

# **MODELING THE IMPACT OF SOCIAL DISTANCING MEASURES ON THE SPREAD OF SARS-CoV-2 IN MINNESOTA**

TECHNICAL DOCUMENTATION MODEL VERSION 3.0  
(UPDATED MAY 13, 2020)

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Eva A. Enns,<sup>1</sup> Marina Kirkeide,<sup>2</sup> Abhinav Mehta,<sup>3</sup> Richard MacLehose,<sup>2</sup> Gregory S. Knowlton,<sup>1</sup> M. Kumi Smith,<sup>2</sup> Kelly M. Searle,<sup>2</sup> Ran Zhao,<sup>2</sup> Erinn Sanstead,<sup>4</sup> Stefan Gildemeister,<sup>4</sup> Pamela Mink,<sup>4</sup> Alisha Simon,<sup>4</sup> Shalini Kulasingam<sup>2</sup>

1. Division of Health Policy and Management, University of Minnesota, School of Public Health
2. Division of Epidemiology and Community Health, University of Minnesota, School of Public Health
3. Computer Science and Engineering, University of Minnesota
4. Minnesota Department of Health



University of Minnesota School of Public Health  
Eva Enns ([eens@umn.edu](mailto:eens@umn.edu)), Shalini Kulasingam ([Kulas016@umn.edu](mailto:Kulas016@umn.edu))  
Media: [unews@umn.edu](mailto:unews@umn.edu)



Minnesota Department of Health  
Stefan Gildemeister ([Stefan.Gildemeister@state.mn.us](mailto:Stefan.Gildemeister@state.mn.us))

Media: [health.media@state.mn.us](mailto:health.media@state.mn.us)

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# Executive Summary

This document details the methods and data sources for the Minnesota COVID-19 transmission model developed as part of a collaborative effort between the University of Minnesota (UMN) and the Minnesota Department of Health (MDH). It reflects updates through May 1, 2020 as part of developing Version 3.0 of the model and associated output. The model structure, methods of calibration, and parameter values are informed by a systematic review of published data, consultation with peers across the US, and other COVID-19 models in the literature. The age and comorbidity distribution of the model population is informed by data specific to Minnesota.

There still remains substantial uncertainty in many key model parameters. Results of this model, not included in this methods documentation, must be interpreted in light of the uncertainty and limitations detailed at the end of this document. As such, updates to the model and revisions to the accompanying documentation should be expected as more research is published on COVID-19 in the United States.

## Background

Eight days after the first case of SARS-CoV-2 infection was reported in Minnesota on March 8, 2020, MDH confirmed “community spread” of the novel virus. Since then, social distancing orders have been issued by Governor Walz, requiring Minnesotans to avoid social contact outside the home as much as possible. In the absence of effective therapies or a vaccine, non-pharmaceutical interventions such as social distancing and case isolation provide the best available strategies for mitigating the impact of the COVID-19 pandemic. To help inform state-level decision-making, MDH partnered with UMN to develop a model of SARS-CoV-2 transmission in Minnesota. This model was one factor among numerous considerations that contributed to the establishment of the series of non-pharmaceutical interventions in Minnesota:

- K-12 school closures were instituted on March 18, 2020<sup>1</sup>
- This was followed by issuance of a statewide stay-at-home order that took effect on March 28, 2020.<sup>2</sup>
- On April 8, 2020, Governor Walz extended the statewide stay-at-home order until May 4, 2020.<sup>3</sup>
- On April 30, 2020, it was announced that the stay-at-home order would be further extended until May 18, 2020.<sup>4</sup>

This document provides an overview of the model, including model structure, assumptions, parameter values, and model calibration. It reflects changes incorporated into model version 3.0 through May 1, 2020. Thus, this technical document supersedes earlier releases and associated documentation. The associated R code has been made publicly available on Github (<https://github.com/orgs/MN-COVID19-Model>) and initial results can be reviewed online at Minnesota's COVID-19 response website (<https://mn.gov/covid19/data/modeling/>).

## Methods

### Model structure

We used an extended susceptible-exposed-infectious-recovered (SEIR) model that accounts for the age and comorbidity distributions of the population of Minnesota to assess the potential impact of specific non-pharmaceutical interventions (Figure 1). The model tracks the number of Minnesota residents who are susceptible, exposed, infectious, and recovered from the virus on a daily basis.

Individuals without prior SARS-CoV-2 infection are initially assumed to be in the susceptible state (“S”). When susceptible individuals become infected, they first transition to the exposed state (“E”), which reflects a pre-symptomatic, pre-infectious incubation period. From the exposed state, a proportion of individuals progress to an asymptomatic infectious state (“AI”), which reflects subclinical infections (e.g. infections that develop mild or no symptoms for the entire duration of infection). Remaining individuals in the exposed state transition to the symptomatic infectious state (“I”). We assume that symptomatic and asymptomatic infections are equally infectious and have the same average infectious period. In the model, we include multiple exposed states ( $E_1, \dots, E_m$ ) and multiple infectious states ( $AI_1, \dots, AI_n; I_1, \dots, I_n$ ) to reflect more realistic heterogeneity in the duration of the incubation and infectious periods than is typically reflected in a standard SEIR model. Additional detail is provided below.

Symptomatic infections have a probability of requiring hospitalization with or without mechanical ventilation (“ICU” and “H” states, respectively). Following infection, individuals can recover to the recovered state (“R”), where we assume individuals retain complete immunity over the modeled time horizon. We also model the risk of death (“D”) for those in the “H” and “ICU” states, and the possibility of out-of-hospital death directly from the “I” state for symptomatic individuals. The model is implemented as a set of difference equations, which approximate ordinary differential equations that describe how individuals move between states. These equations are provided in the Appendix.

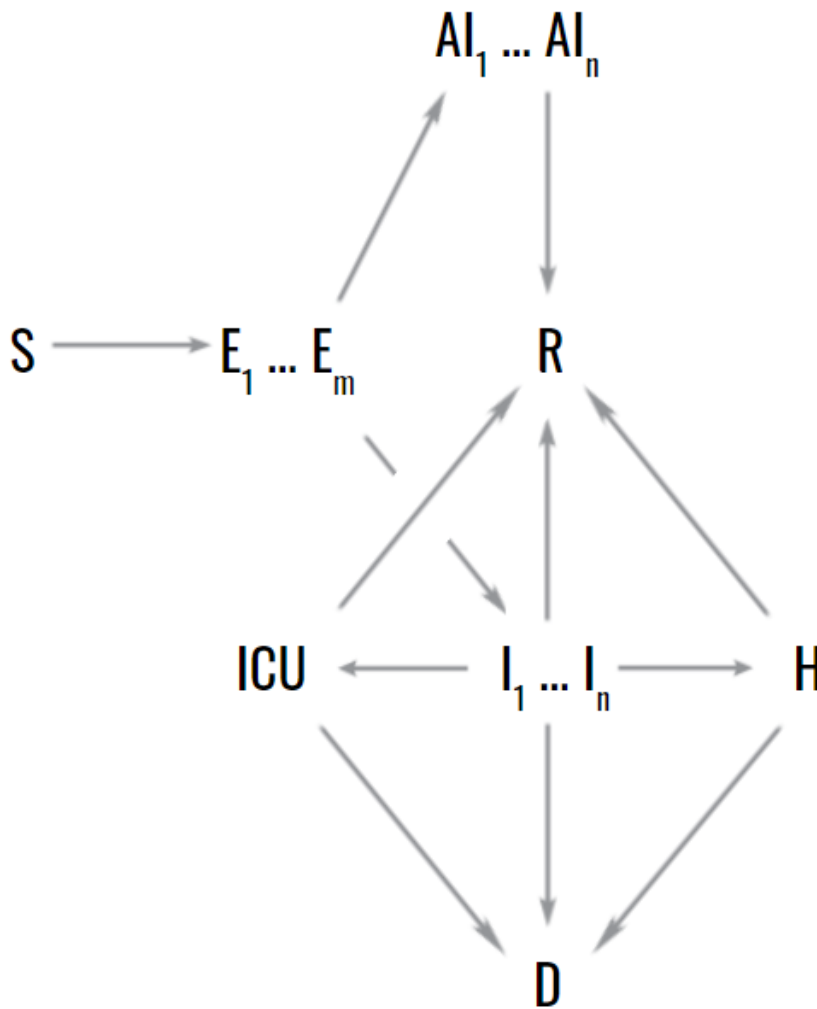


Figure 1: SEIR model diagram for the Minnesota (MN) COVID-19 Model. S: Susceptible;  $E_1 \dots E_m$ : Exposed;  $AI_1 \dots AI_n$ : Subclinical infection;  $I_1 \dots I_n$ : Symptomatic infection; H: Hospitalized and not ventilated; ICU: In ICU and ventilated; R: Recovered; D: Dead.

## Analysis

We used the model to predict epidemiological outcomes for one year (March 23, 2020 through March 22, 2021) to capture both the short- and long-term effects of different mitigation strategies under currently available evidence about the pathogen and the resulting disease. Epidemiological outcomes include the cumulative number of SARS-CoV-2 infections, the cumulative number of COVID-19 deaths, the number of intensive care unit (ICU) beds (equipped with ventilators) needed at peak demand, and time to reach ICU bed (with ventilator) capacity under assumptions of surge capabilities. All analyses were run in R v3.5.3, an open source programming language and software environment used widely for statistical computation, mathematical modeling, and data visualization.

## Key Model Parameters

Model parameters are summarized in Appendix Table S1.

### *Population structure*

In light of evidence of substantial heterogeneity in COVID-19 mortality by age and underlying comorbidities, we stratified our model population by nine 10-year age groups (0-9, ..., 70-79, 80+; indexed by  $\alpha$ ) and by comorbidity status (no comorbidities vs.  $\geq 1$  comorbidity; indexed by  $\kappa$ ). The size and age distribution of the population of Minnesota was informed by data from the Minnesota State Demographics Center.<sup>5</sup> Age-specific prevalence of relevant underlying conditions was determined from an analysis of the Minnesota All Payer Claims Database (Appendix Table S2).<sup>6</sup> Underlying conditions included chronic obstructive pulmonary diseases (COPD), cardiovascular disease (ischemic heart disease or heart failure), diabetes, poorly managed hypertension, and cancer, which are indicated as potential risk factors for poor COVID-19 outcomes.<sup>7</sup>

### *Disease progression*

Durations for the incubation and infectious periods were taken from estimates reported in the literature.<sup>8,9</sup> Unlike traditional compartmental models which assume that these periods are exponentially distributed, we model individual heterogeneity in incubation and infectious periods as gamma distributed, which is more realistic.<sup>10</sup> This is achieved by including multiple “E” (e.g.  $E_1, \dots, E_m$ ) and multiple “I” and “AI” states (e.g.  $I_1, \dots, I_n; AI_1, \dots, AI_n$ ).<sup>11</sup> Gamma distributions are parameterized in terms of shape,  $k$ , and scale parameters,  $\theta$ . In a compartmental model, the number of states corresponds to the shape parameter,  $k$ , while the transition rate between states correspond to  $1/\theta$ . Note that the mean of a gamma distribution is equal to  $k\theta$ . The shape and scale parameters were selected to match the mean and/or percentiles characterizing incubation and infectious periods reported in the literature. For the incubation period, the mean was estimated to be 5.2 days with a 95th percentile of 12.5 days.<sup>8</sup> This was best fit by having two exposed compartments with a daily transition rate of  $2/5.2=0.38$  ( $\text{Gamma}(k = 2, \theta = \frac{5.2}{2})$ , mean: 5.2; 95th percentile: 12.3). For the infectious period, parameters were selected to match a median of 7 days and interquartile range (IQR) of 3-9 days.<sup>9</sup> This was best fit by having three infectious compartments and a daily transition rate of  $3/7.8=0.38$  ( $\text{Gamma}(k = 3, \theta = \frac{7.8}{3})$ , mean: 7.8; median: 7.0; IQR: 4.5 – 10.4).

### *Contact and Transmission*

An age-based contact matrix (included with the code),  $CM[i,j]$ , was used to indicate the frequency of daily contact between age groups  $i$  and  $j$ . The contact structure was taken from a study that extrapolated the 2008 POLYMOD study in Europe to reflect the US population.<sup>12</sup> The contact matrix was further scaled to reflect the demographics of the Minnesota population. We assumed the same contact patterns for those with and without underlying comorbidities.

The rate at which a susceptible individual in age group  $i$  become infected is equal to the product of the probability of transmission per infected contact ( $\beta$ ) and the total number of infected contacts per time step,  $\lambda_i$ :

$$\sum_{\alpha=1}^9 \frac{I_{\alpha} + AI_{\alpha}}{n_{\alpha}} * CM[i, \alpha]$$

where  $I_{\alpha}$  and  $AI_{\alpha}$  are the number of symptomatic and asymptomatic infectious individuals in age group  $\alpha$  and  $n_{\alpha}$  is the number of alive individuals in age group  $\alpha$ . Those who are asymptomatic are assumed to be equally infectious as those who have symptomatic infections.

Due to the inclusion of population stratification, age-specific mixing patterns, and gamma-distributed incubation and infectious periods, the analytical calculation of  $R_0$  is complex. We therefore used empirical methods to estimate  $R_0$  based on doubling times in the first 20 days of our simulation (without mitigation).<sup>13</sup> We varied  $\beta$  until we achieved an  $R_0$  of 3.87, which was consistent with  $R_0$  estimates from 11 European countries in the early un-mitigated phases of their COVID-19 epidemics.<sup>14</sup>

### *Hospitalization and Mortality*

A mean duration of 11 days from hospitalization to recovery or death was used for those who did not receive mechanical ventilation and a mean duration of 8 days was used for those who did receive mechanical ventilation in the ICU.<sup>15</sup> Average lengths of hospital and ICU stay used in the model do not currently depend on age due to a lack of sufficiently complete data. Age-specific proportions of symptomatic cases requiring hospitalization or ICU care, as well as the proportion of hospitalized or ICU cases who die, were informed by recently published data from the CDC and a study of outcomes among hospitalized patients in New York.<sup>7,16</sup> We equated being in the ICU with requiring a ventilator, thus estimates for ICU are based on those who required a ventilator. We also allow for mortality to occur outside of the ICU or hospital. Parameters governing this process were estimated via calibration (described below).

The reported data on hospitalization and mortality did not align with our 10-year age group categories. To allow us to estimate the necessary age-specific probabilities of hospitalization, of admission to the ICU conditioned on hospitalization, of dying in the ICU (on ventilator), and of dying in the hospital but outside of the ICU (off ventilator), we fit linear regression models to the observed proportions. The midpoint of the reported categories was used as the predictor with polynomial terms included to improve fit. Predicted probabilities for the midpoint of our 10-year age group were computed for each regression model. Logit transformations of the observed probabilities were used when they improved fit. Model fit to the observed probabilities was excellent (R-squares between 90% and 99%).

The number of available ICU beds with ventilators in the state of Minnesota assumed to be available for COVID-19 patients was obtained through communication with MDH (capacity as of March 22, 2020 was 235; as of April 4, 2020, this has been expanded to 2,200). If at a given time step the number of individuals requiring ICU care exceeded the state's capacity, we calculated the  $p_{ICUoverflow}$  parameter that reflects the proportion of COVID-19 patients requiring an ICU bed (with ventilator) who will be unable to access one, as follows:

$$p_{ICUoverflow} = \frac{\sum_{\alpha=1}^9 ICU_{\alpha} - N_{ICUcapacity}}{\sum_{\alpha=1}^9 ICU_{\alpha}}$$



where  $ICU_{\alpha}$  is the number of individuals of age  $\alpha$  requiring an ICU bed (with ventilator) in the current time step and  $N_{ICUcapacity}$  is the statewide capacity of ICU beds with a ventilator available for COVID-19 patients. In each age group, the  $p_{ICUoverflow}$  proportion of patients needing ICU care (with ventilator), representing those patients needing care in excess of statewide capacity, were assumed to die after 1 day of unmet need. The remaining  $(1 - p_{ICUoverflow})$  proportion of patients needing ICU care (with a ventilator) were assumed to experience an average length of stay and face age-specific ICU mortality risks, as summarized in Table S3.

### *Model initialization*

The initial number of infections in the model was estimated from the number of confirmed COVID-19 cases reported by MDH as of March 22, 2020. Due to limited testing at the time, confirmed cases likely reflected just a small fraction of the total number of infections in the state at the time. Thus, the model was initialized with a total number of infections calculated by scaling up the total confirmed cases as of March 22, 2020 to account for undetected cases. Because the probability of infections being detected in Minnesota at that time was highly uncertain, we estimated this parameter by calibrating the model to observed COVID-19 outcomes in Minnesota (described below). It is important to note that this parameter was only used in the initialization of the model and was not used at any point later in the simulation.

Once the total initial number of infections was determined, confirmed cases were assigned to the appropriate state, stratified by age and hospitalization/ICU status. Non-hospitalized confirmed cases were assigned to the last symptomatic state (" $I_n$ ") of the appropriate age stratum. Estimated undetected infections were assigned across the exposed, asymptomatic, and symptomatic infected states and according to each age group based on the age distribution of infections observed in our model when 20,000 cumulative infections were reached. The age distribution at this number of infections was chosen because this was approximately the number of infections predicted to be in Minnesota on March 22, 2020 under input parameter values that resulted in a well-calibrated model. The age distribution of infections was also fairly stable at this point in the epidemic.

### *Non-pharmaceutical interventions*

The model allows for the inclusion of different non-pharmaceutical interventions in the form of contact reduction strategies. We included four different types of contact reduction:

1. Shelter-in-place: equivalent to Minnesota's stay-at-home order, this strategy is assumed to be the most restrictive and have the greatest reduction in contact rates.
2. General social distancing: equivalent to the early measures taken in Minnesota to mitigate COVID-19 spread, including K-12 school closures and work-from-home recommendations.
3. Social distancing among vulnerable: a targeted social distancing strategy in which only those aged 60 years and older are assumed to engage in reduced contact with others.
4. Sustained social distancing: a modest contact reduction that may be sustained once other measures are lifted.

Each strategy is defined in terms of the percentage contact reduction achieved and in which population it applies. All strategies are assumed to result in the same contact reduction for all age groups, except for the social distancing strategy targeted to vulnerable groups. Each strategy can have a different start and end date in the model simulation. End dates for strategies can also be defined as some number of days past the peak of some measurable COVID-19 metric, such as deaths or hospitalizations. In general, specifying overlapping start and end dates for multiple mitigation measures results in the most restrictive measure superseding any other measure. That is, structurally, mitigation strategies cannot be combined for additional benefits. The one exception is the targeted social distancing among vulnerable groups and sustained social distancing. If both strategies are in force at the same time, vulnerable individuals reduce their contacts according to the targeted contact reduction rate, while the rest of the population reduces their contacts according to the sustained behavior change contact reduction rate.

### *Model Calibration*

The model was calibrated to reproduce two key outcomes: the cumulative number of COVID-19 deaths and prevalent COVID-19 hospitalizations recorded in Minnesota from March 23 through April 25, 2020. For the model calibration, the model was parameterized to reflect the timing of the different contact reduction strategies instituted in Minnesota over the calibration time period, which included general social distancing (school closures and recommendations to work from home) in force from March 23 – March 27, 2020, followed by the more restrictive stay-at-home order from March 28, 2020 onward (which is still in effect at the writing of this report). Model input parameters estimated through calibration were the initial proportion of infections detected on March 22, 2020 in Minnesota, the proportion of subclinical infections, the proportion of symptomatically infected individuals aged 80 years and older requiring hospitalization, the probability of symptomatically infected individuals aged 70 years and older dying without ever being hospitalized, the percentage contact reduction resulting from the stay-at-home order, and the percentage contact reduction resulting from social distancing. Plausible ranges for these input parameters are summarized in Table 1. It should be noted that while we only vary the probability of hospitalization among symptomatically infected individuals over the age of 80, this value was then used to calculate the proportion of symptomatically infected people in other age groups by multiplying by the age-specific relative risk of hospitalization, as summarized in Table S3. We assumed the relative risk of hospitalization by age compared to those aged 80 years and over (e.g. risk of hospitalization for 20-29 year-olds vs 80+; 30-39 year-olds vs 80+; etc.) was the same as in a recent CDC report on national COVID-19 outcomes.<sup>14</sup> By calibrating the proportion of symptomatic infections requiring hospitalization in 80+ year-olds (the reference category), we are able to increase or decrease hospitalization probability across all age groups to match observed trends in Minnesota.

The goodness-of-fit of model outputs to observed data was measured using a log-likelihood function. We used the Nelder-Mead optimization algorithm to identify best-fitting parameter sets. We ran the Nelder-Mead algorithm<sup>17</sup> 700 times from different, randomly sampled starting conditions to avoid identifying local maxima. The 700 Nelder-Mead runs yielded 408 unique parameter sets. Because we were estimating multiple parameter values through calibration,

there was not a single, unique best-fitting set of parameter values. Instead, 47% (n=191) of runs yielded parameters sets with log-likelihood values within 5% of the maximum log-likelihood. These 191 parameter sets were retained to generate uncertainty intervals around model-predicted outcomes. For the purposes of the public release of the model code, we have set input parameters to the set of parameter values that approximately yielded median results in model outcomes. This set of parameter values is known as our “base case” parameter set and is summarized in Table 1.

Model-predicted prevalent hospitalizations and cumulative deaths are shown for the base case parameter set in Figures 2 and 3, respectively, alongside the MDH data points used as calibration targets. As a point of validation, the calibrated base case parameters were used to generate estimates of the prevalent number of ICU beds occupied over the same calibration time period, which we compared to observed ICU bed occupancy (Figure 4). It should be noted that the definition of the ICU compartment in this model only includes individuals who need invasive mechanical ventilation, not every individual who is admitted for critical care to the ICU. Among hospitalized patients in New York, the majority of COVID-19 patients in the ICU did receive mechanical ventilation,<sup>7</sup> consistent with expert opinion (personal communication, Dr. John Hick, April 13, 2020).

As a point of validation, we calculated the proportion of deaths occurring outside health care settings (e.g., at home or in congregate living settings) predicted by the model and compared that to death information reported by MDH, which was not used as a calibration target. As of April 25, 2020, the model predicted 69.7% of cumulative deaths to occur outside of health care settings, compared to 65.0% observed in MDH data.

**Table 1: Calibrated Parameter Values and Ranges Used for Calibration**

| Parameter  | Plausible initial range | Calibrated value (base case) |
|--|-------------------------|------------------------------|
| Probability of infection being detected (prior to March 22, 2020)              | 0.001 – 0.100           | 0.021                        |
| Proportion of infections which are asymptomatic or mild                        | 0.20 – 0.60             | 0.41                         |
| Proportion of symptomatic, infected individuals aged 80+ who get hospitalized  | 0.05 – 0.40             | 0.103                        |
| Probability that individuals aged 70+ with a symptomatic infection die at home | 0 – 0.15                | 0.139                        |
| Percentage contact reduction under the stay-at-home order                      | 30% – 85%               | 55.1%                        |
| Percentage contact reduction under social distancing                           | 10% – 50%               | 37.6%                        |

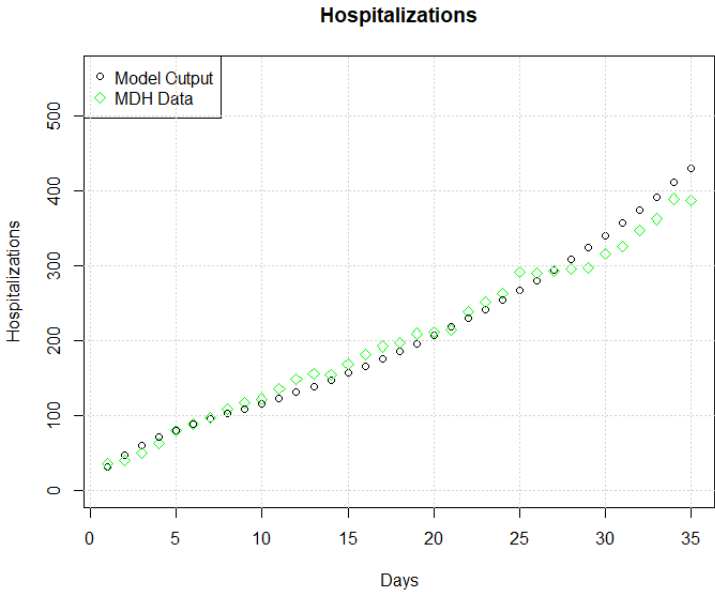


Figure 2: Number of COVID-19 patients receiving care in the hospital from March 22 (day 1) through April 25 (day 35) predicted by the model (black circles) and reported in state surveillance data (green diamonds) from MDH.

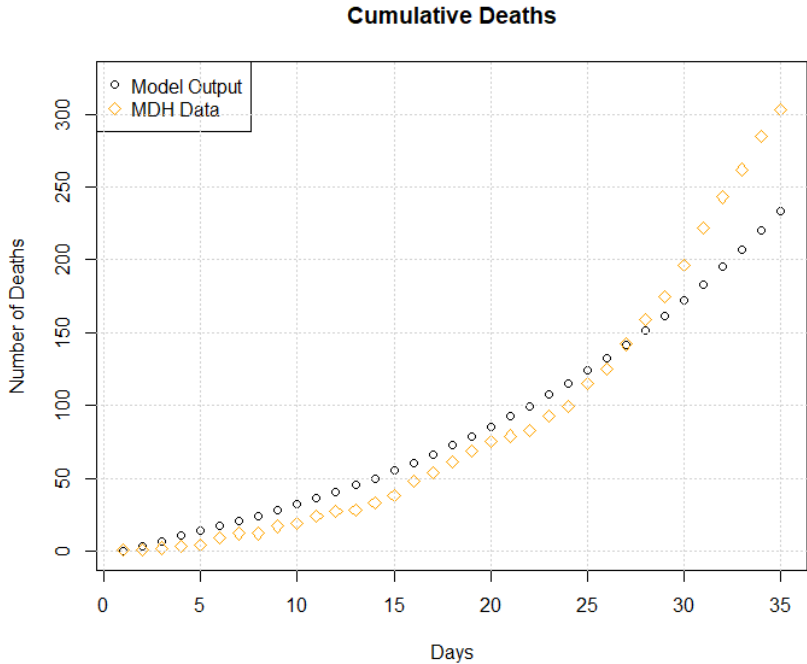


Figure 3: Cumulative number of COVID-19 deaths from March 22 (day 1) through April 25 (day 35) predicted by the model (black circles) and reported in surveillance data (yellow diamonds) from MDH.

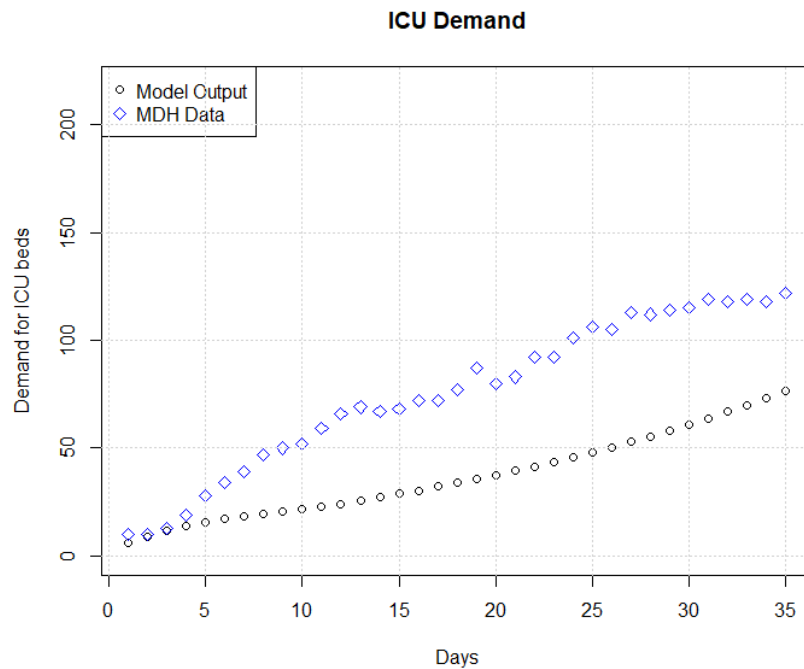


Figure 4: Number of COVID-19 patients receiving care in the ICU from March 22 (day 1) through April 25 (day 35) predicted by the model (black circles) and reported in surveillance data (blue diamonds) from MDH. Note that surveillance data reflect ICU bed occupancy both with and without mechanical ventilation, while ICU demand in the model is parameterized in terms of mechanical ventilation needs.

## Minnesota Mitigation Scenarios

In the code released alongside this documentation, we include several mitigation strategy scenarios that were modeled for the state of Minnesota through May 1, 2020; after that the code was held static to prepare for publication. Although some of the scenarios align roughly with Executive Orders issued by Governor Walz, they should be viewed as hypothetical and static scenarios. This means they represent rough approximations of changes in contact (or lack thereof) and they have been generally designed to end at some point during the summer of 2020. These scenarios should not be viewed as model-derived recommendations – for one, they predict sharp peaks in health care demand and significant mortality – or as likely outcomes of decision-making. Instead, they represent illustrations of different, time-limited mitigation strategies. As noted in the introduction, state leaders are using a variety of data and factors in their decision-making, only one of which are projections from mathematical models.

### *Scenario specifications*

The first scenario (“Scenario 1”) is a no mitigation scenario, projecting outcomes under the assumption that individuals do not reduce their contact with others and that there is no expansion in statewide ICU capacity. All other scenarios include the achieved statewide ICU capacity increase (as of the writing of this report) to 2,200 beds and an initial period of general social distancing (reflecting the policies in effect from March 23 – March 27, 2020 in Minnesota) followed by some period of a shelter-in-place policy (akin to Minnesota’s stay-at-home order that began March 28, 2020). The second scenario (“Scenario 2”) simulates outcomes if the stay-

at-home order had expired after the initially announced two weeks (on April 11, 2020), followed by an additional three weeks of general social distancing. The third scenario (“Scenario 3”) extends the second scenario by including continued social distancing for vulnerable groups (in our model, those 60 aged years and older) until 30 days past the state’s peak in COVID-19 deaths. The fourth scenario (“Scenario 4”) is the same as the third, except that the shelter-in-place policy remains in force for six weeks instead of just two. In these scenarios, general social distancing is defined as reducing contacts by 37.5% across all age groups, while the stay-at-home order is defined as reducing contacts by 55.1% across all age groups, which are the contact reductions we estimated through model calibration. Social distancing among vulnerable groups is assumed to result in a 50% reduction in contacts among those 60 years and older.

### *Uncertainty Analysis*

To generate uncertainty intervals around our model projections for the scenarios described above, we ran the model for each of the 191 “good-fitting” parameter sets retained from the Nelder-Mead calibration. For each parameter set, we generated all model outcomes (cumulative deaths, ICU demand, etc.). We reported the 2.5% and 97.5% percentiles of these outcomes to reflect the uncertainty around our projections. The point estimates given for each scenario are the model-predicted outcomes for the base case parameter set. The base case parameter set was chosen to approximately reflect the median cumulative number of deaths under “Scenario 4” (which most closely reflects policies enacted by state policymakers). Note that generating the uncertainty results is computationally intensive and we have not included this capability in the public code release. Results from the uncertainty analysis are presented in the slides accompanying this release, while the code has default inputs set to base case parameter values, which allows users to generate plots of the base case curves.

## Limitations

- **Published estimates of the basic reproductive number ( $R_0$ ) are highly variable.** The probability of transmission per effective contact is currently estimated by adjusting the model to reflect published values of the  $R_0$  for SARS-CoV-2 under a no mitigation scenario. It is important to note that  $R_0$  can vary by geography and population. Implementation of mitigation strategies also influence rate of infection growth and any empirical estimates of  $R_0$  (or more precisely, the effective reproductive number,  $R_t$ ). We anticipate continual updates to published  $R_0$  values, particularly as more data from the US become available; results of this model will also change accordingly.
- **Death outside of ICU care settings is still poorly understood.** While our model has been expanded to account for mortality that occurs in the hospital setting as well as outside the hospital itself, these mortality risks are uncertain. Estimates may change as the epidemic progresses, and COVID-19 deaths outside of healthcare settings may be undercounted.
- **There is still great uncertainty around proportions of infections that remain undetected or are asymptomatic.** Testing availability for SARS-CoV-2 is suboptimal across the US; more challenging for model-based predictions, however, is the heterogeneity in testing policies across states and over time. In addition, new information is continually emerging regarding

infections acquired from presumably asymptomatic cases. Updates on these epidemiologic features will also necessarily alter estimates generated by this model.

- **The role of asymptomatic infection in contributing to the spread of SARS-CoV-2 is uncertain.** The role of asymptomatic infections and whether and how they contribute to the spread of SARS-CoV-2 is still being determined. Although we have expanded the model to specifically account for asymptomatic infections, the estimated proportion of infections that are asymptomatic remains uncertain. As more robust data become available, this parameter and range will be updated accordingly.
- **The increased risk of death from COVID-19 due to an existing co-morbid condition is not accounted for in this version of the model.** The limited quality and completeness of currently published U.S. data on COVID 19 mortality does not allow us to separately model the increased risk due to underlying co-morbidities. As such, while the majority of people in the ICU who were ventilated had a co-morbidity, in this version of the model we include but do not apply a multiplier. In future iterations, as more robust data become available on specific comorbid conditions and the increased risk of death in the ICU, hospital or other settings become available, we will update our model accordingly.
- **Hotspot outbreaks.** A limitation of our model is that it has been developed to reflect the dynamics of SARS-CoV-2 transmission for Minnesota as a whole. While we are able to reproduce the deaths occurring in the general population, deaths occurring in specialized settings such as nursing homes may be underestimated. We do validate our model's projections by comparing the proportion of deaths occurring out-of-hospital projected by our model against surveillance data and find similar results (69.7% vs. 65.0%). COVID-19 outcomes associated with unique settings, such as nursing homes, would need to be addressed in future iterations.
- **Death rates in and out of hospitals have not been established.** Information on the probability of death (either in ICU, in the hospital but not in the ICU, or at home) is inadequate. Adequate data are not available in U.S. settings. The data we used to parameterize our model from NYU hospital admissions includes cases that have not yet resolved. A number of cases may yet die from COVID-19, in which case our fatality rates could be underestimates.

## Next Steps

In the service of informing decision-making and public interest into the pandemic and its response, the research partnership between the UMN School of Public Health and MDH is committed to continuing to refine and expand this disease model.

This will consist of reviewing the literature and updating parameter estimates on an ongoing basis, which is particularly important as more robust U.S. or Minnesota data (where applicable) become available. The research team is currently exploring ways to make the model useful to a broader set of applications, including accounting for testing and newly available treatments,<sup>18</sup> examining methods for accounting for hotspots such as nursing homes, incorporating information on local contact patterns as these become available, exploring ways to incorporate geographic differences in disease spread and impact, and considering ways to model cyclical mitigation strategies.

## Acknowledgements

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## Appendix

### Equations E1-11

$$dS_{\alpha,\kappa} = -\beta * \lambda_{\alpha} * S_{\alpha,\kappa} \quad (1)$$

$$dE1_{\alpha,\kappa} = \beta * \lambda_{\alpha} * S_{\alpha,\kappa} - \text{prob}(t_E) * E1_{\alpha,\kappa} \quad (2)$$

For states E2-Em the following equation is used:

$$dEn_{\alpha,\kappa} = \text{prob}(t_E) * E(m-1)_{\alpha,\kappa} - \text{prob}(t_E) * En_{\alpha,\kappa} \quad (3)$$

$$dI1_{\alpha,\kappa} = (1 - \text{proportion asymptomatic}) * \text{prob}(t_E) * Em_{\alpha,\kappa} - \text{prob}(t_I) * I1_{\alpha,\kappa} \quad (4)$$

For states I2-In the following equation is used:

$$dIn_{\alpha,\kappa} = \text{prob}(t_I) * I(n-1)_{\alpha,\kappa} - \text{prob}(t_I) * In_{\alpha,\kappa} \quad (5)$$

$$dAI1_{\alpha,\kappa} = (\text{proportion asymptomatic}) * \text{prob}(t_E) * Em_{\alpha,\kappa} - \text{prob}(t_I) * AI1_{\alpha,\kappa} \quad (6)$$

For states AI2-AIn the following equation is used:

$$dAIIn_{\alpha,\kappa} = \text{prob}(t_I) * AI(n-1)_{\alpha,\kappa} - \text{prob}(t_I) * AIIn_{\alpha,\kappa} \quad (7)$$

$$dH_{\alpha,\kappa} = \text{prob}(t_I) * \text{prop}_{\text{hosp},\alpha} * (1 - \text{prop}_{\text{ICU},\alpha}) * In_{\alpha,\kappa} - \text{prob}(t_H) * H_{\alpha,\kappa} \quad (8)$$

$$\begin{aligned} dICU_{\alpha,\kappa} = & \text{prob}(t_I) * \text{prop}_{\text{hosp},\alpha} * \text{prop}_{\text{ICU},\alpha} * In_{\alpha,\kappa} \\ & - \text{prob}(t_{\text{ICU},b}) * (1 - \text{ICU}_{\text{overflow}}) * ICU_{\alpha,\kappa} \\ & - \text{prob}(t_{\text{ICU},n}) * \text{ICU}_{\text{overflow}} * ICU_{\alpha,\kappa} \end{aligned} \quad (9)$$

$$\begin{aligned} dR_{\alpha,\kappa} = & \text{prob}(t_I) * AIIn_{\alpha,\kappa} + \text{prob}(t_I) * (1 - \text{prob}(\text{die}_{I,\alpha,\kappa})) * (1 - \text{prop}_{\text{hosp},\alpha}) * In_{\alpha,\kappa} + \\ & (1 - \text{prob}(\text{die}_{H,\alpha,\kappa})) * \text{prob}(t_H) * H_{\alpha,\kappa} + \\ & (1 - \text{prob}(\text{die}_{\text{ICU},b,\alpha,\kappa})) * \text{prob}(t_{\text{ICU},b}) * (1 - \text{ICU}_{\text{overflow}}) * ICU_{\alpha,\kappa} + \\ & (1 - \text{prob}(\text{die}_{\text{ICU},n,\alpha,\kappa})) * \text{prob}(t_{\text{ICU},n}) * \text{ICU}_{\text{overflow}} * ICU_{\alpha,\kappa} \end{aligned} \quad (10)$$

$$\begin{aligned} dD_{\alpha,\kappa} = & \text{prob}(\text{die}_{\text{ICU},b,\alpha,\kappa}) * \text{prob}(t_{\text{ICU},b}) * (1 - \text{ICU}_{\text{overflow}}) * ICU_{\alpha,\kappa} + \\ & \text{prob}(\text{die}_{\text{ICU},n,\alpha,\kappa}) * \text{prob}(t_{\text{ICU},n}) * \text{ICU}_{\text{overflow}} * ICU_{\alpha,\kappa} + \\ & \text{prob}(\text{die}_{I,\alpha,\kappa}) * \text{prob}(t_I) * (1 - \text{prop}_{\text{hosp},\alpha}) * In_{\alpha,\kappa} + \text{prob}(\text{die}_{H,\alpha,\kappa}) * \text{prob}(t_H) * H_{\alpha,\kappa} \end{aligned} \quad (11)$$

Footnote: The subscripts “I”, “ICU”, and “H” are used to denote when a probability applies only to that state. The subscripts “ $\alpha$ ” and “ $\kappa$ ” indicate a parameter’s dependence on age group or comorbidity group respectively. The subscripts “n” and “b” refer to whether a ventilator is available for those who need one; “n” indicates no ventilator is available, “b” indicates a ventilator is available. For example,  $\text{prob}(\text{die}_{\text{ICU},n,\alpha,\kappa})$  is the probability that someone who needs a ventilator in the ICU when a ventilator is not available will die, and this value is dependent on the age of the person.

**Table S1. Parameter definitions, values, and sources**

| Name                     | Definition   | Estimate  | Data source setting  |
|--------------------------|--|---|--|
| $\beta$                  | Probability that contact with an infectious person results in an infection                       | Calculated using estimates of $R_0$ : 3.87<br><br>(details of $\beta$ calculations in methods section)  | Multiple European countries <sup>14</sup>                          |
| $\lambda$                | Number of contacts per time step that one age group has with infected individuals                | See methods section for calculation   | European countries scaled to US population structure <sup>12</sup> |
| $\text{prob}(t_E)$       | Probability of transitioning through an exposed state at each time step                          | Calculated from estimated mean incubation period: 5.2 days  | China, national <sup>8</sup>                                       |
| $\text{prob}(t_I)$       | Probability of transitioning through an infected state at each time step                         | Calculated using estimated mean time from symptom onset to hospital: 7.8 days                           | United States (14 states) <sup>9</sup>                             |
| $\text{prob}(t_{ICU,b})$ | Probability of transitioning out of the ICU at each time step when a ventilator is available     | Calculated using estimated time from ICU admission to recovery or death: 8 days                         | China (Wuhan) <sup>15</sup>  |
| $\text{prob}(t_{ICU,n})$ | Probability of transitioning out of the ICU at each time step when a ventilator is not available | Calculated assuming that people who need a ventilator but do not get one will spend an average of 1 day | Assumption   |

|  |  |   |                                 |
|--|--|---|---------------------------------|
|  |  | in the ICU compartment  |                                 |
| $\text{prop}_{\text{hosp}}$              | Proportion of symptomatic infections requiring hospitalization   | See table S3  | US, national <sup>16</sup>      |
| $\text{prop}_{\text{ICU}}$               | Proportion of hospitalized individuals who need ICU with ventilator  | See table S3  | US (New York City) <sup>7</sup> |
| $\text{prob}(t_H)$                       | Probability transitioning out of the hospitalized state (per time step)  | Calculated from estimated duration of hospitalization:<br>11 days | China (Wuhan) <sup>15</sup>     |
| $\text{prob}(\text{die}_H)$              | Probability of dying in the hospital when not in need of ICU with ventilation                                    | See table S3  | US (New York City) <sup>7</sup> |
| $\text{prob}(\text{die}_{\text{ICU},b})$ | Probability of dying when ventilated and in the ICU when a bed is accessible                                     | See table S3  | US (New York City) <sup>7</sup> |
| $\text{prob}(\text{die}_{\text{ICU},n})$ | Probability of dying when in the ICU when a ventilator is not accessible   | 1   | Assumption                      |
| $\text{ICU}_{\text{overflow}}$           | Proportion of individuals who require an ICU bed with ventilator but cannot access due to capacity being reached | Calculated, see methods section                                   | Calculated                      |

**Table S2. Age distribution and age-stratified proportion of Minnesotans with one or more underlying conditions.**

| Age group (years) | Population size <sup>i</sup><br>(N) | Proportion of total<br>population <sup>i</sup><br>(%) | 1 or more underlying<br>condition <sup>ii</sup><br>(%) |
|-------------------|-------------------------------------|---|--|
| 0 to 9            | 643,010                             | 11.3  | 1.2  |
| 10 to 19          | 732,001                             | 12.9  | 2.3  |
| 20 to 29          | 731,088                             | 12.9  | 3.8  |
| 30 to 39          | 764,590                             | 13.4  | 6.9  |
| 40 to 49          | 678,395                             | 11.9  | 12.5   |
| 50 to 59          | 717,300                             | 12.6  | 21.4   |
| 60 to 69          | 714,641                             | 12.6  | 30.1   |
| 70 to 79          | 440,582                             | 7.7   | 43.6   |
| 80+               | 265,554                             | 4.7   | 55.9   |

<sup>i</sup>Minnesota State Demographic Center, 2020 projections.<sup>5</sup>

<sup>ii</sup>Minnesota All Payer Claims Database, 2017.<sup>6</sup> Underlying conditions included chronic obstructive pulmonary disease, cardiovascular disease (ischemic heart disease or heart failure), diabetes, poorly managed hypertension, and cancer.

**Table S3. Age-specific hospitalization parameter estimates**

| Age group (years) | Proportion of symptomatic infections requiring hospitalization <sup>i</sup> | Relative proportion of symptomatic cases requiring hospitalization (ref: 80+) <sup>ii</sup> | Proportion of hospitalized cases requiring ICU care (ventilation)<br>prob <sub>(icu)</sub> | Proportion of deaths among hospitalized cases (no ventilator)<br>prob <sub>(die<sub>H</sub>)</sub> | Proportion of deaths among ICU cases ever on a ventilator<br>prob <sub>(die<sub>ICU,b</sub>)</sub> |
|-------------------|---|---|--|--|--|
| 0-9               | 0.0115  | 0.0184  | 0.1304   | 0.0000   | 0.0005   |
| 10-19             | 0.0496  | 0.0793  | 0.1196   | 0.0000   | 0.0424   |
| 20-29             | 0.1234  | 0.1972  | 0.1351   | 0.0003   | 0.1002   |
| 30-39             | 0.2060  | 0.3293  | 0.1711   | 0.0043   | 0.1738   |
| 40-49             | 0.2712  | 0.4333  | 0.2219   | 0.0186   | 0.2633   |
| 50-59             | 0.3206  | 0.5123  | 0.2719   | 0.0365   | 0.3686   |
| 60-69             | 0.3758  | 0.6006  | 0.2962   | 0.0538   | 0.4897   |
| 70-79             | 0.4679  | 0.7477  | 0.2703   | 0.0957   | 0.6267   |
| 80+               | 0.6258  | 1.0000  | 0.1877   | 0.2874   | 0.7795   |

<sup>i</sup>Data on COVID-19 hospitalization rates reported by CDC<sup>16</sup> was used to calculate the relative proportion of symptomatic infections needing hospitalization by age group rather than used as direct input.

<sup>ii</sup>To calculate age-specific hospitalization probabilities,  $\text{prop}_{\text{hosp}}$ , the relative proportion of symptomatic cases by age is multiplied by the calibrated values for the probability of 80+ year-olds who are hospitalized.