Supplementary Material for "An Agent Based Modeling of COVID-19: Validation, Analysis, and Recommendations"

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1. Supplementary Tables for Ford County, Kansas, USA:

Table 1: Part 1 of location-specific data for Ford county including total population, initial cases, average family size, life expectancy, lock-down declaration etc.

Table 2: Part 2 of location-specific data for Ford county including percentage of the total population belonging to different professions.

Table 3: The lower and upper bounds of duration, probability of occurrence, starting and ending times for different tasks performed by an agent in Ford county.

Table 4: Values of different thresholds for Ford county.

2. Supplementary Tables for New York City, USA:

Table 5: Part 1 of location-specific data for New York City including total population, initial cases, average family size, life expectancy, lock-down declaration etc. The values have been scaled to accommodate for a population of 10000 from 8.3 million.

Table 6: Part 2 of location-specific data for New York City including percentage of the total population belonging to different professions.

Table 7: Values of different thresholds for New York City.

Table 8: The lower and upper bounds of duration, probability of occurrence, starting and ending times for different tasks performed by an agent in New York City.

3. Supplementary Tables for Physiological Data

Table 9: Lower and upper bounds of time interval between actions, probability of occurrence, effects on oneself and others etc. Here, min, max and prob refer to minimum, maximum and probability respectively.

4. Scaled-down version of New York City

For conducting our experiments in the case of New York City, we have chosen to run the simulations for 10,000 people. This involves scaling the location-specific input parameters for the smaller population. Table 6 shows that the proportion of people engaged in different professions are supplied as percentages to the model. However, some parameters are adjusted for the population of size = 10000. This can be understood from Table 10.

Table 10: Scaling of parameters for New York City for a population of 10000.

Data pertaining to Table 10 has been collected from various sources.^{1,2,3,4} Moreover, we have considered each working group to contain 10-12 people approximately. In the case of the gatherings, we have considered approximately 100 people or less to be present.

To compare the daily values of effective reproduction number (R_t) of our scaled-down ABM model with an SIR model, we calculate the R_t values for each day using the following formula:

$$
R_t(x) = \frac{\sum\limits_{i \in I(x)} d_i^{out}}{|I(x)|}
$$

Here, $R_t(x)$ denotes the R_t value on day x. $I(x)$ is the set of persons infected on day x. d_i^{out} is the number of secondary infections caused by person *i* . Venkatramanan *et al.* provided a formula for calculating the weekly values of R_t that has been adopted for determining daily values in the above equation.⁵ To remove noise generated by randomness of each day, the R_t curve was smoothened.

The methodology of SIR model:

We have used the well-known SIR model,⁶ which divides the total population into three different compartments, namely *Susceptible*, *Infectious* and *Removed*. We have assumed the total population to be *Susceptible* initially. The rate of change from *Susceptible* to *Infectious* is defined as *Transmission Rate* (β). On the other hand, the rate of change from *Infectious* to *Removed* is termed as *Removal Rate* (ɣ). *Removal Rate* is assumed to be constant over the period of time, while the *Transmission Rate* is assumed to be time-variant. We performed a grid search among the plausible values of *Removal Rate* and the value with maximum likelihood is used as *Removal Rate* henceforth. On the other hand, based on the work of *Kurchaski et al., ⁷* we have modeled transmission (i.e., *Transmission Rate*) as a stochastic random walk process. We have used Sequential Monte Carlo simulation (i.e., Particle Filter),^{8,9} in order to find *Transmission Rate* with time, and consequently **R^t** as well. Sequential Monte Carlo simulation is run 100 times with bootstrap fits to deduce various confidence intervals of \mathbf{R}_t . Our model is fitted with the number of daily confirmed cases. While fitting the model, we have tried to maximize the negative log-likelihood.

Figure 1: $R₁$ curves by ABM model with the scaled-down population (blue) and SIR model with the full population (red) of NYC. The blue curve appears to be similar to the red curve with an RMSE value of 0·4626, although converging to zero sooner than the red curve because of the smaller size of the population.

Figure 1 shows that the R, curves obtained in the ABM and SIR models are consistent, thus supporting the reasoning behind choosing to scale down the parameters of New York City.

The comparison between ABM and SIR models are shown to provide a preliminary validation of our scaled-down ABM model. These two models were run with different population sizes and because of that, the number of infections must be different. But given the characteristics of a certain population, the initial spread pattern in a scaled-down model should keep a resemblance with that of a full sized model. Both R, curves should match during this period. At some point, the susceptible population becomes significantly lower in the scaled-down (ABM) model and it starts to make it difficult for the disease to spread. Then the spread starts to get contained in the scaled-down model due to less susceptible people left, and as a result, from that point, the ABM's R_t goes down before SIR's R_t .

5. References

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