Estimation of COVID-19 Impact in Virginia

March 3rd, 2021
(data current to March 1st-2nd)
Biocomplexity Institute Technical report: TR 2021-024
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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Biocomplexity COVID-19 Response Team
Overview

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

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

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

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

- **Case rate growth in Virginia continues to decline with a few hotspots emerging**
  - VA mean weekly incidence down to 19/100K from 23/100K, US levels decline (to 18 from 19 per 100K)
  - Significant progress made in last month, however 88% of VA counties above mean rate of Summer 2020
  - Projections continue to be down across Commonwealth

- Recent updates:
  - Adjustment to death outcome modeling to correct for delays in reporting, higher resolution hospital data incorporated for hospital calibration
  - Ascertainment rate adjusted to better capture total infections to date
  - Further updates to vaccination schedules, with fitting now including partially vaccinated population and future vaccinations based on current levels instead of goals

- The situation is changing rapidly. Models continue to be updated regularly.
Situation Assessment
Case Rate (per 100k) by VDH District

Declines continue across the Commonwealth

• Majority of districts have decreasing rates
• Rates remain high in many districts
• University districts (New River, Blue Ridge) experiencing outbreaks
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”
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

<table>
<thead>
<tr>
<th>Trajectory</th>
<th>Description</th>
<th>Weekly Case Rate (per 100K) bounds</th>
<th># Districts (prev week)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Declining</td>
<td>Sustained decreases following a recent peak</td>
<td>below -0.9</td>
<td>33 (32)</td>
</tr>
<tr>
<td>Plateau</td>
<td>Steady level with minimal trend up or down</td>
<td>above -0.9 and below 0.5</td>
<td>2 (0)</td>
</tr>
<tr>
<td>Slow Growth</td>
<td>Sustained growth not rapid enough to be considered a Surge</td>
<td>above 0.5 and below 2.5</td>
<td>0 (2)</td>
</tr>
<tr>
<td>In Surge</td>
<td>Currently experiencing sustained rapid and significant growth</td>
<td>2.5 or greater</td>
<td>0 (1)</td>
</tr>
</tbody>
</table>
District Trajectories – last 10 weeks

<table>
<thead>
<tr>
<th>Status</th>
<th># Districts (prev week)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Declining</td>
<td>33 (32)</td>
</tr>
<tr>
<td>Plateau</td>
<td>2 (0)</td>
</tr>
<tr>
<td>Slow Growth</td>
<td>0 (2)</td>
</tr>
<tr>
<td>In Surge</td>
<td>0 (1)</td>
</tr>
</tbody>
</table>

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

- Variants are defined by collection of co-occurring mutations that make it distinct from the other various variations in the genome.
  - Some subsets of mutations, including single amino acid substitutions, make the change that alters the virus pathogenicity

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  - Some subsets of mutations, including single amino acid substitutions, make the change that alters the virus pathogenicity
SARS-CoV2 Variants of Concern

**Lineage B.1.1.7**

- B.1.1.7 has been detected in Virginia as well as in at least 2,506 cases across 45 states as of Mar 2nd (10-20 day delay for genotyping), will continue to grow rapidly. Current estimates place national frequency at ~10% and Virginia at 16%

- **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

- **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

- **Evidence mounts** supporting increased risks of hospitalization and mortality for B.1.1.7 infected individuals

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](https://dash.harvard.edu/handle/1/37366884)
New variants of SARS-CoV2

**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 Cell** demonstrates immune escape across a bank of sera from different COVID-19 patients and vaccine recipients (Pfizer and AstraZeneca)
- **Additional study** demonstrates that T cell response from mRNA vaccinated individuals are not significantly degraded across these “immune escaping” variants

**Additional Variants**
- **Lineage P.1**: [First case reported in Minnesota](https://www.cdc.gov/coronavirus/2019-ncov/variants/lineage-p1.html) on Jan 25th, now at least 10 cases in 5 states caused a [resurgence of hospitalizations in Manaus, Brazil](https://www.cdc.gov/coronavirus/2019-ncov/variants/lineage-p1.html) and is now estimated to be 1.4-2.2 times more transmissible and able to partially evade protective immunity.
- **Lineage B.1.429 (similar mutations as in B.1.1.7 and B.1.351)**: Initially found in Southern California, coincided with surge in Nov and Dec, [found in over half of sequenced samples in LA](https://www.cdc.gov/coronavirus/2019-ncov/variants/lineage-b1-429.html)
- New naming conventions in the works. May cluster these with bird names: Robin 1, Robin 2, Pelican, Yellowhammer, Mockingbird, Bluebird, Quail, etc.

Results demonstrate that CD4+ and CD8+ T cell responses in convalescent COVID-19 subjects or COVID-19 mRNA vaccinees are not substantially affected by mutations found in the SARS-CoV-2 variants

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.
Estimating Daily Reproductive Number

March 1\textsuperscript{st} Estimates

<table>
<thead>
<tr>
<th>Region</th>
<th>Date Confirmed $R_e$</th>
<th>Date Confirmed</th>
<th>Diff Last Week</th>
</tr>
</thead>
<tbody>
<tr>
<td>State-wide</td>
<td>0.836</td>
<td>0.115</td>
<td></td>
</tr>
<tr>
<td>Central</td>
<td>0.819</td>
<td>0.200</td>
<td></td>
</tr>
<tr>
<td>Eastern</td>
<td>0.827</td>
<td>0.051</td>
<td></td>
</tr>
<tr>
<td>Far SW</td>
<td>1.085</td>
<td>0.476</td>
<td></td>
</tr>
<tr>
<td>Near SW</td>
<td>0.810</td>
<td>0.005</td>
<td></td>
</tr>
<tr>
<td>Northern</td>
<td>0.943</td>
<td>0.300</td>
<td></td>
</tr>
<tr>
<td>Northwest</td>
<td>0.641</td>
<td>-0.331</td>
<td></td>
</tr>
</tbody>
</table>

Methodology

- Wallinga-Teunis method (EpiEstim\textsuperscript{3}) for cases by \textbf{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

Changes in Case Detection

<table>
<thead>
<tr>
<th>Timeframe (weeks)</th>
<th>Mean days</th>
<th>% difference from overall mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>July (26-30)</td>
<td>6.2</td>
<td>-10%</td>
</tr>
<tr>
<td>Aug (31-34)</td>
<td>4.9</td>
<td>-29%</td>
</tr>
<tr>
<td>Sept (35-38)</td>
<td>4.5</td>
<td>-34%</td>
</tr>
<tr>
<td>Oct (39-43)</td>
<td>4.5</td>
<td>-35%</td>
</tr>
<tr>
<td>Nov (44-47)</td>
<td>4.5</td>
<td>-35%</td>
</tr>
<tr>
<td>Dec (48-49)</td>
<td>4.2</td>
<td>-39%</td>
</tr>
<tr>
<td>Jan (00-04)</td>
<td>3.9</td>
<td>-43%</td>
</tr>
<tr>
<td>Feb (05-06)</td>
<td>3.4</td>
<td>-51%</td>
</tr>
<tr>
<td>Overall (13-05)</td>
<td>6.9</td>
<td>--</td>
</tr>
</tbody>
</table>

Test positivity vs. Onset to Diagnosis

Positivity continues its rapid decline
Mask Usage and Vaccine Acceptance in Virginia

Reported mask usage for Virginia remains high
• Facebook surveys have shown steady increase over past three months
• ~88% (early Nov) to ~96% (late Feb)
• Some variance across the Commonwealth
• ~3000 daily responses from VA

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

Data Source: https://covidcast.cmu.edu
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**
Race and Ethnicity cases per 100K

Rates per 100K of each Racial-Ethnic population by Health District
- Each Health District’s Racial-Ethnic population is plotted by their Hospitalization and Case Rate
- Points are sized based on their overall population size (overlapping labels removed)

Case rates by zip codes broken into income quintiles

VDH 7-day moving average rate of new COVID-19 cases by zip code average household income (dollars/ household years) quantile
Other State Comparisons

Trajectories of States

- All states are declining (11) or plateaued (43)
- Re ticks up in many states indicating possible return to growth
- Rates remain elevated, as more declines are level off

Virginia and her neighbors

- 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
Still some way to go to return to rates experienced during the summer of 2020 (June through August)

- 68% 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 92% last week
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

### Point Prevalence by Zip Code (2021-02-27)

<table>
<thead>
<tr>
<th>Rank</th>
<th>Zip Code</th>
<th>Name</th>
<th>Prevalence</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>22904</td>
<td>Charlottesville</td>
<td>4,890</td>
</tr>
<tr>
<td>2</td>
<td>22607</td>
<td>Harrisonburg</td>
<td>2,610</td>
</tr>
<tr>
<td>3</td>
<td>23964</td>
<td>Red Oak</td>
<td>1,710</td>
</tr>
<tr>
<td>4</td>
<td>23027</td>
<td>Cartersville</td>
<td>1,650</td>
</tr>
<tr>
<td>5</td>
<td>24060</td>
<td>Blacksburg</td>
<td>1,630</td>
</tr>
<tr>
<td>6</td>
<td>22903</td>
<td>Charlottesville</td>
<td>1,610</td>
</tr>
<tr>
<td>7</td>
<td>23315</td>
<td>Carrsville</td>
<td>1,560</td>
</tr>
<tr>
<td>8</td>
<td>22211</td>
<td>Fort Myer</td>
<td>1,520</td>
</tr>
<tr>
<td>9</td>
<td>24558</td>
<td>Halifax</td>
<td>1,490</td>
</tr>
<tr>
<td>10</td>
<td>23882</td>
<td>Stony Creek</td>
<td>1,450</td>
</tr>
</tbody>
</table>

* 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 (e.g., in a group of 14 in Charlottesville, there is a 50% chance someone will be infected)
- Some zip codes have high likelihood of exposure even in groups of 25
Current Spatial Hot Spots

<table>
<thead>
<tr>
<th>Spot</th>
<th>Zip Code</th>
<th>Name</th>
<th>Conf.</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>22904</td>
<td>Charlottesville</td>
<td>99%</td>
</tr>
<tr>
<td>2</td>
<td>22807</td>
<td>Harrisonburg</td>
<td>99%</td>
</tr>
<tr>
<td>3</td>
<td>24060</td>
<td>Blacksburg</td>
<td>99%</td>
</tr>
<tr>
<td>4</td>
<td>22903</td>
<td>Charlottesville</td>
<td>99%</td>
</tr>
<tr>
<td>5</td>
<td>24558</td>
<td>Halifax</td>
<td>95%</td>
</tr>
<tr>
<td>6</td>
<td>23055</td>
<td>Fork Union</td>
<td>90%</td>
</tr>
<tr>
<td>7</td>
<td>23964</td>
<td>Red Oak</td>
<td>90%</td>
</tr>
<tr>
<td>8</td>
<td>23456</td>
<td>Virginia Beach</td>
<td>90%</td>
</tr>
</tbody>
</table>

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.
Current Spatial Hot Spots

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
Model Update – Adaptive Fitting
Adaptive Fitting Approach

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

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

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

- Allows for future “what-if” Scenarios to be layered on top of calibrated model
- Eliminates connectivity between patches, to allow calibration to capture the increasingly unsynchronized epidemic

**External Seeding:** Steady low-level importation

- Widespread pandemic eliminates sensitivity to initial conditions
- Uses steady 1 case per 10M population per day external seeding
Using Ensemble Model to Guide Projections

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

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

Weekly forecasts done at county level.

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

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

Also submitted to CDC Forecast Hub.
Seroprevalence updates to model design

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

- CDC Nationwide Commercial Laboratory Seroprevalence Survey estimated 5.7% [3.8% – 8.5%] seroprevalence as of Dec 10th – 23rd, from 4.6% 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 ascertainment as was consistent earlier in the pandemic were being used)

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

<table>
<thead>
<tr>
<th>Cases, Hospitalizations and Deaths</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Cases*</td>
</tr>
<tr>
<td>Total Hospitalizations**</td>
</tr>
<tr>
<td>Total Deaths</td>
</tr>
<tr>
<td>(New Cases: 1,549)*</td>
</tr>
<tr>
<td>** Includes both people with a positive test (Confirmed), and symptomatic with a known exposure to COVID-19 (Probable).</td>
</tr>
<tr>
<td>* Includes both people with a positive test (Confirmed), and symptomatic with a known exposure to COVID-19 (Probable).</td>
</tr>
</tbody>
</table>

Outbreaks

| Total Outbreaks* | 2,647 |
| Outbreak Associated Cases | 65,272 |

Testing (PCR Only)

| Testing Encounters PCR Only* | 5,946,972 |
| Current 7-Day Positivity Rate PCR Only** | 6.6% |

* PCR testing is "Reverse transcription polymerase chain reaction laboratory testing." |
** Lab reports may not have been received yet. Percent positivity is not calculated for days with incomplete data.

Multiorgan Inflammatory Syndrome in Children

| Total Cases* | 36 |
| Total Deaths | 0 |

*Cases defined by CDC-HAN case definition: https://www.cdc.gov/han/case_definitions/2019NovelCoronavirus.html

Accessed 9:00am March 3, 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, 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%
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

Accessed 8:30pm March 2, 2021
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)
  • Vaccination rate specific to each county (as obtained through VDH dashboard) vax data in data package
  • Future courses based on sustaining daily average of most recent week
    • Rate: 299 FIRST DOSES per 100K per day or a total of ~25K 1st doses per day, which is up from last week’s levels
    • Total Amount: This pace leads to eventually reaching 50K administered a day, implying 25K 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
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
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
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
Adaptive projections by District

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

**Capacities* by Region – Adaptive-FatigueControl-VariantB117**

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

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

https://nssac.bii.virginia.edu/covid-19/vmrddash/
### Weekly Cases and Hospitalizations

#### Weekly confirmed cases

<table>
<thead>
<tr>
<th></th>
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<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>2/28/21</td>
<td>13,381</td>
<td>13,380</td>
<td>13,380</td>
<td>13,380</td>
<td>13,380</td>
</tr>
<tr>
<td>3/7/21</td>
<td>10,897</td>
<td>10,898</td>
<td>10,904</td>
<td>11,074</td>
<td>11,079</td>
</tr>
<tr>
<td>3/14/21</td>
<td>8,856</td>
<td>8,868</td>
<td>8,878</td>
<td>9,642</td>
<td>9,642</td>
</tr>
<tr>
<td>3/21/21</td>
<td>7,256</td>
<td>7,278</td>
<td>7,292</td>
<td>8,568</td>
<td>8,559</td>
</tr>
<tr>
<td>3/28/21</td>
<td>5,989</td>
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#### Weekly Hospitalizations

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Key Takeaways

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

• **Case rate growth in Virginia continues to decline with a few hotspots emerging**
  • VA mean weekly incidence down to 19/100K from 23/100K, US levels decline (to 18 from 19 per 100K)
  • Significant progress made in last month, however 88% of VA counties above mean rate of Summer 2020
  • Projections continue to be down across Commonwealth

• Recent updates:
  • Adjustment to death outcome modeling to correct for delays in reporting, higher resolution hospital data incorporated for hospital calibration
  • Ascertainment rate adjusted to better capture total infections to date
  • Further updates to vaccination schedules, with fitting now including partially vaccinated population and future vaccinations based on current levels instead of goals

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


Google. COVID-19 community mobility reports. [https://www.google.com/covid19/mobility/](https://www.google.com/covid19/mobility/)

Questions?

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

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Supplemental Slides
Date of Onset Reproductive Number

Feb 20th Estimates

<table>
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<tr>
<th>Region</th>
<th>Date of Onset</th>
<th>Date Onset Diff</th>
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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

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"

 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