

AMST Technical Report 2020-01

Effect of Mitigation Strategies on the Spread of COVID-19 in New Jersey

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Modelling Results

Following the typical mathematical modelling of infectious disease using deterministic compartmental models, a Susceptible-Exposed-Symptomatic Infectious-Asymptomatic Infectious-Recovered-Dead population model has been developed to understand the transmission of COVID-19 throughout New Jersey. The model is also used to understand the effect that social distancing and other mitigation policies have on the spread of the disease, as well as the harm that can arise if the mitigation strategies are removed too soon.

Figure 1 shows the number of infectious individuals and cumulative deaths over a six month period beginning on April 5, 2020. The implementation of social distancing and other mitigation policies lowers the reproductive number, which provides a measure of number of social interactions and the infectiousness of the disease. As mitigation policies reduce disease transmission as seen by a reduction in the reproductive number, one sees a reduction in the size of the epidemic as well as in the total number of deaths.

Figure 2 shows the number of infectious individuals and cumulative deaths over a six month period beginning on April 5, 2020 for the case of no mitigation and for the case with a 40% reduction in disease transmission. The figure also shows the effect of removing the mitigation policies on May 17, 2020. One sees an increase in the spread of the disease with an end result that is very similar to the case when no mitigation was ever performed. Figure 3 is similar to Figure 2, and shows the number of infectious individuals and cumulative deaths over a nine month period beginning on April 5, 2020 for the case of no mitigation and for the case with a 60% reduction in disease transmission. The figure also shows the effect of removing the mitigation policies on August 01, 2020. One sees an increase in the spread of the disease with an end result that is very similar to the case when no mitigation was ever performed.

Figures 2 and 3 demonstrate that mitigation policies cannot simply be removed. A phased removal is required, and excellent testing, contact tracing, and serological testing must be in place before removing the mitigation policies. An even better scenario involves having antiviral treatments and a vaccine in place before completely removing the mitigation strategies.

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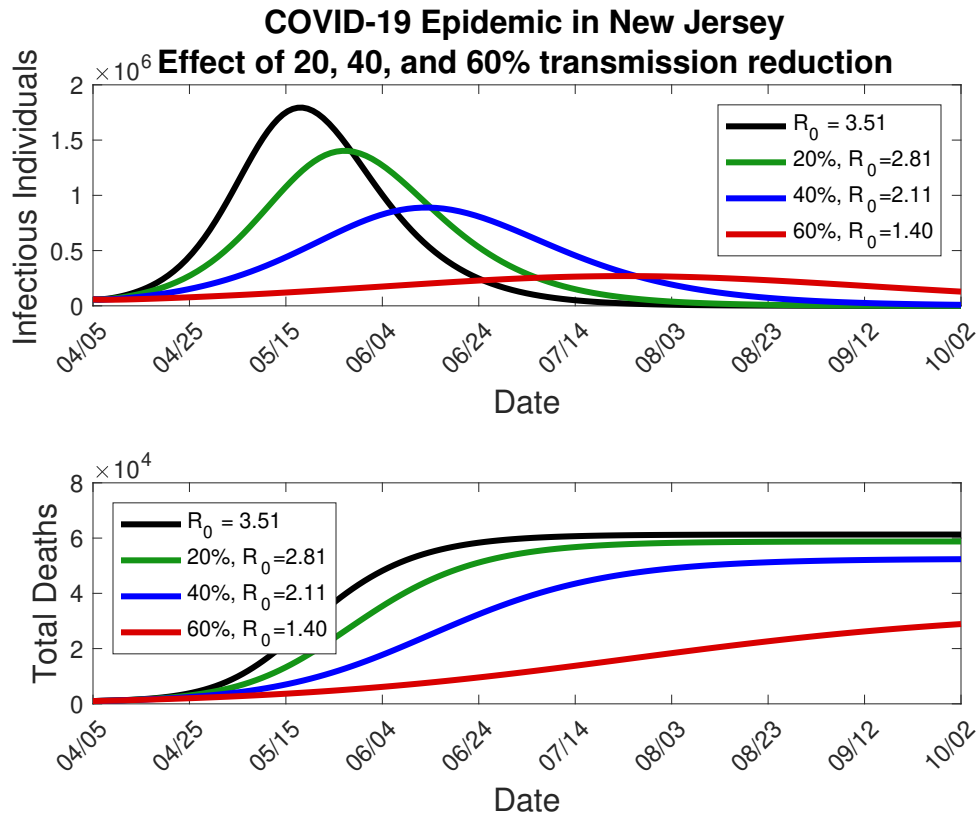


Figure 1: Number of infectious individuals and cumulative deaths over a six month period beginning on April 5, 2020. One can see how the reduction of disease transmission through mitigation policies reduces the size of the epidemic and the cumulative number of deaths.

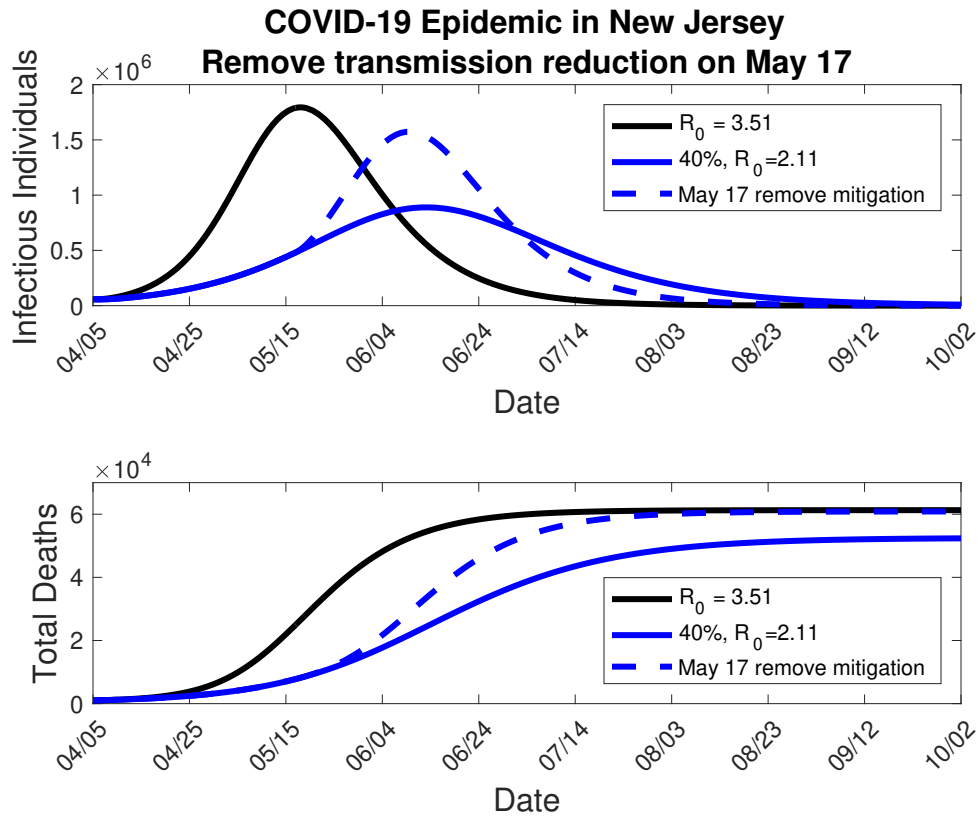


Figure 2: Number of infectious individuals and cumulative deaths over a six month period beginning on April 5, 2020. Implementation of a mitigation policy that reduces disease transmission by 40% leads to a decrease in the size of the epidemic if carried out for long enough. If instead, the mitigation policies are removed on May 17, 2020, one sees an increase in the spread of the disease with a final size that is similar to that which would have occurred if no mitigation had ever been implemented.

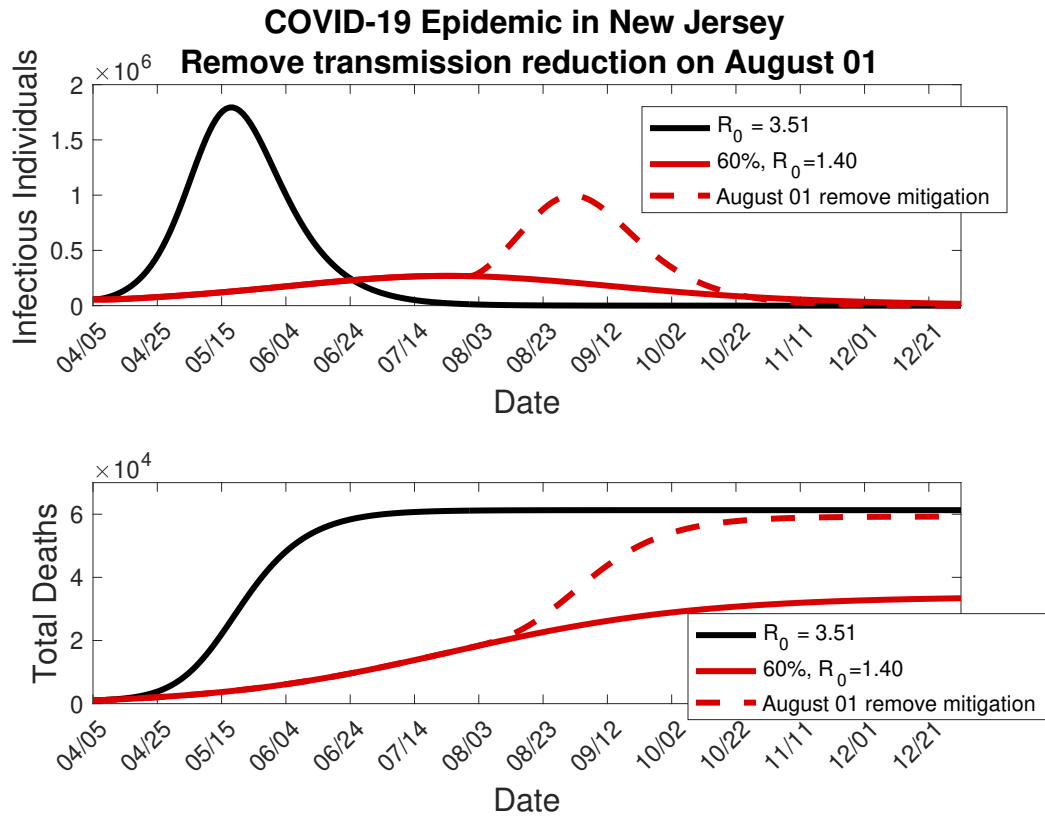


Figure 3: Number of infectious individuals and cumulative deaths over a nine month period beginning on April 5, 2020. Implementation of a mitigation policy that reduces disease transmission by 60% leads to a decrease in the size of the epidemic if carried out for long enough. If the mitigation policies are removed on August 01, 2020, one sees an increase in the spread of the disease with a final size that is similar to that which would have occurred if no mitigation had ever been implemented.

Mathematical Model

This population model includes Susceptible, Exposed, symptomatic Infectious, asymptomatic Infectious, Recovered, and Dead individuals. The governing equations are

$$\dot{S} = -\frac{\beta_{\text{symp}} S I_{\text{symp}}}{N} - \frac{\beta_{\text{asymp}} S I_{\text{asymp}}}{N}, \quad (1)$$

$$\dot{E} = \frac{\beta_{\text{symp}} S I_{\text{symp}}}{N} + \frac{\beta_{\text{asymp}} S I_{\text{asymp}}}{N} - \gamma E, \quad (2)$$

$$\dot{I}_{\text{symp}} = f\gamma E - \sigma_{\text{symp}} I_{\text{symp}}, \quad (3)$$

$$\dot{I}_{\text{asymp}} = (1-f)\gamma E - \sigma_{\text{asymp}} I_{\text{asymp}}, \quad (4)$$

$$\dot{R} = (1-d)\sigma_{\text{symp}} I_{\text{symp}} + \sigma_{\text{asymp}} I_{\text{asymp}}, \quad (5)$$

$$\dot{D} = d\sigma_{\text{symp}} I_{\text{symp}}, \quad (6)$$

where S , E , I_{symp} , I_{asymp} , R , and D respectively denote Susceptible, Exposed, symptomatic Infectious, asymptomatic Infectious, Recovered, and Dead individuals. In addition, β_{symp} and β_{asymp} respectively denote the symptomatic and asymptomatic contact rates, N is the population size of New Jersey, $1/\gamma$ is the mean exposure time, f is the fraction of infected individuals who become symptomatic, $1/\sigma_{\text{symp}}$ and $1/\sigma_{\text{asymp}}$ respectively represent the mean symptomatic and asymptomatic time, and d is the fraction of symptomatic infectious individuals who die.

The basic reproductive number, R_0 , is the number of secondary infections produced by a single infectious individual who is placed in an entirely susceptible population. For example, if the reproductive number is three, we would expect an infectious individual placed in an entirely susceptible population to infect on average three more individuals. In this COVID-19 model, the reproductive number is given by

$$R_0 = f \frac{\beta_{\text{symp}}}{\sigma_{\text{symp}}} + (1-f) \frac{\beta_{\text{asymp}}}{\sigma_{\text{asymp}}}. \quad (7)$$

Population sizes were obtained from U.S. Census data, and epidemiological parameter values were chosen to be consistent with a doubling time of three days and COVID-19 reports from the MRC Centre for Global Infectious Disease Analysis, Imperial College, London, UK¹. All values are listed in Table 1.

It is important to note that due to a lack of testing, there is great uncertainty in the parameter values, which leads to uncertainty in model simulations. Although the model output is robust to changes in parameter values, one should not rely solely on the predictions made by an individual model using a single set of parameter values. Instead, these results should be used to qualitatively improve understanding of the spread of the disease. In particular, the results contained within this document show the relative effect of mitigation policies, and the danger in removing the policies before adequate testing and contact tracing have been implemented.

¹URL: <https://www.imperial.ac.uk/mrc-global-infectious-disease-analysis/covid-19/>

Parameter	Denotation	Value
β_{symp}	symptomatic contact rate	0.45/day
β_{asymp}	asymptomatic contact rate	0.3/day
$1/\gamma$	mean exposure time	5 days
f	fraction of infected individuals who become symptomatic	0.7
$1/\sigma_{\text{symp}}$	mean symptomatic time	10 days
$1/\sigma_{\text{asymp}}$	mean asymptomatic time	4 days
d	fraction of symptomatic infectious individuals who die	0.1
N	population of New Jersey	8 909 000

Table 1: COVID-19 model parameter values.