Reaction-diffusion spatial modeling of COVID-19 in Chicago

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Abstract

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1 Introduction

2 Materials and methods

2.1 Confirmed and death data

In this study, we used the publicly available data set of COVID-19 provided by the City of Chicago Data Portal [2]. This data set includes daily counts of confirmed infected cases, hospitalizations, and deaths.

2.2 Mathematical model

We focus our study on four components of the epidemic flow (Figure 1). That is, the populations of Susceptible individuals (S), Asymptomatic infected individuals (A), symptomatic Infected individuals (I), and Removed individuals (R). Our model is known as the SAIR model [1], which
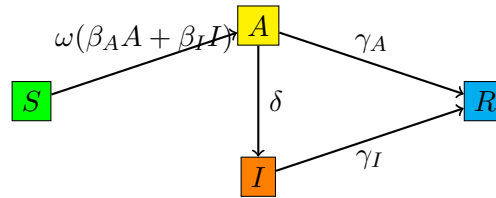

Figure 1: Compartmental representation of the SAIR model.

substitutes the E compartment of the SEIR model by the A compartment. This model is relevant when there are many undetected asymptomatic infectious individuals, which is known to be the case for COVID-19.

We motivate the use of this simple model for the following reasons:

- We do not consider the E group in this work because we feel this population can be merged with the A group.

- We do not distinguish between quarantined, hospitalized, or nursing-home populations. Including these additional compartments would over parameterize the model. Additionally, the way in which data has been collected and is provided by authorities has varied over time,

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making its usage rather difficult [6]. For the same reasons, we do not distinguish between deceased and recovered.

To build the mathematical model, we followed the standard strategy developed in the literature concerning SIR models [3]. We assume that individuals in S can be infected by both members of A and I. We suppose that the individuals in the A and I compartments may have different contact rates β_A and β_I, and different recovery rates γ_A and γ_I. Furthermore, we consider a rate δ at which individuals in A may develop symptoms or are otherwise detected and so will move to the I compartment. Lastly, we assume that only members of S and A are mobile.

The dynamics is governed by a system of two partial differential equations (PDE) and two ordinary differential equations (ODE) as follows, for $\mathbf{x} = (x, y) \in \Omega \subset \mathbf{R}^2, t > 0$,

$$
\begin{aligned}
S_t - D(t)\Delta S &= -\omega(t)\frac{\beta_A A + \beta_I I}{N}S, \\
A_t - D(t)\Delta A &= \omega(t)\frac{\beta_A A + \beta_I I}{N}S - (\gamma_A - \delta)A, \\
I_t &= -\gamma_I I + \delta A, \\
R_t &= \gamma_A A + \gamma_I.
\end{aligned}
\tag{1}
$$

Since travel into the city of Chicago was heavily restricted for the early stages of the pandemic, the homogeneous Neumann boundary condition is imposed [5]. The population compartments are considered fractions, such that $S + A + I + R = 1$.

2.3 Parameter estimation

To account for the lockdown, the average number of of contacts is updated as in [4]

$$
\omega(t) = \omega_0 \left[\eta + (1 - \eta)\frac{1 - \tanh\left[2(t - t_q)\right]}{2} \right].
\tag{2}
$$

Here, $t_q = (t_{\text{eol}} + t_{\text{bol}})/5$, where bol denotes the beginning of the lockdown and eol denotes the end of the lockdown. The parameter $0 \leq \eta \leq 1$ is a varying coefficient translating respect for social distancing and other preventative measures. Note that ω_0 is the average number of contacts before any intervention, and is a constant.

The parameters ω_0, β_A, and β_I are not independently identifiable, so the optimization problem reduces to five parameters $\theta = (\omega_0\beta_A, \omega_0\beta_I, \delta, \gamma_A, \gamma_I)$. Given, for n days, the observations $I_{\text{obs}}(t_i)$, the objective function is the least square function

$$
J(\theta) = \sum_{i=1}^{n} \left[I_{\text{obs}}(t_i) - I(t_i)\right]^2
\tag{3}
$$

with constraints $0 \leq \theta \leq 1$. $I(t_i)$ denotes the output of the mathematical model at time t_i computed with parameters θ.

The optimization problem is solved using the MATLAB nonlinear optimization function `fmincon`. The initial parameter guesses to seed `fmincon` were randomly sampled from a uniform distribution over 1000 iterations. The median of each resulting parameter was selected. Figure 2 shows the estimated parameters.

2.4 Numerical discretization

while the diffusion coefficient is

$$
D(t) = D_0 - \eta H(t - t_q)
\tag{4}
$$

where $H(t)$ is the Heaviside step function.

3 Results

3.1 Existence of solutions and basic reproduction numbers

We show that we are justified in searching for suitable parameters to solve the model. Let $\mathbf{x} = (S, A, I, R)$ and $\mathbf{x}_0 = (S_0, A_0, I_0, R_0)$. First we show that the solution of the initial value problem (1) exists for the case with no diffusion.

Theorem 1. *Let $0 \leq \mathbf{x}_0 \leq N$ be the initial datum. Then there exists a unique in time solution $\mathbf{x}$ of the initial value problem (1) without diffusion over $C \subset U \subset \mathbf{R}^4 \times \mathbf{R}^1$ where C is a compact set that contains $(\mathbf{x}_0, t_0)$. Moreover, the solution is $\mathbf{C}^1$.*

Proof. Since $\mathbf{x}_t = f(\mathbf{x}, t)$ is $\mathbf{C}^1$ on the open set $U \subset \mathbf{R}^4 \times \mathbf{R}^1$, it follows that there exists a solution of (1) without diffusion through the point $\mathbf{x}_0$ at $t = t_0$ for $|t - t_0|$ sufficiently small. Moreover, $\mathbf{x}(t, t_0, \mathbf{x_0})$ is a $\mathbf{C}^1$ function [7]. Since C is a compact set containing $(\mathbf{x}_0, t_0)$, then the solution $\mathbf{x}(t, t_0, \mathbf{x_0})$ can be uniquely extended backward and forward in t up to the boundary of C [7]. $\square$

We do provide a proof for the existence of solutions to the initial boundary value problem (1) with diffusion terms, but we assume it exists.

Conjecture 1. *Let $0 \leq \mathbf{x}_0 \leq N$ the initial datum. Then there exists a unique global in time solution $\mathbf{x}$ of the initial boundary value problem (1).*

A proof for this conjecture will be similar to the one given in [5].

An important parameter in understanding the initial growth of the virus is the basic reproduction number.

Definition 1 (Basic Reproduction Number). *The basic reproduction number $\mathcal{R}_0$ can be computed using the next generation of the model without diffusion. Since the infected individuals are in A and I, new infections ($\mathcal{F}$) and transitions between compartments ($\mathcal{V}$) can be rewritten as*

$$\mathcal{F} = \begin{pmatrix} \omega(\beta_A A + \beta_I I)S \\ 0 \end{pmatrix}, \qquad \mathcal{V} = \begin{pmatrix} (\gamma_A + \delta)A \\ \gamma_I - \delta A \end{pmatrix}.$$

Thus, $\mathcal{R}_0 = \rho(\mathsf{F}\mathsf{V}^{-1})$ of the next generation matrix

$$\mathsf{F}\mathsf{V}^{-1} = \begin{pmatrix} \frac{S_0 \omega_0 \beta_A}{\gamma_A + \delta} + \frac{S_0 \omega_0 \beta_I \delta}{\gamma_I(\gamma_A + \delta)} & \frac{S_0 \omega_0 \beta_I}{\gamma_I} \\ 0 & 0 \end{pmatrix}.$$

So,

$$\mathcal{R}_0 = \frac{S_0 \omega_0}{\gamma_A + \delta}\left(\beta_A + \beta_I \frac{\delta}{\gamma_I}\right). \tag{5}$$

This number is dimensionless and has an epidemiological meaning. The first term represents the transmission rate by asymptomatic individuals, and the second term represents the transmission rate by symptomatic individuals.

3.2 Model resolution

Calibration of the model is done from March 18, 2020 to June 24, 2020. This range corresponds approximately to the first "wave" of cases seen in Chicago. The lockdown time points match exactly to the imposed lockdown of the city. That is, $t_{\text{bol}} = $ March 21, 2020 and $t_{\text{eol}} = $ May 29, 2020.

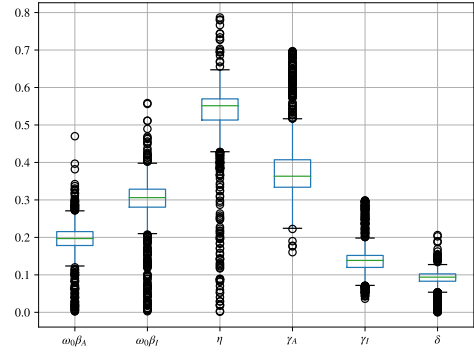|			
$\omega_0\beta_A$	transmission rate due to A	0.1969	days^{-1}
$\omega_0\beta_I$	transmission rate due to I	0.3061	days^{-1}
η	lockdown scale factor	0.5514	1
δ	symptom onset rate	0.0939	days^{-1}
γ_A	removal rate of A	0.3632	days^{-1}
γ_I	removal rate of I	0.1385	days^{-1}

Figure 2: Parameters calibrated according to data from the Chicago Data Portal. On the right is a boxplot of the parameter distribution from 1000 optimization iterations.
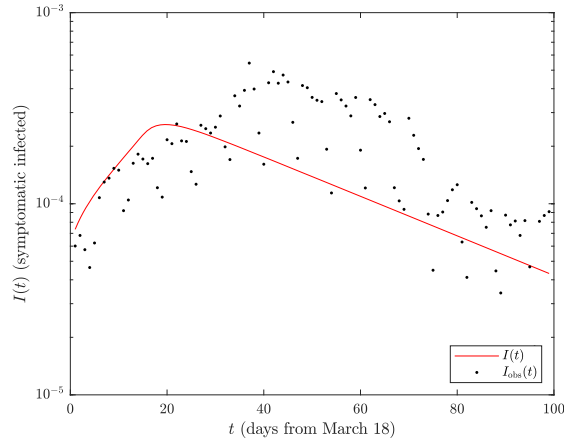

Figure 3: Fitting symptomatic infected by the median value. Note the logarithmic scale on the y-axis.

3.3 Spatial spread of COVID-19

4 Discussion

Conflicts of Interest:

Appendix

Nomenclature (Units are indicated in brackets.)

Latin symbols

A	Asymptomatic infected individuals	[individuals]
D	Diffusivity	
I	Symptomatic infected individuals	[individuals]
N	Total population of individuals	[individuals]

R	Removed individuals	[individuals]
S	Susceptible individuals	[individuals]
Greek symbols		
β_j	Contact rate of compartment j	[days^{-1}]
γ_j	Recovery rate of compartment j	[days^{-1}]
δ	Rate of asymptomatic individuals that may develop symptoms	[days^{-1}]
ω	Contacts	

References

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