

## Small-Area Projections of COVID-19 Transmission in the United States

### Background

The novel coronavirus SARS-CoV-2 has caused a pandemic that has already infected 1.56 million people with 92,000 deaths in the United States by May 20, 2020. As local areas seek to respond to emerging risk of outbreaks, most models that are predicting the case burden over the next few months project for large areas (state or national), using a fixed R estimated from national data, do not consider city characteristics (e.g., population density, demographics) that could impact transmissibility, and don't directly measure the effect of social distancing. In addition, these models do not consider time-varying exposures such as temperature and humidity that might affect SARS-CoV-2 transmission. There is an urgent need to project how SARS-CoV-2 transmission will occur in the coming months more selectively across U.S. cities that are very different geographically and with respect to the underlying risks of their populations. Our objective is to project the trajectory of the COVID-19 epidemic in major U.S. cities by assuming that R is not fixed, will vary significantly across the country, and will vary specifically in relationship to temperature, humidity and social distancing strategies. In conjunction with other national models, these data can provide complementary information to better guide communities as they respond to emerging risk in the weeks ahead.

### Methods

We have expanded our projections to include 389 counties with active outbreaks (up from 211 in our original analyses), representing 68% of the total U.S. population, based on the following characteristics: 1) population exceeding 100,000 persons; 2) includes a state capital; or 3) is the largest county within a less populous state. Of the nearly 600 counties that met these criteria, we model only those whose SARS-CoV-2 daily case rates exceeded an absolute count of five, thus prioritizing counties within a minimum threshold of disease activity. Daily case counts of SARS-CoV-2 infection by county were obtained from The New York Times and USAFACTS (usafacts.org). We obtained data about county and population characteristics from the American Community Survey, Behavioral Risk Factor Surveillance System and other surveys of the population. For each county, we obtained data on social distancing, defined as the percent change in visits to non-essential businesses in each county (Unacast). We obtained daily dry-bulb temperatures and absolute humidity from the National Oceanic and Atmospheric Administration Local Climatological Data from 2010 to the current date. Estimates for R values in each county were informed by methods from Wallinga & Teunis 2004 and Cori et al. 2013. Distributed lag non-linear mixed effects models (Gasparrini et al. 2010) allowed us to examine simultaneously the cumulative exposure-response relationship between daily temperatures over a lag period of 4 to 14 days with R, including an interaction between a lagged 4-14 day rolling average of absolute humidity. In addition to the coefficients from the distributed lag non-linear models, the predictive models also include, at the county level, a rolling average of lagged social distancing between 4-14 days, population density, diabetes prevalence, percent of residents over 65 years of age, percent of population below 200% of poverty level, household crowding and change of testing capacity (using a rolling test positivity rate that can account for elevation of cases based on increased testing capacity). Models predicting R and daily cases over the next four weeks were trained using data between April 1 and May 14. The final model was selected from six models based on predictive accuracy of observed data in the first two weeks of May. For predictions, we use historical averages of daily temperature and humidity; testing positivity rate and social distancing are held constant at their current 7-day averages.

### Preliminary Findings

The trajectory of real-time R has varied greatly across counties, with variance in both the peak and slope of R over time and resultant surge of SARS-CoV-2 cases. Social distancing, population density, and temperature/humidity significantly affect the estimations of R over time, while standardizing on population characteristics. The ability of rising temperatures or humidity to mitigate transmissibility (or Rs) erodes for counties with higher population density and among communities that reopen too quickly, compared to their peak social distancing in April.

### Implications

These small-area analyses allow real-time modeling of SARS-CoV-2 transmission and provide complementary information to the other national models currently used to project coronavirus transmission. The consideration of county-level characteristics, daily temperatures, and direct measurement of the effect of social distancing directives reveal marked heterogeneity in the magnitude and timing of surges of SARS-CoV-2 cases in the United States. These results might inform consideration of selective strategies to mitigate SARS-CoV-2 transmission and assess health care system capacity constraints across the country. They can also serve as an early warning indicator for communities and their residents to reassess and modify behavior in response to forecasted resurgence risk.

### Statistical References:

Wallinga, Jacco, and Peter Teunis. "Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures." *American Journal of epidemiology* 160, no. 6 (2004): 509-516.

Cori, Anne, Neil M. Ferguson, Christophe Fraser, and Simon Cauchemez. "A new framework and software to estimate time-varying reproduction numbers during epidemics." *American journal of epidemiology* 178, no. 9 (2013): 1505-1512.

Gasparri A1, Armstrong B, Kenward MG. Distributed lag non-linear models. *Statistics in Medicine*. 2010 Sep 20;29(21):2224-34. doi: 10.1002/sim.3940.

We are available to discuss our models at your earliest convenience.

David Rubin, MD, MSCE ([rubin@email.chop.edu](mailto:rubin@email.chop.edu))

Greg Tasian, MD MSCE ([tasiang@email.chop.edu](mailto:tasiang@email.chop.edu))

Jing Huang, PhD ([huangj5@email.chop.edu](mailto:huangj5@email.chop.edu))