Reaction-diffusion spatial modeling of COVID-19 in Chicago

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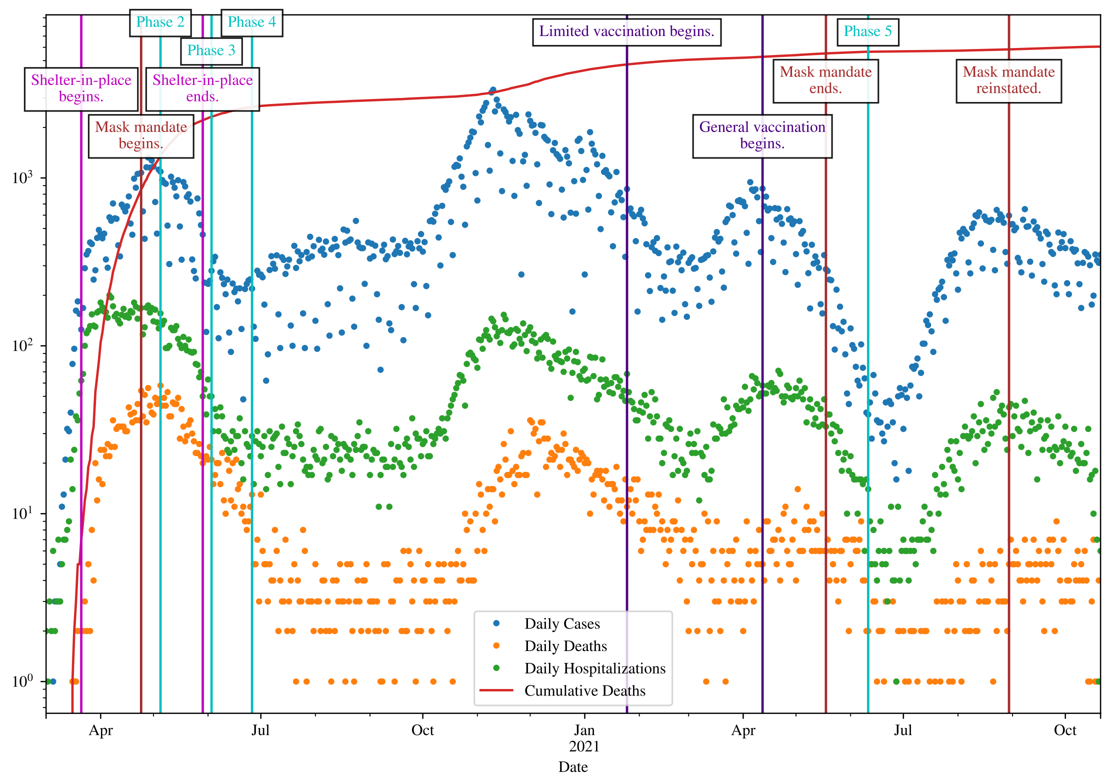

Figure 1: Timeline of the progression of COVID-19 in Chicago with key public policy events marked. The COVID-19 data was obtained from the City of Chicago Data Portal [3]. The dates of the policy events were gathered from the Illinois.gov press releases [9], [7], [8], [10], [6], the Chicago Tribune [2], 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 (2)-(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
$t_i = 1$	$t_q = 4$	$t_q = 15$	$t_f = 99$

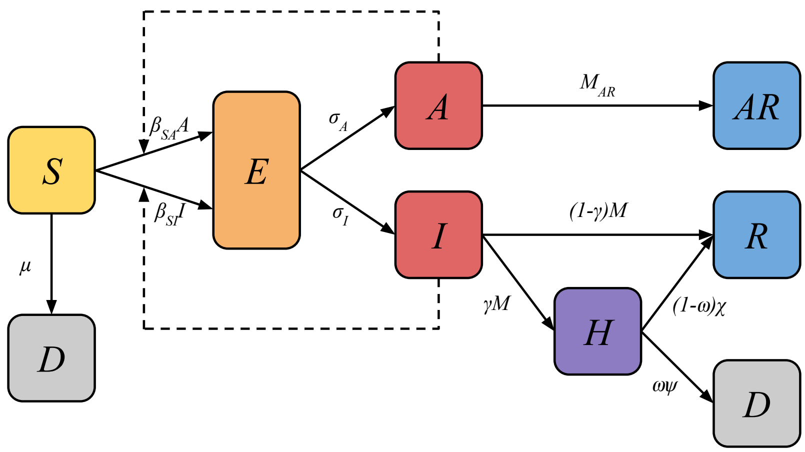


Figure 2: Schematic diagram of the model. The dashed lines indicate the interaction of the infected populations with the susceptible populations that leads to infection.

$$
\begin{aligned}
S_t &= \mathfrak{D}_S \Delta S - \frac{\beta_A A}{N} S - \frac{\beta_I I}{N} S - \mu S, \\
E_t &= \mathfrak{D}_E \Delta E + \frac{\beta_A A}{N} S + \frac{\beta_I I}{N} S - (\sigma_A + \sigma_I) E, \\
AR_t &= M_{AR} A, \\
A_t &= \mathfrak{D}_A \Delta A + \sigma_A E - M_{AR} A, \\
I_t &= \sigma_I E - M I, \\
H_t &= \gamma M I - (1-\omega)\chi H - \omega \psi H, \\
R_t &= (1-\gamma) M I + (1-\omega)\chi H, \\
D_t &= \omega \psi H.
\end{aligned}
$$

We begin by reducing the model. First, we ignore non-COVID deaths, so $\mu = 0$. Next we introduce the fractions

$$
\begin{aligned}
s &= \frac{S}{N}, & e &= \frac{E}{N}, & ar &= \frac{AR}{N}, & a &= \frac{A}{N}, \\
i &= \frac{I}{N}, & h &= \frac{H}{N}, & r &= \frac{R}{N}, & d &= \frac{D}{N}.
\end{aligned}
$$

With these fractions and $\mu = 0$, we have the conservation law

$$
s + e + ar + a + i + h + r + d = 1. \tag{1}
$$

The ODE system becomes

$$
\begin{aligned}
s_t &= -\beta_A a s - \beta_I i s,\\
e_t &= \beta_A a s + \beta_I i s - (\sigma_A + \sigma_I)e,\\
ar_t &= M_{AR} a,\\
a_t &= \sigma_A e - M_{AR} a,\\
i_t &= \sigma_I e - M i,\\
h_t &= \gamma M i - (1-\omega)\chi h - \omega\psi h,\\
r_t &= (1-\gamma) M i + (1-\omega)\chi h,\\
d_t &= \omega\psi h.
\end{aligned}
$$

At this point it is worth noting the dimensions of the components of the system. Since $[X] =$ population where $X \in \{N, S, E, AR, A, I, H, R, D\}$, then $[x] = 1$ where $x \in \{s, e, ar, a, i, h, r, d\}$. Then,

$$[\beta_A] = [\beta_I] = [\sigma_A] = [\sigma_I] = [M_{AR}] = [M] = [\chi] = [\psi] = \frac{1}{T}$$

and $[\omega] = [\gamma] = 1$. We introduce the non-dimensional time variable $\tau = tM$. Then by the chain rule, $x_t = M x_\tau$. Next, we define the following non-dimensional parameters

$$
\begin{aligned}
\alpha_A &= \frac{\beta_A}{M}, & \alpha_I &= \frac{\beta_I}{M}, & \lambda_A &= \frac{\sigma_A}{M}, & \lambda_I &= \frac{\sigma_I}{M},\\
\eta &= \frac{M_{AR}}{M}, & \theta &= \frac{\chi}{M}, & \kappa &= \frac{\psi}{M}.
\end{aligned}
$$

Using these non-dimensional parameters and the conservation law in Equation 1, we can replace the ODE system with

$$
\begin{aligned}
s_\tau &= -\alpha_A a s - \alpha_I i s, &(2)\\
e_\tau &= \alpha_A a s + \alpha_I i s - (\lambda_A + \lambda_I)e, &(3)\\
ar_\tau &= \xi a, &(4)\\
a_\tau &= \lambda_A e - \xi a, &(5)\\
i_\tau &= \lambda_I e - i, &(6)\\
r_\tau &= (1-\gamma) i + (1-\omega)\theta h. &(7)
\end{aligned}
$$

Then by the conservation law, we have

$$d = n - (s + e + ar + a + i + r). \tag{8}$$

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")

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

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).

$$\beta_I(t) = \beta_I \left(\eta_I + (1 - \eta_I) \frac{1 - \tanh[2(t - t_q)]}{2} \right) \tag{10}$$

$$\beta_A(t) = \beta_A \left(\eta_A + (1 - \eta_A) \frac{1 - \tanh[2(t - t_q)]}{2} \right) \tag{11}$$

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.

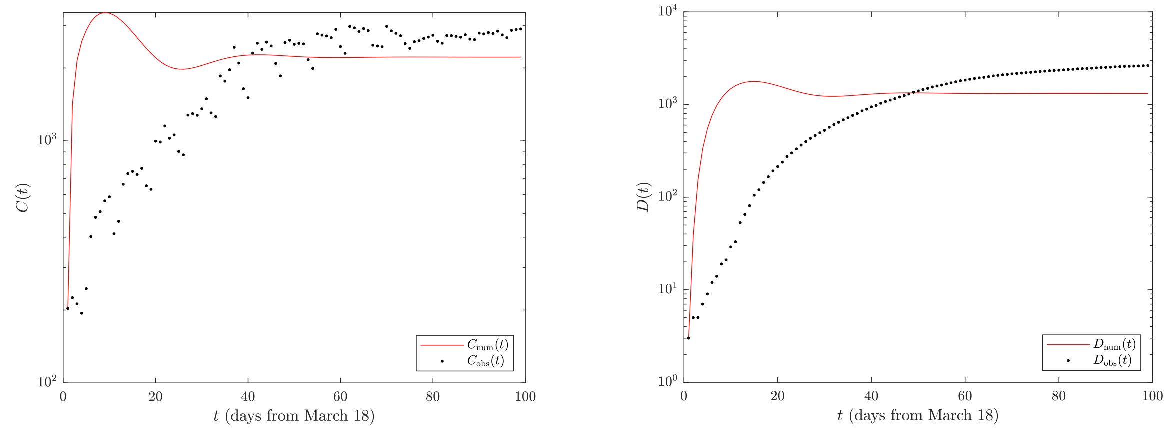
		Median (IQR)	Initial value
Transmission rate, $S \to I$	β_I		$c \in \mathcal{U}[0,1]$
Transmission rate, $S \to A$	β_A		$c \in \mathcal{U}[0,1]$
Lockdown effect, $S \to I$	η_I		$c \in \mathcal{U}[0,1]$
Lockdown effect, $S \to A$	η_A		$c \in \mathcal{U}[0,1]$
Incubation period, $E \to I$ [days]	$1/\sigma_I$		$1/k, k \in \mathcal{U}[2,7]$
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		$c \in \mathcal{U}[1,5]$

2 ODE Dynamics

We want to understand the trajectories of the dynamics of the ODE system (2)-(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 $4 \leq i \leq 8$. Since all the system parameters are positive, this implies $\lambda_i < 0$ for $4 \leq i \leq 7$. 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. $0 < \omega \leq 1$ 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 (2)-(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

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

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

$$\mathsf{F} = \begin{pmatrix} 0 & \beta_{SA}S^* & \beta_{SI}S^* & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \qquad \mathsf{V} = \begin{pmatrix} \sigma_A + \sigma_I & 0 & 0 & 0 \\ -\sigma_A & M_{AR} & 0 & 0 \\ -\sigma_I & 0 & M & 0 \\ 0 & 0 & -\gamma M & \chi(1-\omega) + \psi\omega \end{pmatrix}.$$

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

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

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