

Rejoinder: “Evaluate the Risk of Resumption of Business for the States of New York, New Jersey and Connecticut via a Pre-Symptomatic and Asymptomatic Transmission Model of COVID-19”

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1 The Implication of the SIHC model

We appreciate the efforts made by Yu et al. (2021) to apply our proposed SIHC model for Iowa state data. We agree with them and Xue et al. (2021) that the SIHC model should be made readily applicable for other states. As a modified version of the SIR model, the SIHC model evaluates the real-time risk of the outbreak by considering the pre-symptomatic and asymptomatic transmission of COVID-19 and the impact of intervention policies. We used the estimated latent number of the infected individuals without being confirmed per 100,000 as of the benchmark criterion for the current magnitude of spread (Figure 6 in the original study) and simulated the hypothetical second outbreak after the resumption at different timing to visualize the potential risk (Figure 7 in the original study). If the number of infected individuals without being confirmed per 100,000 is below 20 in a state, we suppose that this state is ready to resume its business.

2 The Quality of Collected Data

As mentioned by Zhang and Li (2021), the collected confirmed cases were difficult to cover the infections with mild or no symptoms, which may undermine the reliability of modeling estimation and prediction. To take into account these uncertainties, we defined two latent compartments: infectious class without confirmation (I) and self-healing class (H), and estimated them by assuming the hidden dynamic of compartments.

Also, the comparison between the estimated and the observed newly infected individuals was presented (Figure 5 in the original study) to display the impact of the lagging effect, which indicated that the SIHC model could be adequate to identify this kind of disturbance from the

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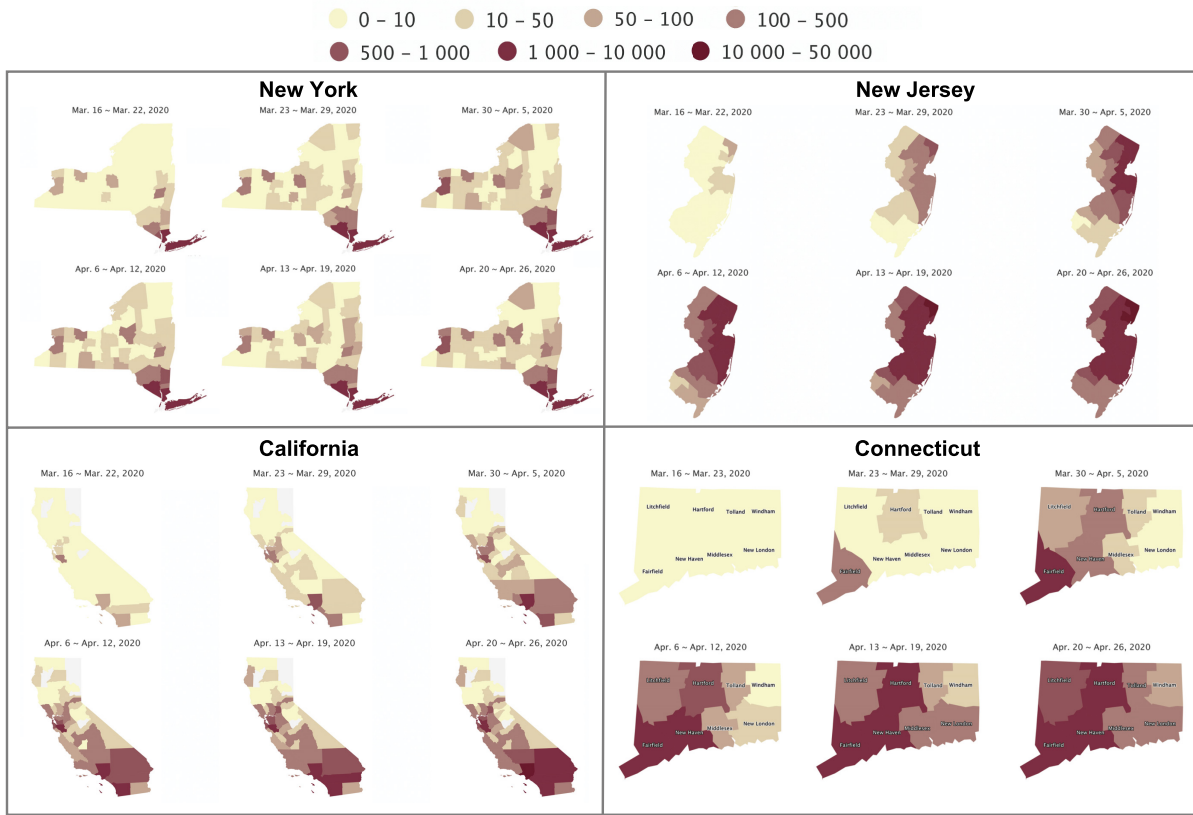


Figure 1: The disease mappings of COVID-19 for the counties of New York, New Jersey, California, and Connecticut.

observed data. In practice, it may not be possible to address the data uncertainty entirely by a mathematical model. Our approach was based on the assumed mechanisms capturing some typical features of COVID-19. Although our assumptions are reasonable, they are also limited.

3 The Spatial Pattern of the COVID-19 Transmission

As discussed by Zhang and Li (2021), Xue et al. (2021), Yu et al. (2021), and Morris and Huang (2021), the spatial heterogeneity of the transmission is crucial to evaluate the outbreak of epidemic for the states in the United States. This is an effective and flexible approach to modeling the epidemic and improving the accuracy of the prediction by considering the spatial correlation. To elaborate this, we present the disease mapping of our targeted states by county-level cumulative confirmed cases in Figure 1:

We observed that there is significant spatial diffusion among the counties network in the four states, which may be caused by the migration of infectious individuals. Based on these considerations, we explored a modification of our SIHC model as follows:

$$\frac{dS^i(t)}{dt} = -\rho_i \theta^i(t) S^i(t) \frac{I^i(t)}{N_i(t)} - \sum_{j \neq i} \omega_{ji} S^i(t) + \sum_{j \neq i} \omega_{ij} S^j(t),$$

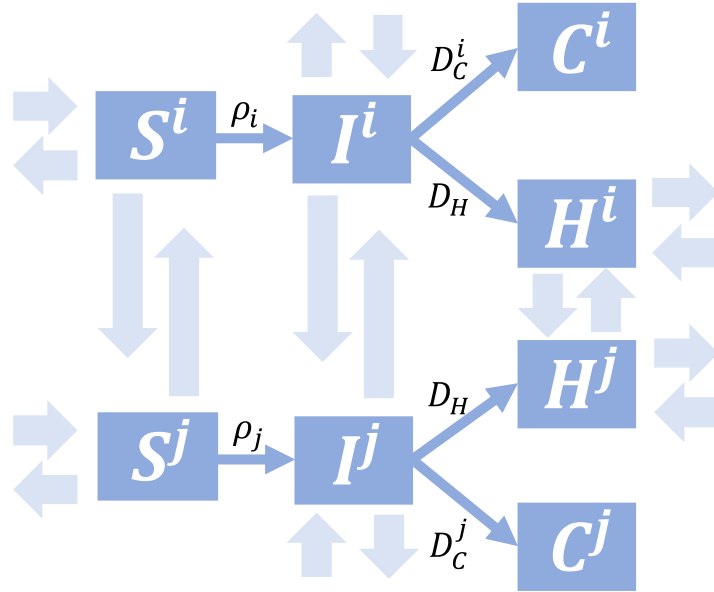


Figure 2: The transition diagram of the compartmental model.

$$\begin{aligned}\frac{dI^i(t)}{dt} &= \rho_i \theta^i(t) S^i(t) \frac{I^i(t)}{N_i(t)} - I^i(t) \left(\frac{1}{D_C^i} + \frac{1}{D_H} \right) - \sum_{j \neq i} \omega_{ji} I^i(t) + \sum_{j \neq i} \omega_{ij} I^j(t), \\ \frac{dH^i(t)}{dt} &= \frac{I^i(t)}{D_H} - \sum_{j \neq i} \omega_{ji} H^i(t) + \sum_{j \neq i} \omega_{ij} H^j(t), \\ \frac{dC^i(t)}{dt} &= \frac{I^i(t)}{D_C^i},\end{aligned}$$

where $S^i(t)$, $I^i(t)$, $H^i(t)$, and $C^i(t)$ are the numbers of individuals in compartments S , I , H , and C in the i^{th} county at time t . ω_{ij} represents the ratio of the removed population in the j^{th} to i^{th} counties. We assume that the removed population in the j^{th} county is uniformly distributed in compartments S , I , and H . The confirmed cases C would stay at home or be isolated in hospital, and hence are immovable. $N_i(t)$, ρ_i , $\theta^i(t)$, D_H , and D_C^i denote the total number of population in the i^{th} county at time t , the transmissibility in i^{th} county, the time-varying average contact numbers per person in the i^{th} county, the mean duration from catching the virus to self-healing without being confirmed, and the mean duration between catching the virus and to being confirmed by testing in the i^{th} county, respectively. The transition diagram of different compartments is presented in Figure 2.

Specifically, $\Omega = (\omega_{ij})$ could be viewed as the weighted adjacent matrix for the spatial network, which could be estimated by the human mobility data (Kraemer et al., 2020) or other spatial characteristics (e.g., the longitude and latitude).

4 Covariates in the SIHC model

As discussed by Morris and Huang (2021) and Quick and Lin (2021), covariates related to the dynamic of the epidemic could be introduced to explain part of the uncertainty of the observed

data. For example, as reported by a previous study, the transmissibility ρ_i , which is defined as the probability to be infected through a contact of an infection, is significantly influenced by the age structure of the population (Davies et al., 2020). The testing rate (mentioned in the original study) of a county is also crucial for D_C^i . Let X_1^i and X_2^i be the vectors of the covariates related to the transmissibility ρ_i and D_C^i . We can use the Bayesian hierarchical model (Bolstad and Curran, 2016) to combine different covariates into the SIHC model and assume that:

$$\begin{aligned}g^{-1}(\mathbb{E}\rho_i) &= (X_1^i)^T \beta_1, \\h^{-1}(\mathbb{E}D_C^i) &= (X_2^i)^T \beta_2,\end{aligned}$$

where g and h are the link functions for modeling the ρ_i and D_C^i by generalized linear models. It is a useful future project to fully implement this idea, and we expect it also to be challenging due to the complex dynamic of COVID-19 transmission.

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