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

Estimation of COVID-19 Impact in Virginia

September 30th, 2020

(data current to September 28th) Biocomplexity Institute Technical report: TR 2020-117

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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



Points of Contact

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Biocomplexity COVID-19 Response Team



Overview

- Goal: Understand impact of COVID-19 mitigations in Virginia
- Approach:
 - Calibrate explanatory mechanistic model to observed cases
 - Project infections through December
 - 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:

- Holding steady with declines outpacing growth.
- VA weekly incidence (9.2/100K) continues to decline and now well below the national average (15/100K) which has been climbing, fueled by growth in the Plains and Mountain West.
- Projections are also mixed across commonwealth with declines outpacing growth.
- Recent updates:
 - Adaptive Fitting projection process has been streamlined.
 - Planning Scenarios moved to Nov 1st.
- The situation is changing rapidly. Models will be updated regularly.



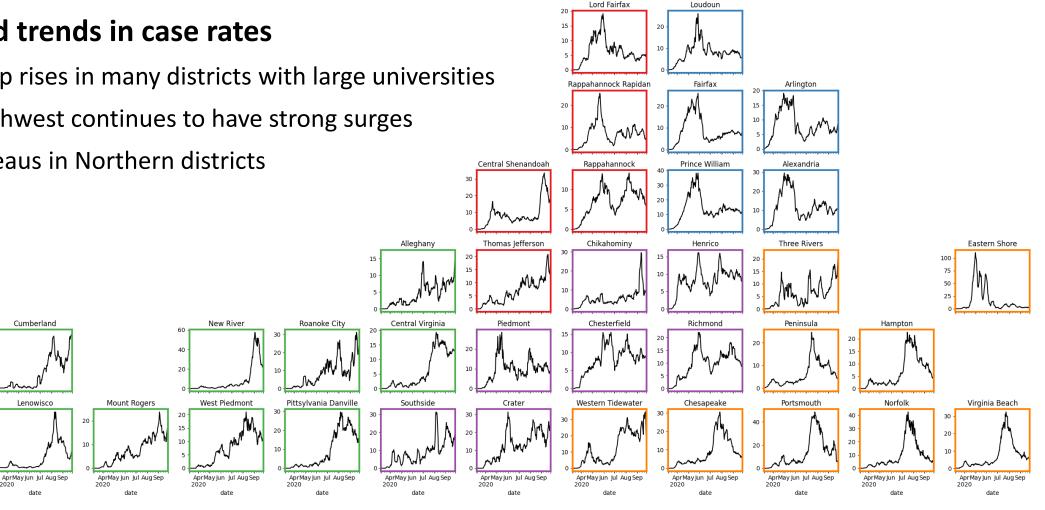
Situation Assessment



Case Rate (per 100k) by VDH District

Mixed trends in case rates

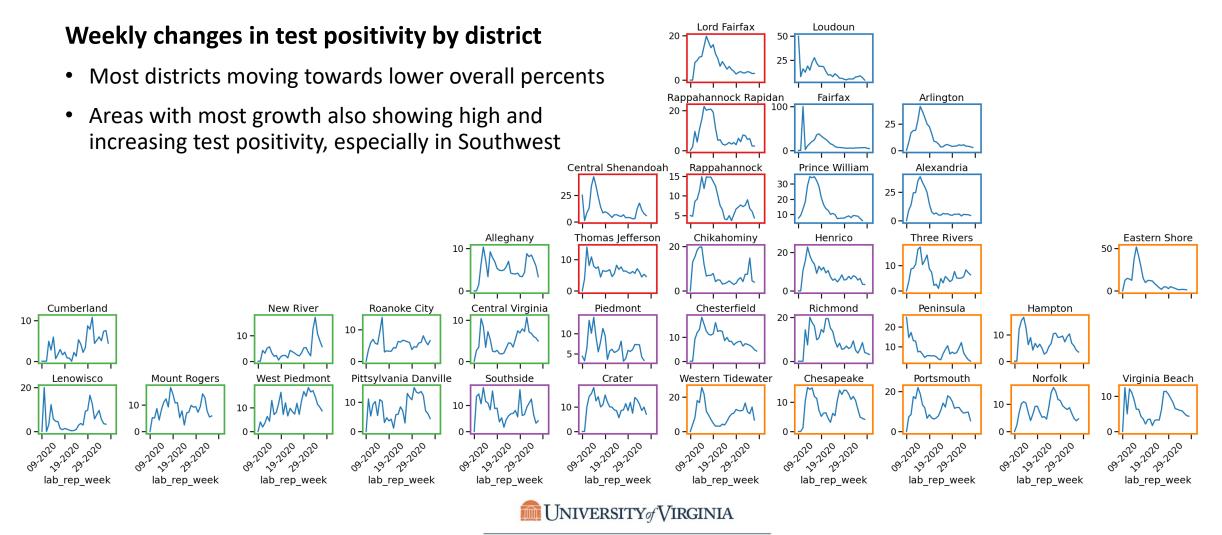
- Sharp rises in many districts with large universities
- Southwest continues to have strong surges
- Plateaus in Northern districts



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Test Positivity by VDH District



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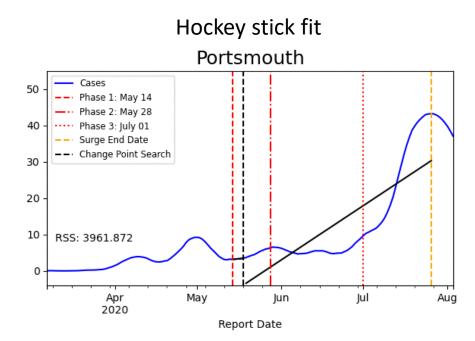
District Trajectories – New Surges starting

Hockey stick fit used to describe recent growth patterns based on recent trends from last peak or inflection points (based on smoothed case rates per 100k)

Declining: Sustained decreases following a recent peak
Plateau: Steady level with minimal trend up or down
Slow Growth: Sustained growth not rapid enough to be considered a Surge

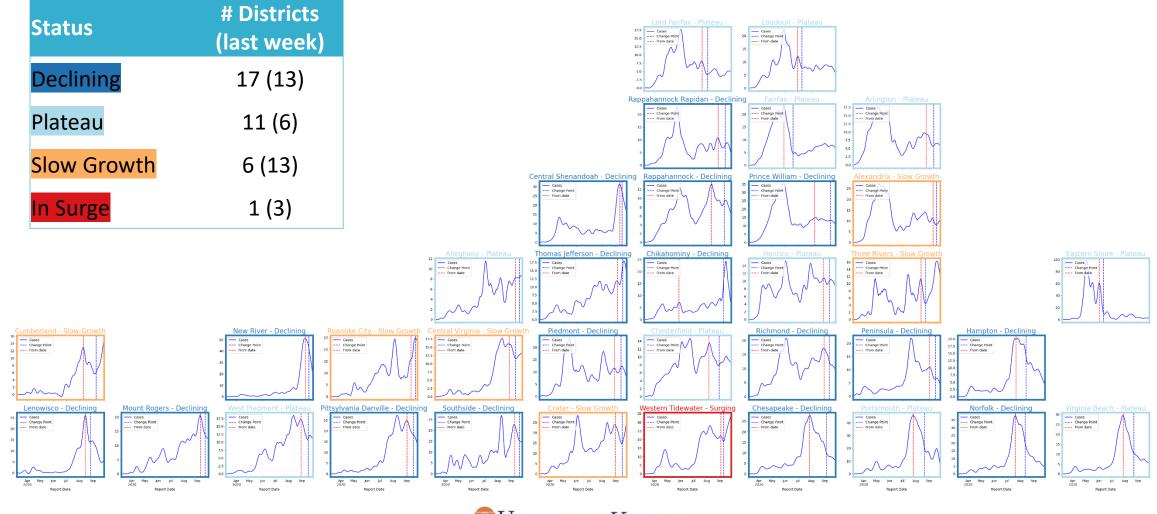
In Surge: Currently experiencing sustained rapid growth and exceeds recent inflection points





Status	# Districts (last week)
Declining	17 (13)
Plateau	11 (6)
<mark>Slow Growth</mark>	6 (13)
In Surge	1 (3)

District Trajectories – Declines outpace Growth



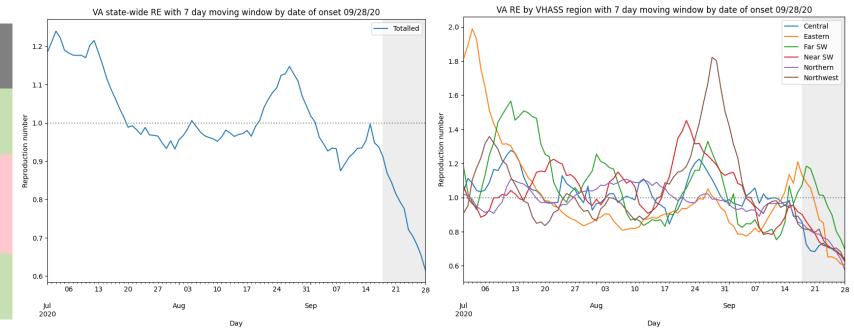
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Estimating Daily Reproductive Number

September 19th Estimates

	Current	Diff Last
Region	R _e	Week
State-wide	0.868	-0.015
Central	0.724	-0.175
Eastern	1.088	0.167
Far SW	1.184	0.415
Near SW	0.858	0.094
Northern	0.824	-0.105
Northwest	0.813	-0.135

30-Sep-20



Methodology

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

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

Changes in Case Detection

10

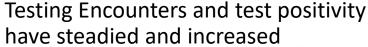
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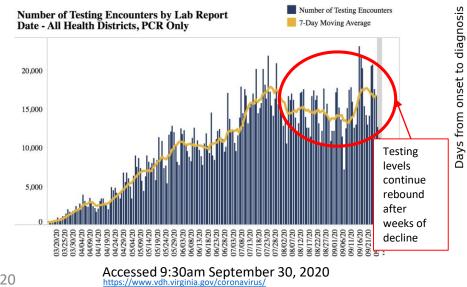
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2

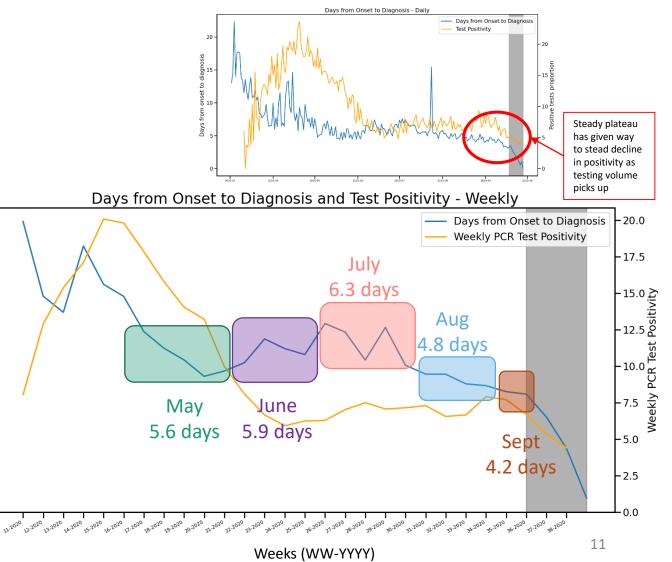
0.

Timeframe (weeks)	Mean days	% difference from overall mean
April (13-16)	8.54	42%
May (17-21)	5.63	-7%
June (22-25)	5.88	-2%
July (26-30)	6.26	4%
Aug (31-34)	4.75	-21%
Sept (2w,35-36)	4.21	-30%
Overall (13-33)	6.02	0%





Test positivity vs. Onset to Diagnosis

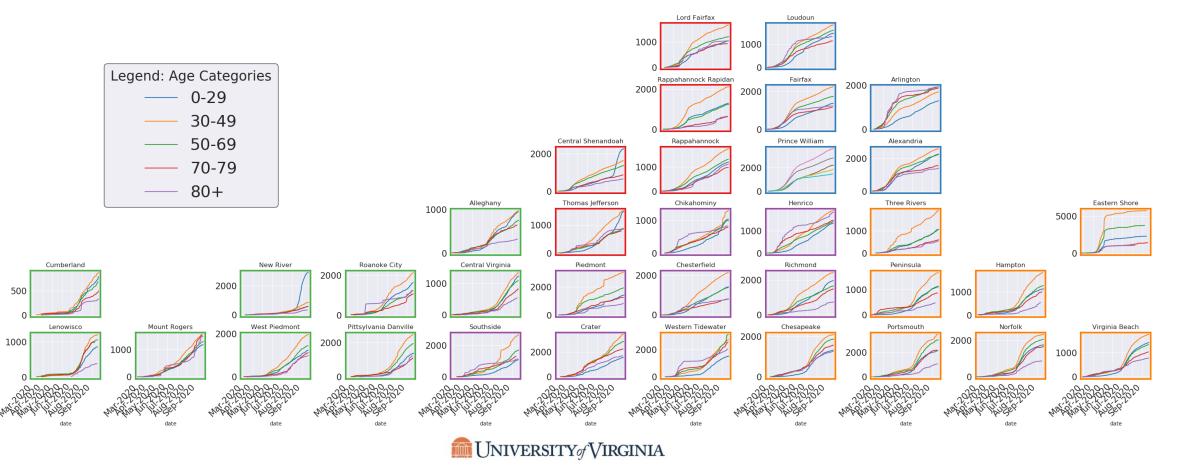


Age-Specific Attack Rates (per 100K)

Cumulative Age-specific Attack Rates (per 100k)

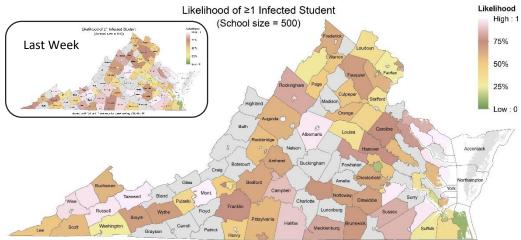
• Younger age groups outpace older in many districts

Age-adjusted Cumulative Prevelance Rate Per 100k District Population



Age-Specific Case Prevalence

During this past week, what might we find in a fully open school?

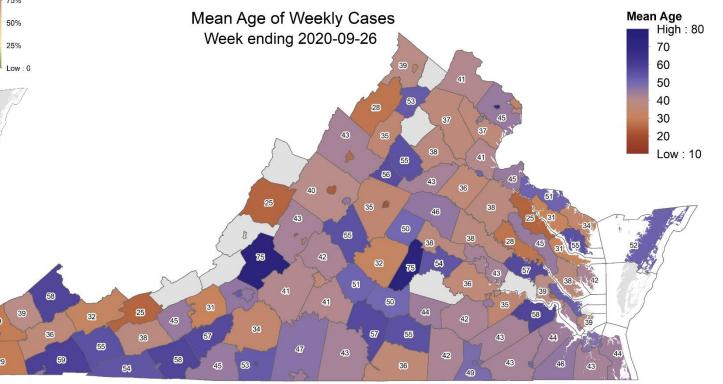


Based on 0-19 Point Prevelence for week ending 2020-09-26

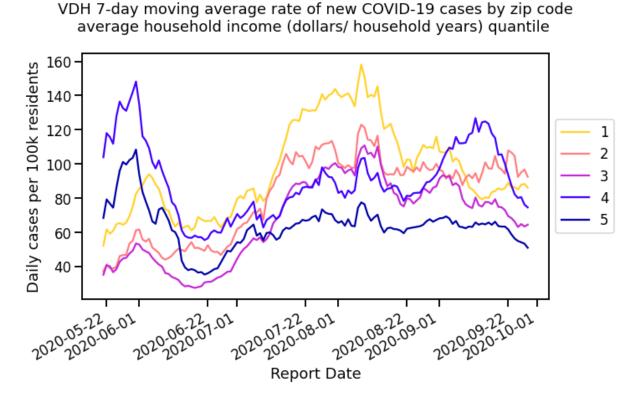
Based on prevalence during week of Sept 19th – Sept 26thof school-aged cases, what is the likelihood any collection of school age kids in a school size of 500 will have at least one infection

What is the average age of the cases by county?

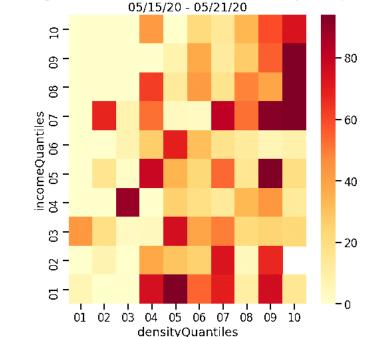
Younger cases in Northern VA, Tidewater, and around universities



Impact across Density and Income



VDH mean cases per 100k by zip code population density (person/ sq mile) and average household income (dollars/ household years) quantiles



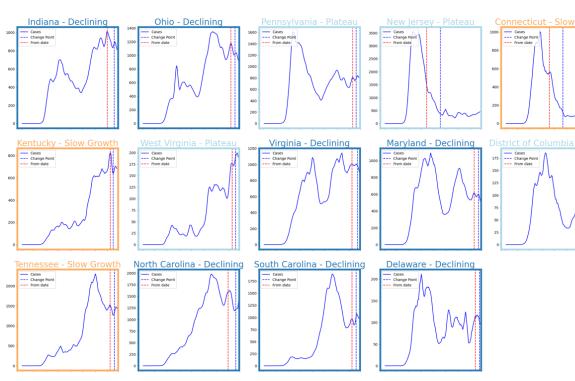
Shift back to higher income zip codes partially driven by surges in areas surrounding universities

Can see the evolution from denser and wealthier zip codes to poorer and less dense zip codes, then recently back to denser wealthier zip codes

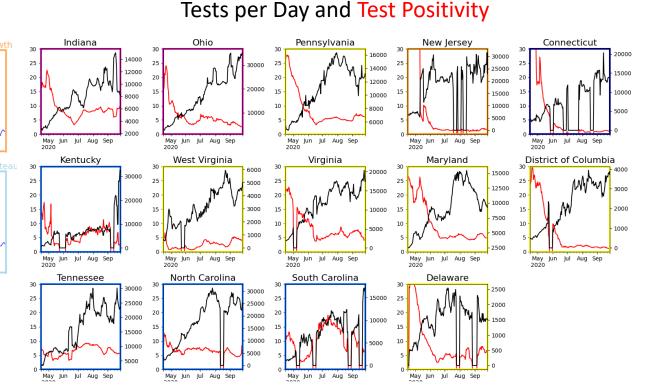


Other State Comparisons

Trajectories of States



- VA declining
- WV previously surging now plateauing along with DC
- MD, DE, and NC now declining
- KY and TN have limited slow growth



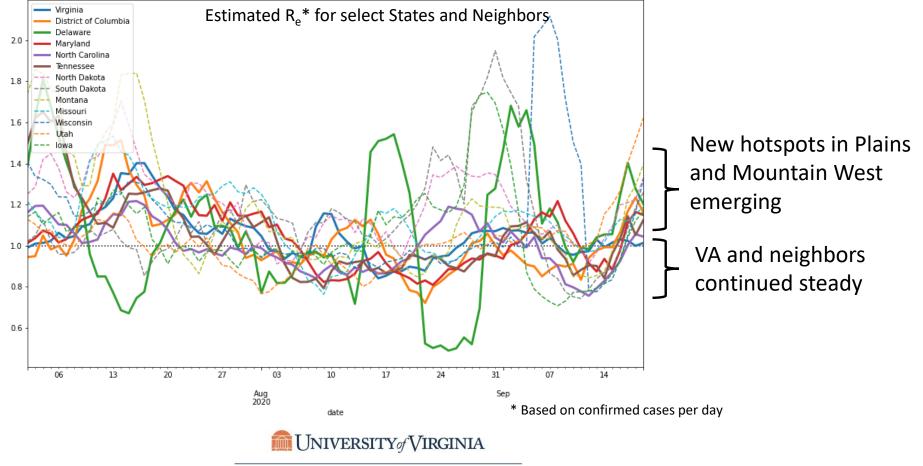
- Test positivity mixed, VA continues to decline.
- Testing volumes steadily growing in VA.



Other State Comparisons

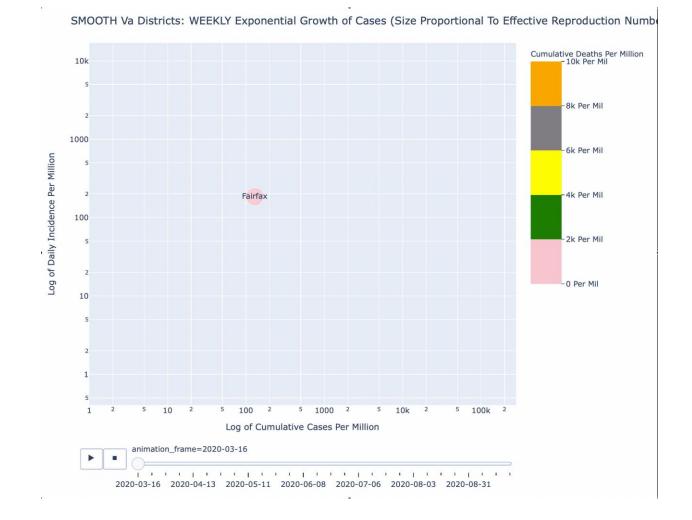
Reproductive Number (R_e) has downward trend across hotspots and Virginia's neighbors

- New states in Plains and Mountain West emerging as hot spots: ND, SD, MT, MO, WI, UT, and IA
- Virginia and neighboring states are mostly at and below 1, though slightly up



Evolution of Infections by District

- From January to Present
- Cumulative cases vs. Daily Incidence
- Placed on log scale to minimize the differences between districts
- Colors represent cumulative deaths per million population
- Size changes based on daily estimated reproductive number

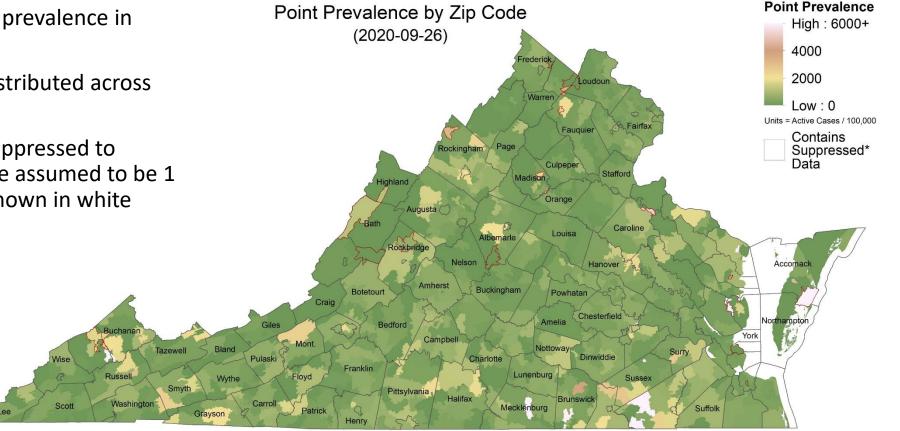




Zip code level weekly Case Rate (per 100K)

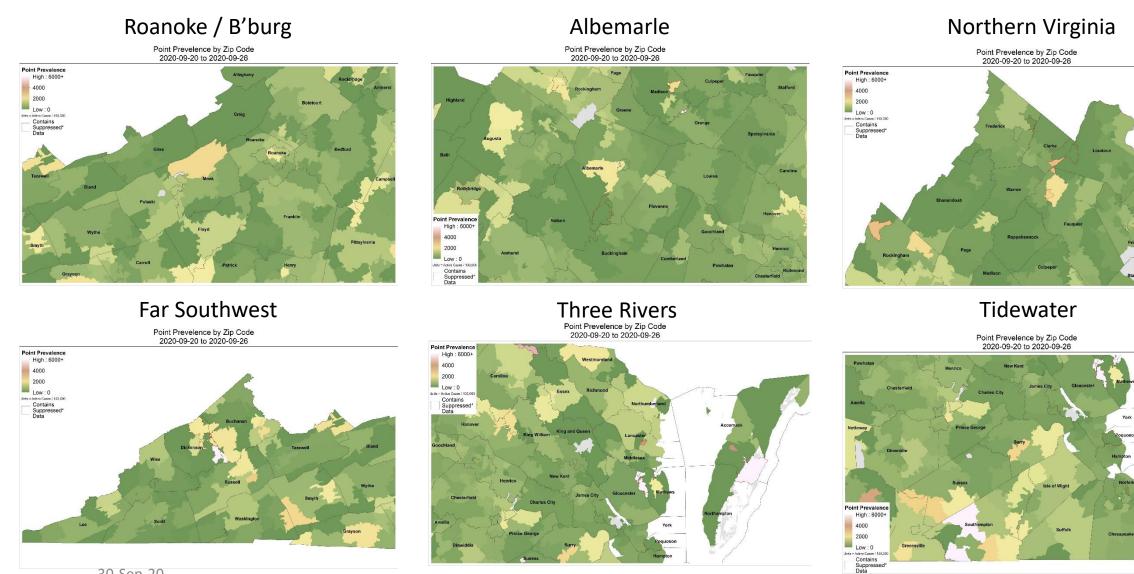
Case Rates in the last week by zip code

- Concentrations of very high prevalence in some zip codes
- High prevalence zips well distributed across the commonwealth
- Many counts are low and suppressed to protect anonymity, those are assumed to be 1 case (per zip per day) and shown in white





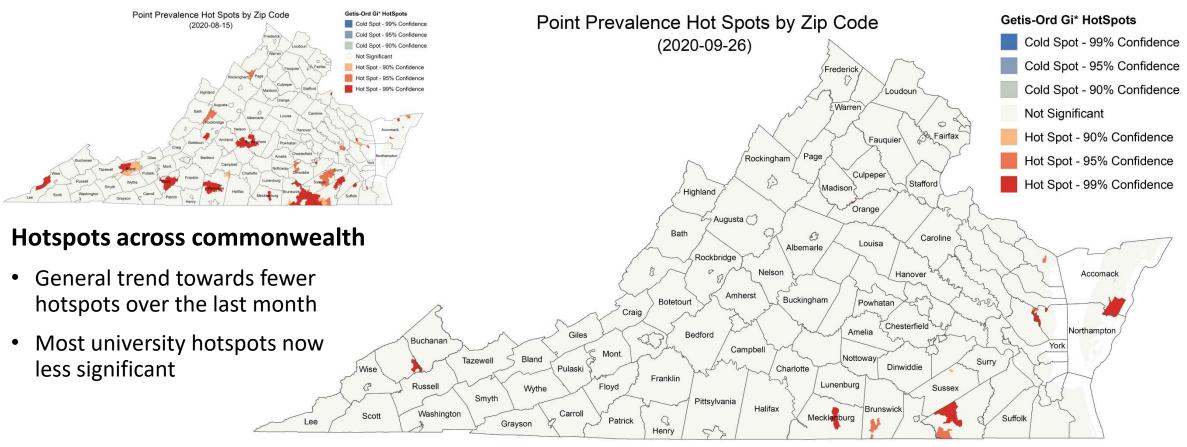
Zip code level weekly Case Rate (per 100K)



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Zip Code Hot Spots

Previous weeks





Model Update – Adaptive Fitting



Adaptive Fitting Approach

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

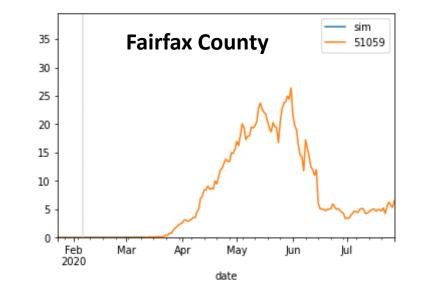
 Allows history to be precisely captured, and used to guide bounds on projections

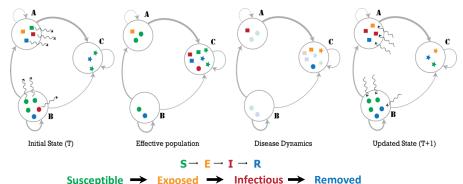
Model: An alternative use of the same meta-population model, PatchSim

- 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

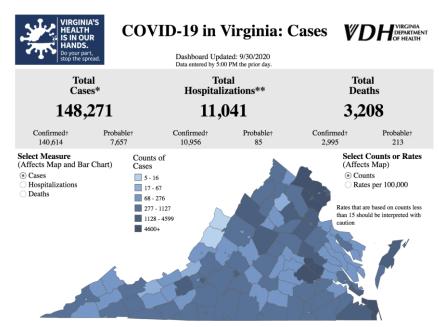


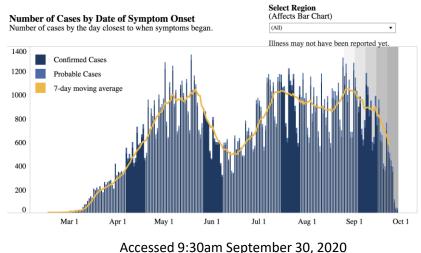


Calibration Approach

- Data:
 - County level case counts by date of onset (from VDH)
 - Confirmed cases for model fitting
- Calibration: fit model to observed data
 - Tune transmissibility across ranges of:
 - Duration of incubation (5-9 days), infectiousness (3-7 days)
 - Undocumented case rate (2x to 15x)
 - 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 using the most recent parameters with constraints learned from the history of the fit parameters
 - Mean trend from last 7 days used, adjusted by variances in the previous 3 weeks
 - 1 week interpolation to smooth transitions in rapidly changing trajectories
 - Particles with high error or variance filtered out







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

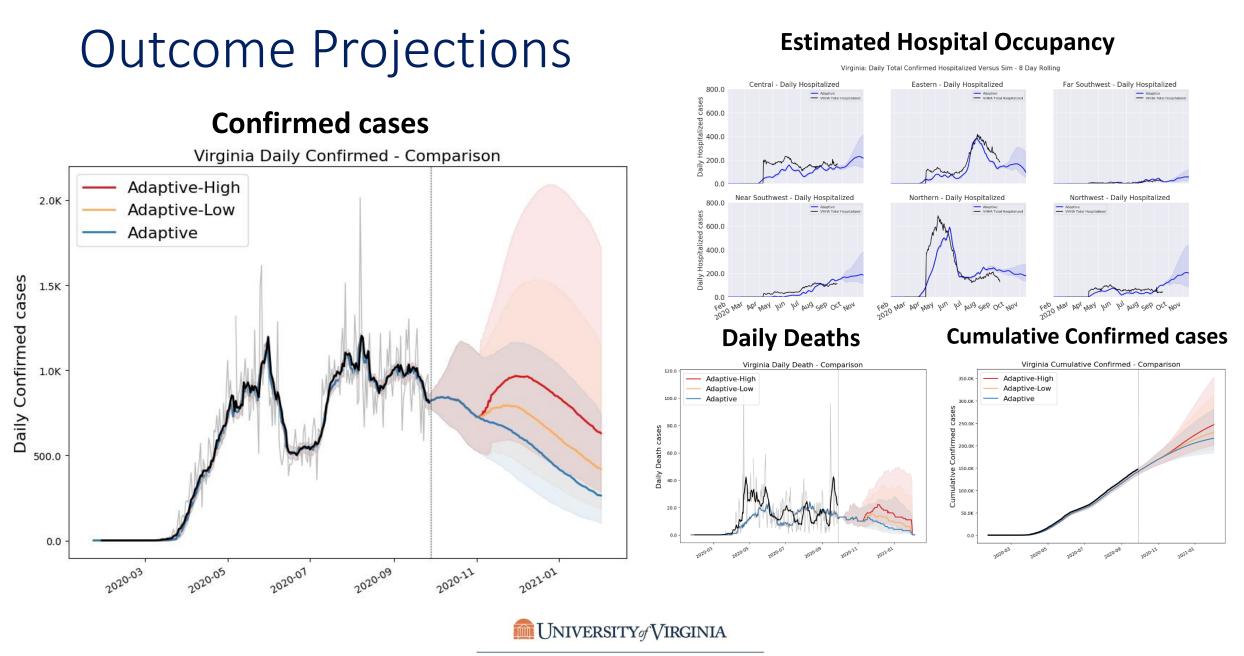
Scenarios – Seasonal Effects

- Societal changes in the coming weeks may lead to an increase in transmission rates
 - Start of in-person school
 - Changes to workplace attendance
 - Seasonal impact of weather patterns
- Three scenarios provided to capture possible trajectories related to these changes starting at beginning of flu season, Oct 1st, 2020
 - Adaptive: No change from base projection
 - Adaptive-Low: 10% increase in transmission starting Nov 1st, 2020
 - Adaptive-High: 20% increase in transmission starting Nov 1st, 2020



Model Results

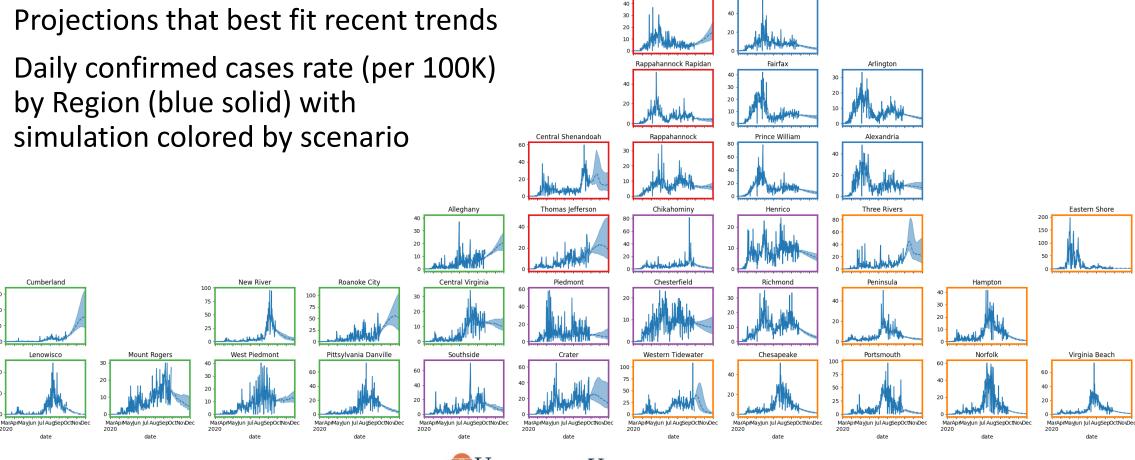




District Level Projections: Adaptive

Adaptive projections by District

- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (blue solid) with simulation colored by scenario



Lord Fairfax

Loudoun

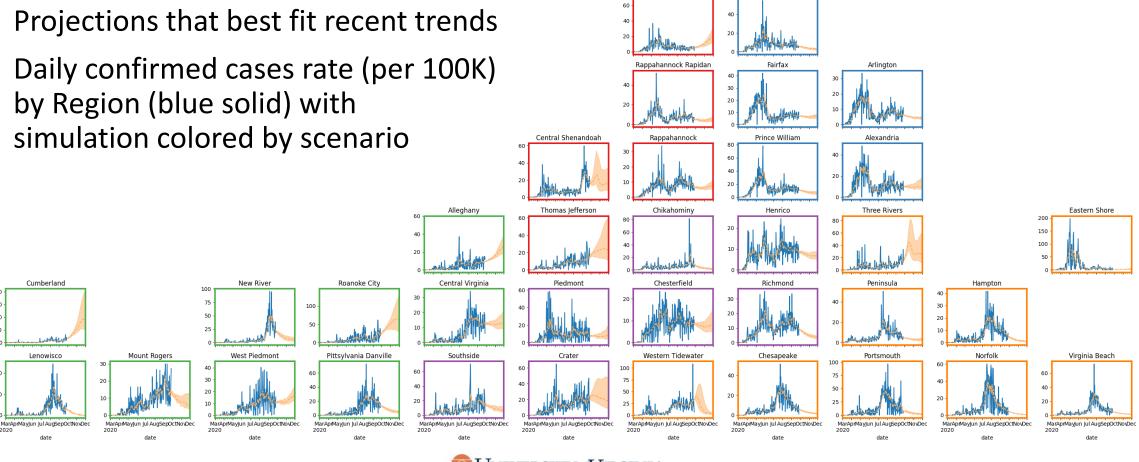
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150 100

District Level Projections: Adaptive-Low

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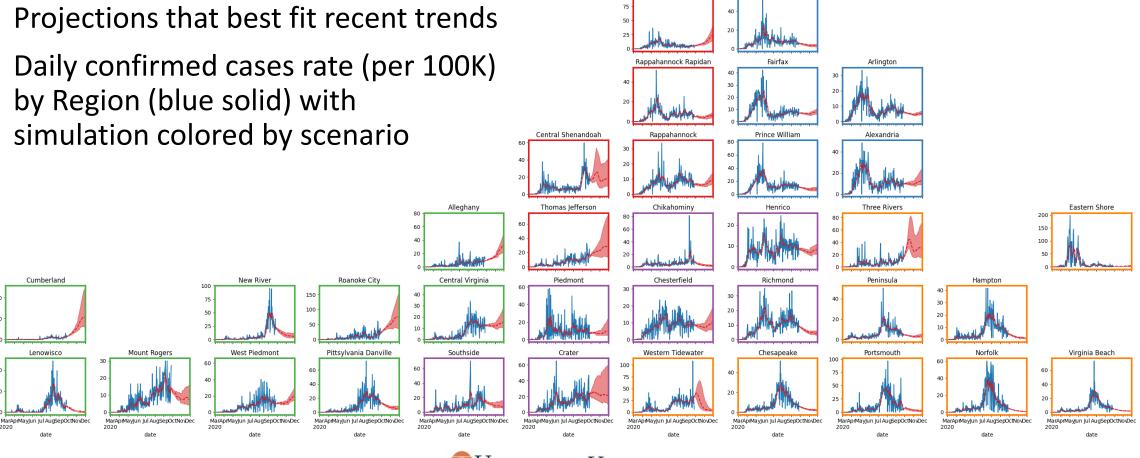
200 150

100

District Level Projections: Adaptive-High

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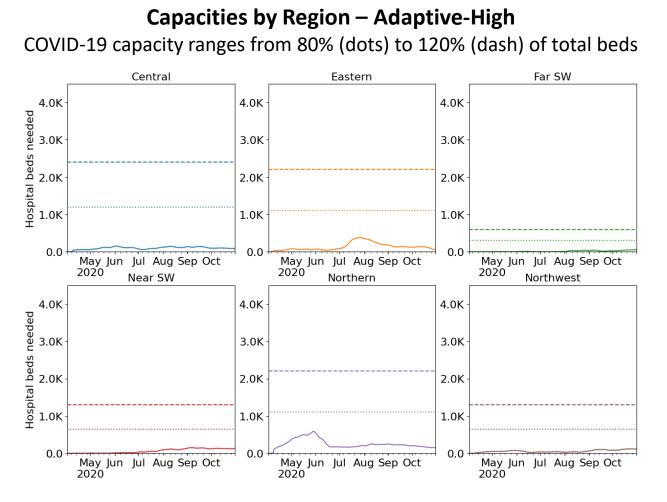
Loudoun

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200

100

Hospital Demand and Capacity by Region



Week Ending	Adaptive	Adaptive-High
9/27/20	5,987	5,987
10/4/20	5,813	5,813
10/11/20	5,881	5,881
10/18/20	5,806	5,806
10/25/20	5,599	5,599
11/1/20	5,236	5,236
11/8/20	4,996	5,208
11/15/20	4,854	5,881
11/22/20	4,726	6,390
11/29/20	4,532	6,678
12/06/20	4,263	6,744
12/13/20	4,005	6,691

Based on Adaptive-High scenario

No regions forecast to exceed capacity

* Assumes average length of stay of 8 days

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Key Takeaways

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

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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. <u>https://github.com/NSSAC/PatchSim</u> (Accessed on 04/10/2020).

Virginia Department of Health. COVID-19 in Virginia. <u>http://www.vdh.virginia.gov/coronavirus/</u> (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. <u>https://www.google.com/covid19/mobility/</u>

Biocomplexity page for data and other resources related to COVID-19: <u>https://covid19.biocomplexity.virginia.edu/</u>



Questions?

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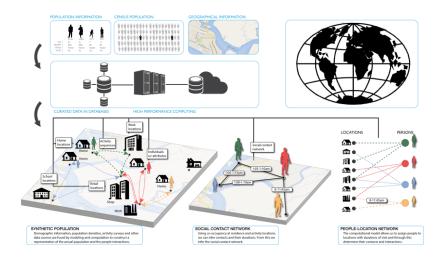
Supplemental Slides



Agent-based Model (ABM)

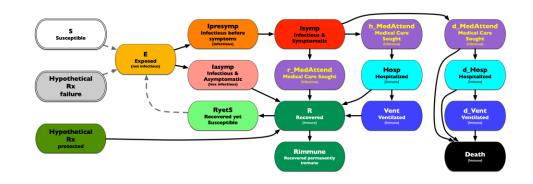
EpiHiper: Distributed network-based stochastic disease transmission simulations

- 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

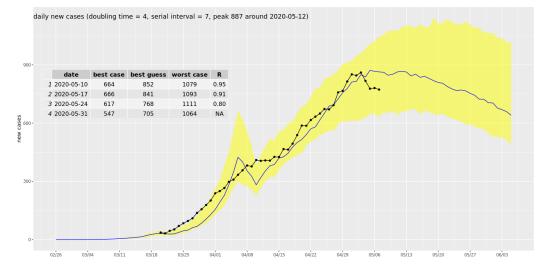
- Literature based probabilities of outcomes with appropriate delays
- Varying levels of infectiousness
- Hypothetical treatments for future developments

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ABM Social Distancing Rebound Study Design

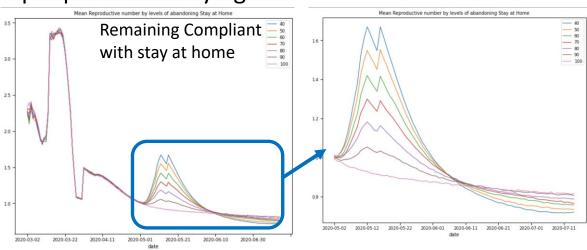
Study of "Stay Home" policy adherence

- 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



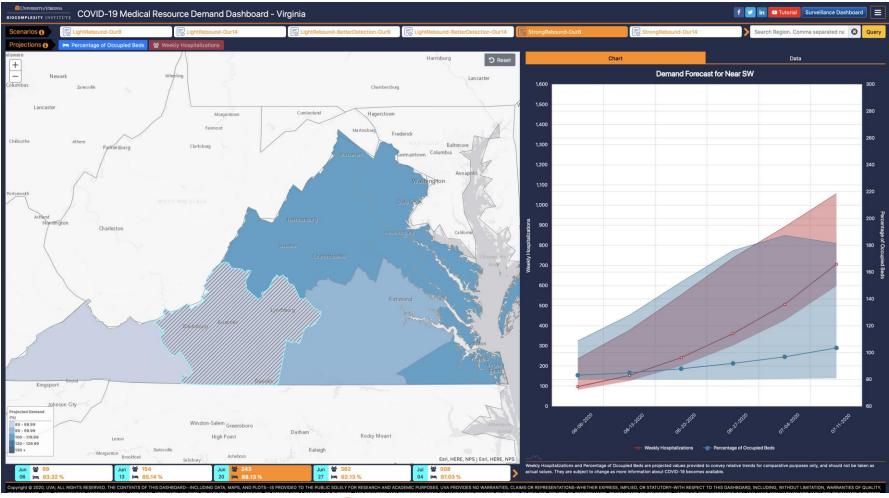
Impacts on Reproductive number with release

- 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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Medical Resource Demand Dashboard

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



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