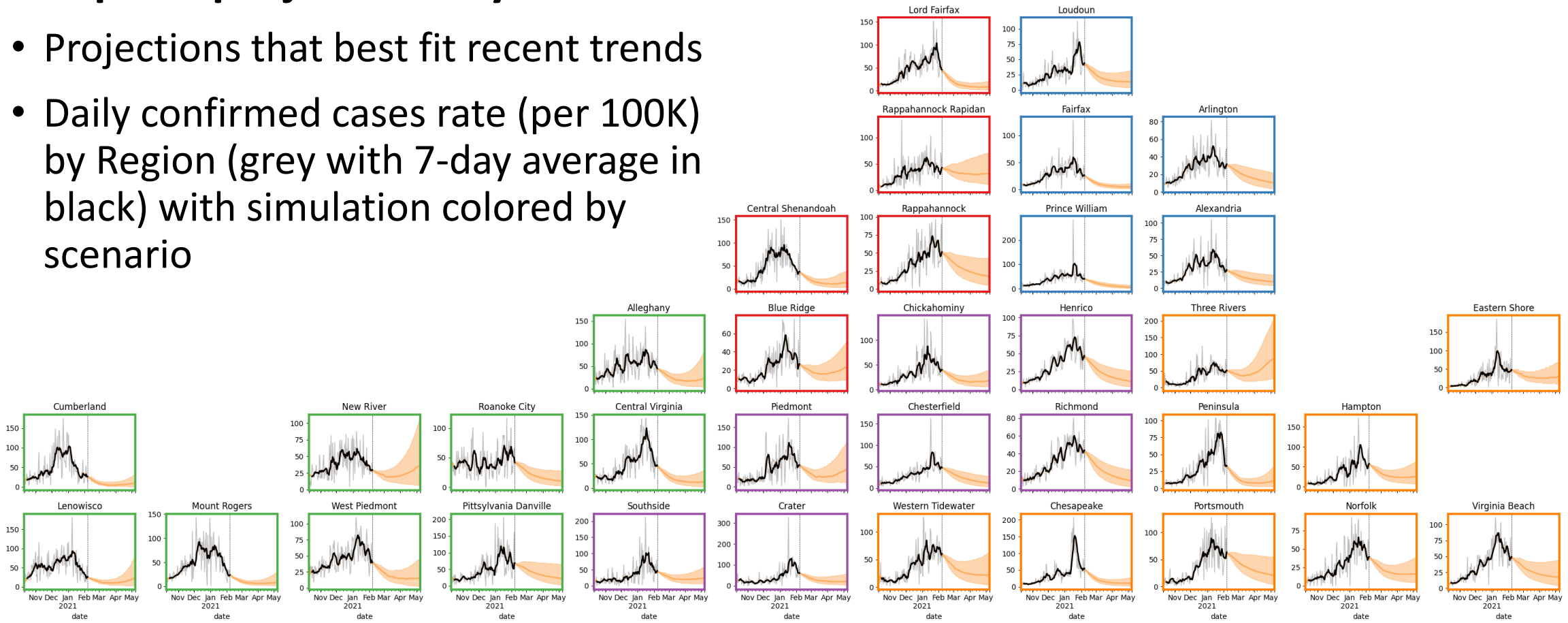


UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

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

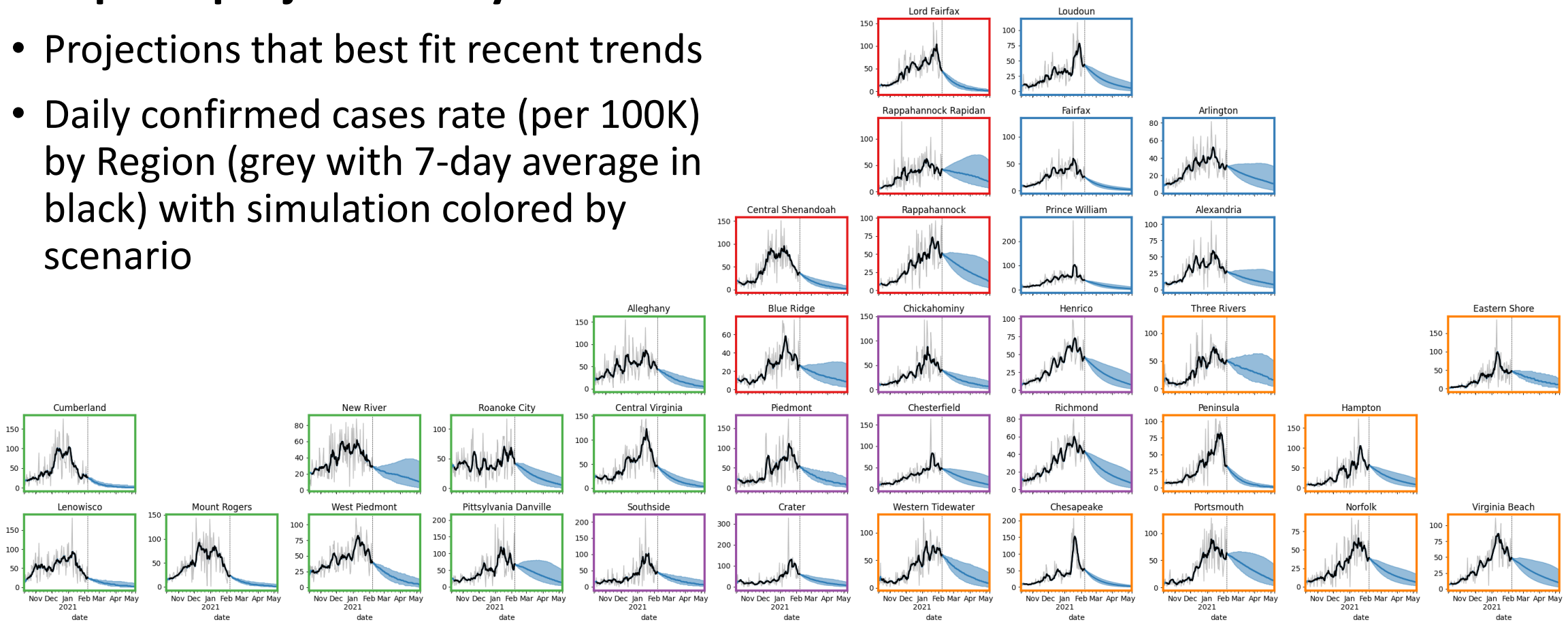


UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

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

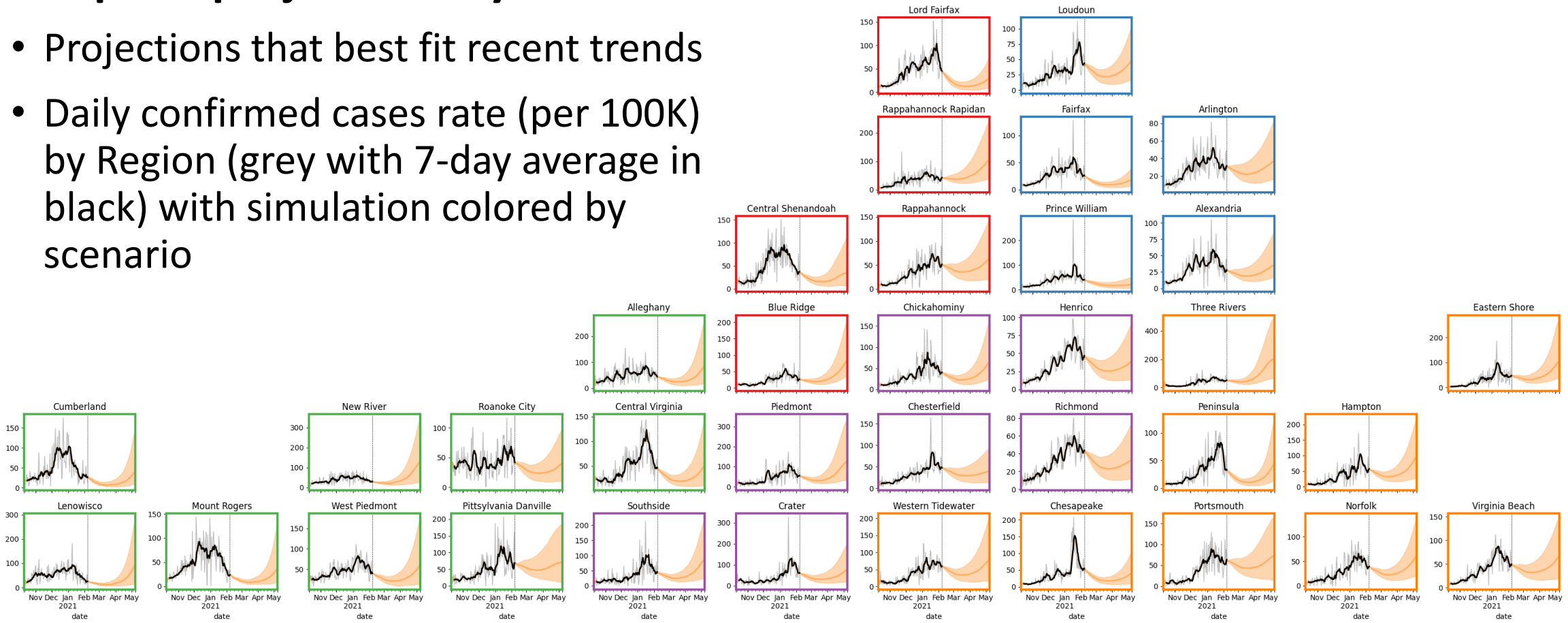


UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

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

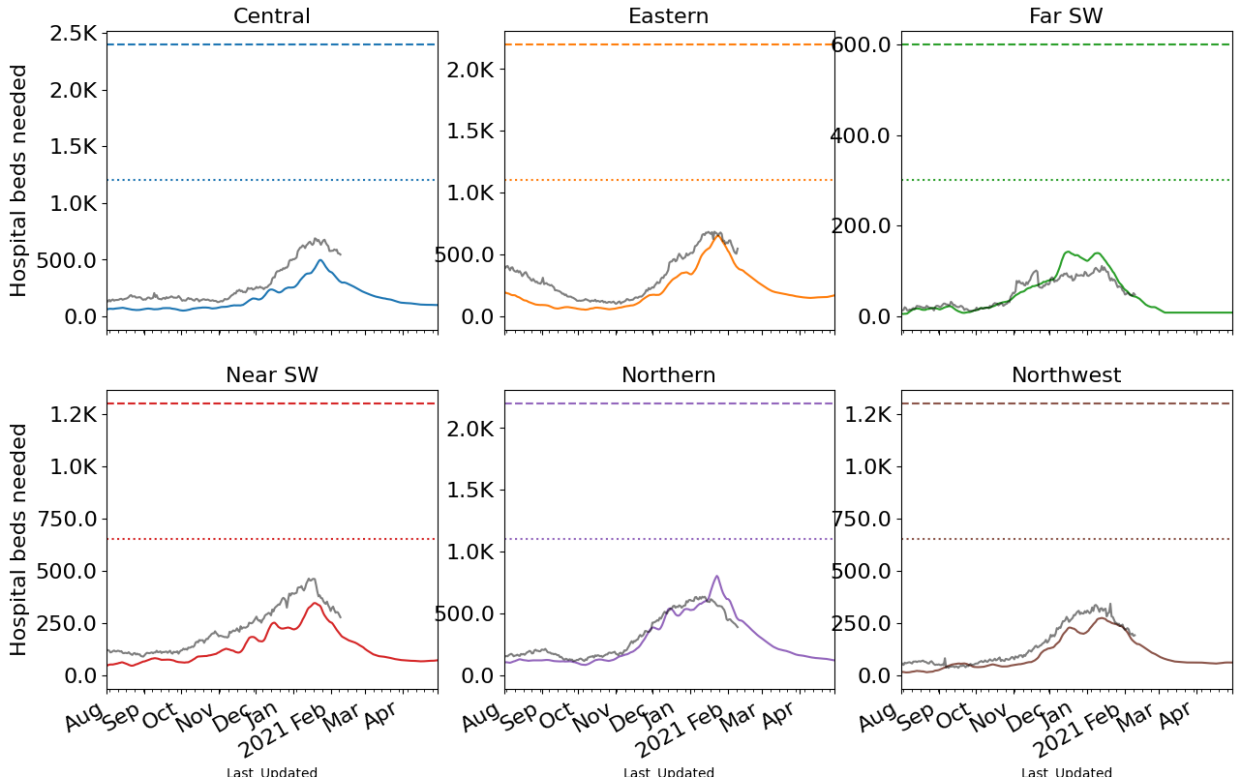


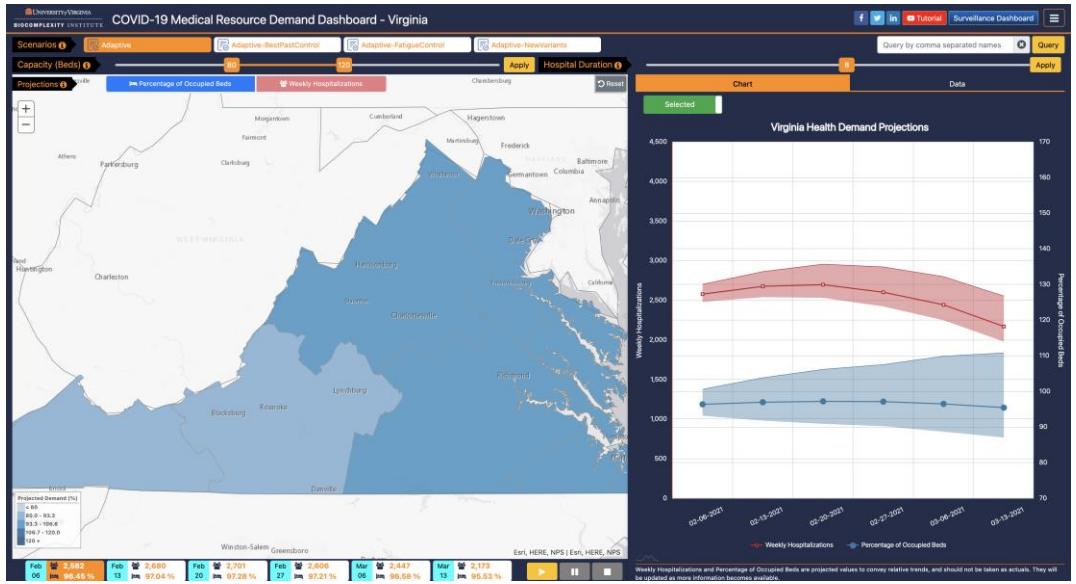
UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

Hospital Demand and Bed Capacity by Region

Capacities* by Region – Adaptive-FatigueControl

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





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

If Adaptive-FatigueControl scenario persists:

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

* Assumes average length of stay of 8 days

Weekly Cases and Hospitalizations

Weekly confirmed cases

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-BestPast	Adaptive-VariantB117	Adaptive-Fatigued Control -VariantB117
2/7/21	25,130	25,130	25,130	25,130	25,130
2/14/21	22,323	22,315	22,309	22,376	22,390
2/21/21	19,062	19,048	19,045	19,426	19,449
2/28/21	16,102	16,074	16,070	16,839	16,859
3/7/21	13,416	13,463	13,372	14,516	14,619
3/14/21	11,003	11,670	10,783	12,542	13,425
3/21/21	8,939	10,617	8,400	10,904	13,159
3/28/21	7,071	9,784	6,254	9,498	13,415
4/4/21	5,536	9,205	4,552	8,275	14,316
4/11/21	4,250	8,813	3,163	7,234	15,852
4/18/21	3,196	8,647	2,145	6,268	18,203
4/25/21	2,356	8,672	1,382	5,371	21,486

Weekly Hospitalizations

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-BestPast	Adaptive-VariantB117	Adaptive-Fatigued Control -VariantB117
2/7/21	1,404	1,404	1,404	1,404	1,404
2/14/21	1,245	1,244	1,244	1,247	1,248
2/21/21	1,057	1,056	1,054	1,075	1,078
2/28/21	884	882	881	930	930
3/7/21	722	725	721	781	789
3/14/21	598	635	583	684	721
3/21/21	471	589	443	590	717
3/28/21	362	526	317	507	723
4/4/21	279	495	216	429	771
4/11/21	206	468	145	371	863
4/18/21	143	457	96	318	997
4/25/21	99	460	54	279	1,195

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**
- VA mean weekly incidence down sharply 45/100K from 54/100K, as national levels continued to decline (to 37/100K from 45/100K)
- Projections are mixed across commonwealth with declines far outpacing growth
- Recent updates:
  - Scenarios expanded to add impact of transmission boosting from Variant B.1.1.7 to control-based (best of past and fatigued) scenarios
  - Further updates to vaccination schedules, with fitting now down on partially vaccinated population and future vaccinations based on current levels instead of goals
- 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

Estimating Daily Reproductive Number

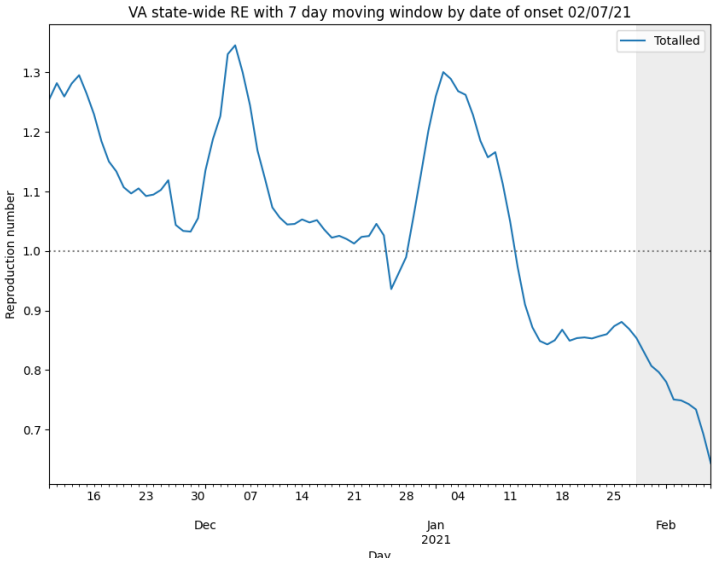
Jan 30th Estimates

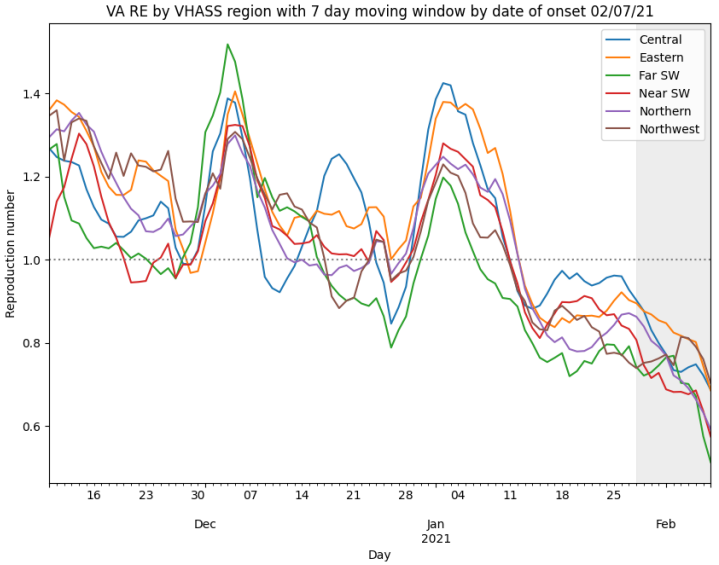
Region	Date of Onset R_e	Date Onset Diff Last Week
State-wide	0.921	0.070
Central	0.831	-0.104
Eastern	0.869	-0.039
Far SW	0.729	-0.033
Near SW	0.716	-0.140
Northern	0.805	0.035
Northwest	0.755	-0.066

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

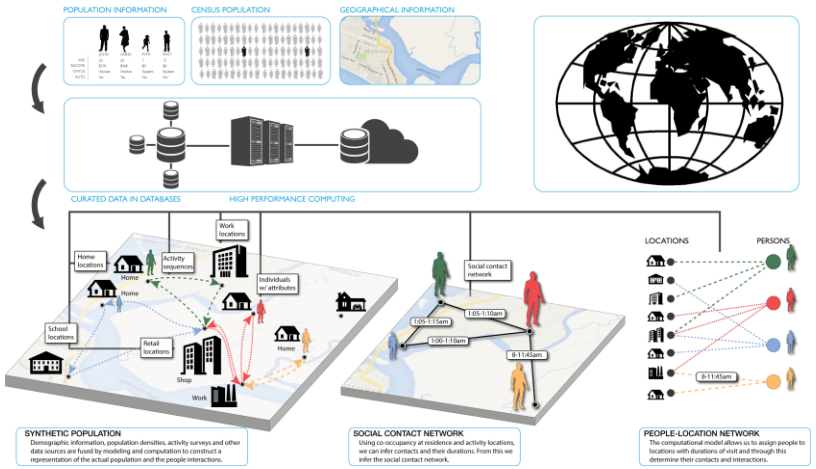




Agent-based Model (ABM)

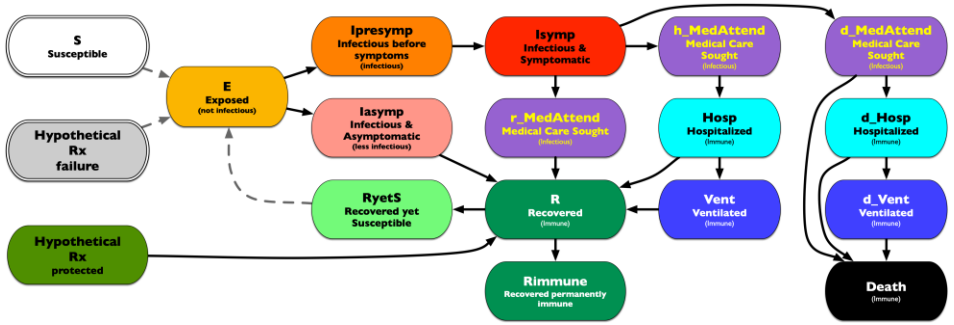
EpiHiper: Distributed network-based stochastic disease transmission simulations

- Assess the impact on transmission under different conditions
- Assess the impacts of contact tracing



Synthetic Population

- Census derived age and household structure
- Time-Use survey driven activities at appropriate locations



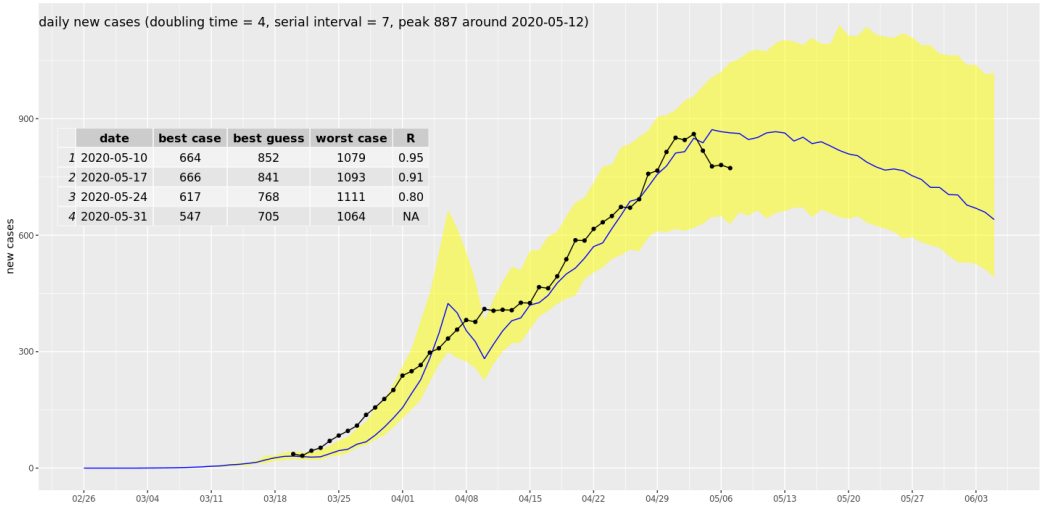
Detailed Disease Course of COVID-19

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

ABM Social Distancing Rebound Study Design

Study of ”Stay Home” policy adherence

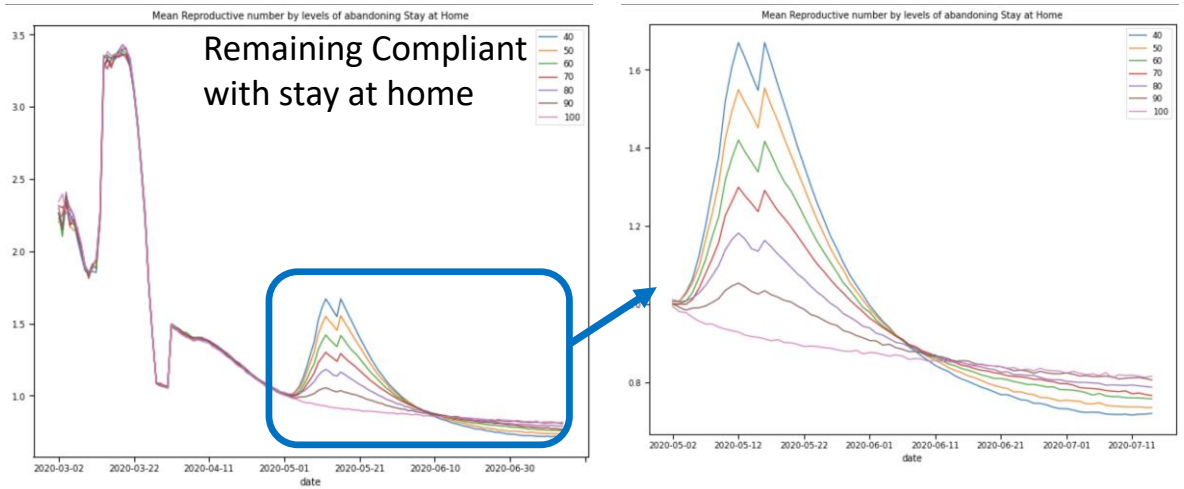
- Calibration to current state in epidemic
- Implement “release” of different proportions of people from ”staying at home”



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

Calibration to Current State

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



Impacts on Reproductive number with release

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