Reaction-diffusion spatial modeling of COVID-19 in Chicago

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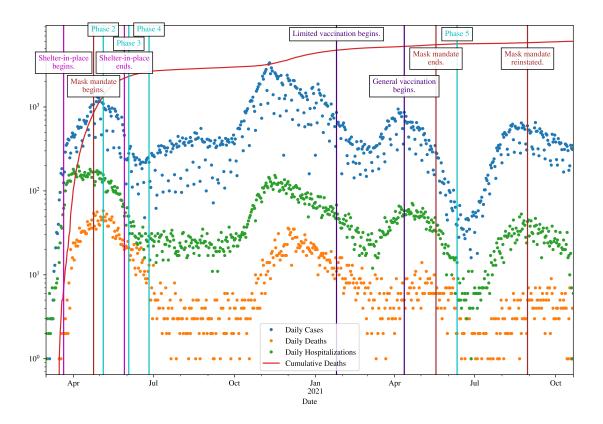


Figure 1: Timeline of the progression of COVID-19 in Chicago with key public policy events marked. The COVID-19 data was obtained from the City of Chicago Data Portal [3]. The dates of the policy events were gathered from the Illinois.gov press releases [9], [7], [8], [10], [6], the Chicago Tribune [2], and NBC Chicago [1]. Note the logarithmic scale.

1 Model Setup

We begin by explaining the ODE model. This is obtained from the full PDE model in Equations (1)-(8) by simply removing the diffusion terms.

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We extend the standard SIR model to incorporate key aspects of the COVID-19 virus.

Given the time scale of the pandemic, we model a weak effect of the change in the susceptible population from births or other mortality factors with the term $-\mu S$. We estimate $\mu = 1.8997 \times 10^{-5}$ [per day] using the average United States death rate in urban regions from 2019 [4].

Table 1: Time sequence of events and simulation times.

Initial simulation time	Imposed lockdown	Effective lockdown	Last fitting day
March 18, 2020	March 21, 2020	April 1, 2020	June 24, 2020
$t_i = 1$	$t_q = 4$	$t_q = 15$	$t_f = 99$

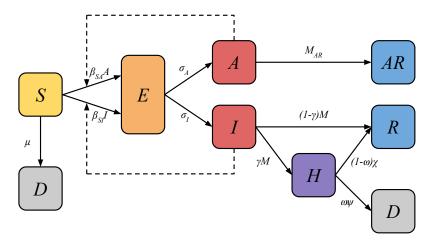


Figure 2: Schematic diagram of the model. The dashed lines indicate the interaction of the infected populations with the susceptible populations that leads to infection.

$$S_t = \mathfrak{D}_S \Delta S - \beta_{SA} SA - \beta_{SI} SI - \mu S, \tag{1}$$

$$E_t = \mathfrak{D}_E \Delta E + \beta_{SA} SA + \beta_{SI} SI - (\sigma_A + \sigma_I) E, \tag{2}$$

$$AR_t = M_{AR}A, (3)$$

$$A_t = \mathfrak{D}_A \Delta A + \sigma_A E - M_{AR} A, \tag{4}$$

$$I_t = \sigma_I E - MI, \tag{5}$$

$$H_t = \gamma M I - (1 - \omega) \chi H - \omega \psi H, \tag{6}$$

$$R_t = (1 - \gamma)MI + (1 - \omega)\chi H,\tag{7}$$

$$D_t = \omega \psi H. \tag{8}$$

To create the PDE model, we first must find suitable parameters using the ODE model as in previous studies. We utilize the MATLAB nonlinear optimization algorithm fminsearch for this purpose. The optimal parameters are determined by minimizing the Euclidean distance \mathcal{N} between the time series generated by the model (subscript "num") and the corresponding observed data time series (subscript "obs")

$$\mathcal{N} = \sum_{i} \left(\left| \ln C_{\text{num}}(t_i) - \ln C_{\text{obs}}(t_i) \right| + \left| \ln D_{\text{num}}(t_i) - \ln D_{\text{obs}}(t_i) \right| \right) \tag{9}$$

where the index i identifies a point in the time series. The parameters are chosen to reproduce the time series of the total number of cases C(t) = I(t) + H(t) + R(t) + D(t), and the total number of deceased D(t).

Table 2: Population values for Chicago. Initial populations are determined from March 13, 2020.

		Population
Total population	N	$2,\!695,\!598$
Initial infected	I_0	162
Initial hospitalized	H_0	38
Initial deceased	D_0	3

To account for changes in virus transmission due to the shelter-in-place order, we impose a time dependence on the transmission rates β as in Equations (10) and (11).

$$\beta_{SI}(t) = \beta_{SI} \left(\eta_{SI} + (1 - \eta_{SI}) \frac{1 - \tanh[2(t - t_q)]}{2} \right)$$
 (10)

$$\beta_{SA}(t) = \beta_{SA} \left(\eta_{SA} + (1 - \eta_{SA}) \frac{1 - \tanh[2(t - t_q)]}{2} \right)$$
(11)

Table 3: ODE parameters: optimal (best-fitting), median and interquartile range, and variation range used in the optimization algorithm. Initial parameter guesses were uniformly sampled within these ranges.

		Median (IQR)	Initial value
Transmission rate, $S \to I$ [per day] ^a	β_{SI}		$c \in \mathcal{U}[0,1]$
Transmission rate, $S \to A$ [per day] ^a	β_{SA}		$c \in \mathcal{U}[0,1]$
Lockdown effect, $S \to I$	η_{SI}		$c \in \mathcal{U}[0,1]$
Lockdown effect, $S \to A$	η_{SA}		$c \in \mathcal{U}[0,1]$
Incubation period, $E \to I$ [days]	$1/\sigma_I$		$1/k, k \in \mathcal{U}[2,7]$
Latent period, $E \to A$ [days]	$1/\sigma_A$		$1/k, k \in \mathcal{U}[2,7]$
Infectivity period [days]	1/M		$1/k, k \in \mathcal{U}[5, 12]$
Recovery period, $A \to AR$ [days]	$1/M_{AR}$		$1/k, k \in \mathcal{U}[5, 12]$
Recovery period, $H \to R$ [days]	$1/\chi$		$1/k, k \in \mathcal{U}[5, 20]$
Period to deceased, $H \to D$ [days]	$1/\psi$		$1/k, k \in \mathcal{U}[5, 20]$
Conversion fraction $(I \xrightarrow{\gamma} H, I \xrightarrow{1-\gamma} R)$	γ		$c \in \mathcal{U}[0.25, 0.75]$
Conversion fraction $(H \xrightarrow{\omega} D, H \xrightarrow{1-\omega} R)$	ω		$c \in \mathcal{U}[0.1, 0.5]$
Initial population fraction, exposed	E_0/I_0		$c \in \mathcal{U}[1,5]$
Initial population fraction, asymptomatic	A_0/I_0		$c \in \mathcal{U}[1,5]$

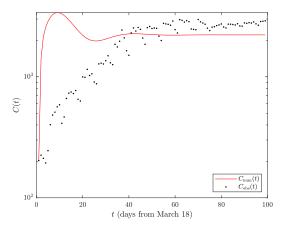
^a Note: The transmission rates β must be divided by N when used in the ODE model.

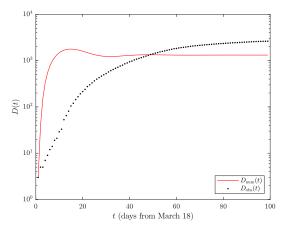
2 ODE Dynamics

We want to understand the trajectories of the dynamics of the ODE system (1)-(8) under different initial conditions. To do this we first find the equilibrium points by solving

$$S_t = E_t = A_t = I_t = H_t = R_t = D_t = 0$$

simultaneously for $\mathbf{x} = (S, E, A, AR, I, H, R, D)^{\intercal}$. The solutions of this system are of the form $\mathbf{x}^* = (0, 0, 0, AR, 0, 0, R, D)^{\intercal}$. This implies there are infinitely many non-isolated equilibrium points. We determine the stability of these equilibrium points by analyzing the linearized system near the





- (a) Confirmed cases C(t) = I(t) + R(t) + H(t) + D(t).
- (b) Number of deaths D(t).

Figure 3: ODE model with fitting to official data from March 18, 2020 ($t_i = 1$) to June 24, 2020 ($t_f = 99$). Here we show the case when β changes exactly on the imposed lockdown on March 21, 2020 ($t_q = 4$).

points. The Jacobian of the system is

$$\mathsf{J} = \begin{pmatrix} -A\beta_{SA} - I\beta_{SI} - \mu & 0 & -S\beta_{SA} & 0 & -S\beta_{SI} & 0 & 0 & 0 \\ A\beta_{SA} + I\beta_{SI} & -\sigma_A - \sigma_I & S\beta_{SA} & 0 & S\beta_{SI} & 0 & 0 & 0 \\ 0 & \sigma_A & -M_{AR} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & M_{AR} & 0 & 0 & 0 & 0 & 0 \\ 0 & \sigma_I & 0 & 0 & -M & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & M\gamma & -\chi(1-\omega) - \psi\omega & 0 & 0 \\ 0 & 0 & 0 & 0 & M(1-\gamma) & \chi(1-\omega) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \psi\omega & 0 & 0 \end{pmatrix}. \tag{12}$$

Now evaluating J at the equilibrium point \mathbf{x}^* and calculating the eigenvalues, we have

$$\lambda = \{0, 0, 0, -M, -M_{AR}, -\mu, -\sigma_A - \sigma_I, -\chi + \chi \omega - \psi \omega\}. \tag{13}$$

Note that the first three eigenvalues are 0, which implies the equilibrium points are non-isolated. This agrees with our earlier observation.

The equilibrium points are stable when $\lambda_i < 0$ for $4 \le i \le 8$. Since all the system parameters are positive, this implies $\lambda_i < 0$ for $4 \le i \le 7$. Thus the stability depends on the sign of λ_8 . There are two cases when $\lambda_8 = -\chi + \chi \omega - \psi \omega < 0$ is true:

- 1. $0 < \omega \le 1$ implies $\lambda_8 < 0$, and
- 2. $\omega > 1$ and $\chi < \frac{\psi \omega}{\omega 1}$ implies $\lambda_8 < 0$.

That is, whenever we have either of these conditions the equilibrium points are stable. If $\lambda_8 > 0$, the equilibrium points are unstable.

We can further analyze the evolution of the pandemic by calculating the basic reproduction number R_0 . We use the next generation matrix approach of the system (1)-(8) without the spatial terms, as in [5] and [11]. In particular, we rewrite the model in the form $\mathbf{x}_t = \mathbf{F} - \mathbf{V}$. The components F_i represents the rate of appearance of new infections in compartment i. The vector $\mathbf{V} = \mathbf{V}^- - \mathbf{V}^+$, where V_i^+ represents the rate of transfer of individuals into compartment i by all other means, and V_i^- represents the rate of transfer of individuals out of compartment i. Reordering the compartments so $\mathbf{x}_t' = (E_t, A_t, I_t, H_t, S_t, AR_t, R_t, D_t)^{\intercal}$, we have

$$\mathbf{F} = \begin{pmatrix} \beta_{SA}SA + \beta_{SI}SI \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, \qquad \mathbf{V} = \begin{pmatrix} (\sigma_A + \sigma_I)E \\ -\sigma_AE + M_{AR}A \\ -\sigma_IE + MI \\ -\gamma MI + (1 - \omega)\chi H + \omega\psi H \\ \beta_{SA}SA + \beta_{SI}SI + \mu S \\ M_{AR}A \\ -(1 - \gamma)MI - (1 - \omega)\chi H \\ -\omega\psi H \end{pmatrix}.$$

We focus on just the infectious/infected compartments, E, A, I, H, and find the Jacobians of \mathbf{F} and \mathbf{V} with respect to these populations in the order in which they appear. Evaluating at the the disease-free equilibrium $(S = S^*, E = AR = A = I = H = R = D = 0)$ yields

The matrix FV^{-1} is the next-generation matrix. Then $R_0 = \rho(FV^{-1})$, which is

$$R_0 = \frac{\beta_{SA} S^* \sigma_A}{m_{AR}(\sigma_A + \sigma_I)} + \frac{\beta_{SI} S^* \sigma_I}{M(\sigma_A + \sigma_I)}.$$
 (14)

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