

# A PDE Model for Epidemics

Jim Toledo

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## 1 Introduction

Differential equations have been widely used in the field of biology and epidemiology to model various aspects of the environment, including the change in population of various species, climate change, and the spread of infectious diseases. In particular, the spread of infectious diseases is commonly modeled by dividing the population up into labeled compartments and writing a system of ordinary differential equations representing how each compartment interacts with each other. One of the simplest compartmental models for modeling an epidemic is the SIR model, which contains three compartments: susceptible individuals, who are not currently infected but may become infected when contacted by an infectious individual; infectious individuals, who are currently infected and may infect any susceptible individuals they come in contact with; and removed individuals, who have either recovered or died from the disease.

While ODE compartmental models can give valuable information on the spread of disease within an entire population group, a PDE-based compartmental model may give further insight into how a disease may spread geographically as populations naturally diffuse. In this study, we describe a primitive model forecasting the spread of COVID-19 in a bounded rectangular region. This model is a slight simplification of a model from Viguerie et al. (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7361091/>). The main difference is that this model only describes linear diffusion whereas the original model has heterogeneous diffusion.

## 2 The Model

Let  $\Omega$  be a rectangular spatial domain and  $[0, T]$  be a generic time interval. We denote  $s(x, y, t)$ ,  $e(x, y, t)$ ,  $i(x, y, t)$ ,  $r(x, y, t)$ , and  $d(x, y, t)$  as functions representing the number of susceptible, exposed, infected, recovered, and deceased individuals, respectively. Also, we let  $n(x, y, t) = s(x, y, t) + e(x, y, t) + i(x, y, t) + r(x, y, t)$  denote the sum of the living population. Then, the model consists of the following system of coupled PDEs over  $\Omega \times [0, T]$ :

$$s_t = \alpha n - (1 - A/n)\beta_i si - (1 - A/n)\beta_e se - \mu s + D_s \Delta s \quad (1)$$

$$e_t = (1 - A/n)\beta_i si + (1 - A/n)\beta_e se - \delta e - \phi_e e - \mu e + D_e \Delta s \quad (2)$$

$$i_t = \delta e - \phi_d i - \phi_r i - \mu i + D_i \Delta s \quad (3)$$

$$r_t = \phi_r i + \phi_e e - \mu r + D_r \Delta r \quad (4)$$

$$d_t = \phi_d i \quad (5)$$

where  $\alpha$  is the birth rate,  $\delta$  is the inverse of the incubation period,  $\phi_e$  is the asymptomatic recovery rate,  $\phi_r$  is the infected recovery rate,  $\phi_d$  is the infected mortality rate,  $\beta_e$  is the asymptomatic contact rate,  $\beta_i$  is the symptomatic contact rate,  $\mu$  is the general (non-COVID) death rate, and  $D_s, D_e, D_i$ , and  $D_r$  are the diffusivity constants corresponding to the different population groups.  $A$  represents the Allee effect, which, in this setting, models the tendency of outbreaks to cluster towards larger population centers. In general, the propensity for viral transmissions is small for smaller populations and large for larger populations.

We see the presence of the exposed compartment  $e$ , which reflects how asymptomatic individuals exposed COVID may still transmit the virus to susceptible individuals at the contact rate  $\beta_e$ . Also, some exposed patients, represented by  $\phi_e$ , may immediately recover without developing any symptoms. This model assumes that recovered individuals are immune and cannot be reinfected, which is currently a topic of debate. We also see that the populations diffuse at a constant rate depending on the compartment they are in. It is expected that the diffusion rate for infected individuals be significantly lower than the others. Besides the exposed class, the diffusion term, and the Allee effect (shown by the  $1 - A/n$  multiplier), the rest of the terms in this system are standard for an ODE compartmental model for a pandemic.

### 3 Numerical Interpretation

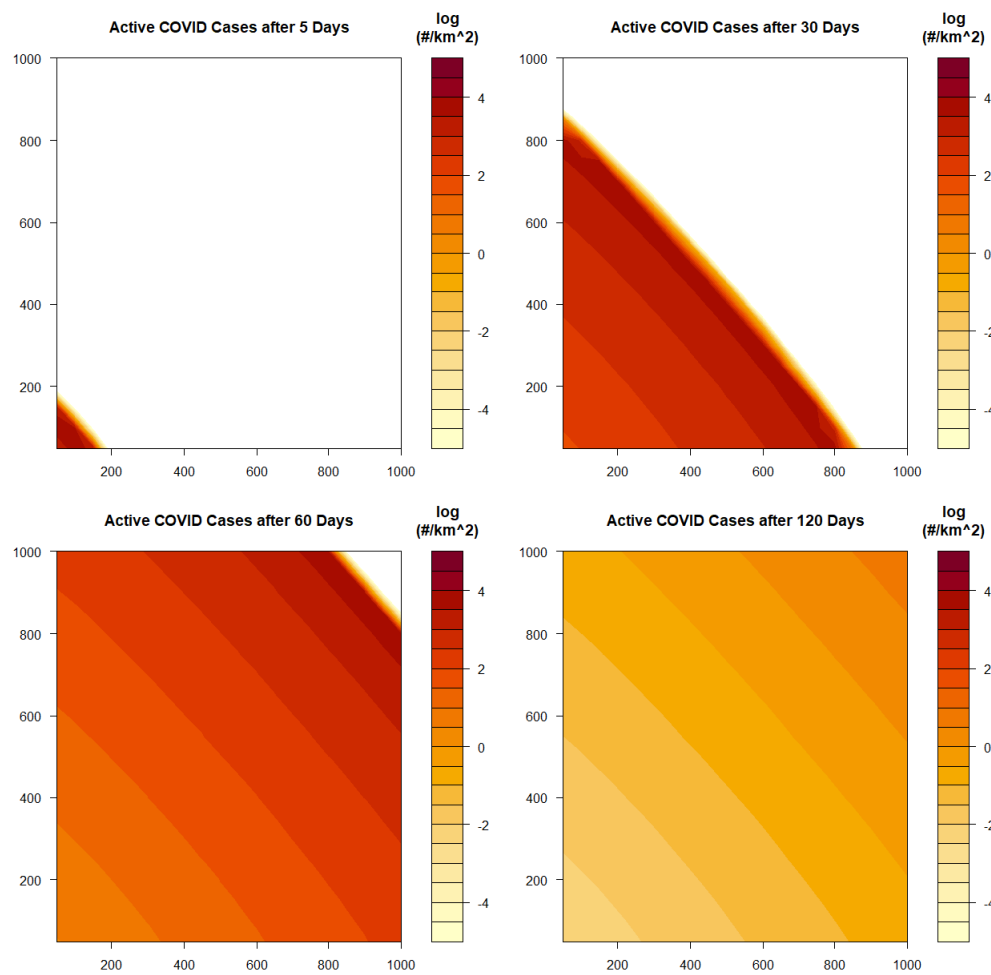
Due to the nature of the compartmental model with various different interactions along with the diffusion term, it would be very difficult to come up with an analytical solution for this model. Thus, we use numeric methods to solve the PDEs for the given region and time interval. For this analysis, we will let  $\Omega$  be a  $1000 \times 1000 \text{ km}^2$  rectangle discretized into a  $20 \times 20$  grid, and we let our time interval be 120 days with discrete time steps of 1 day. We use the *ReacTran* package from R to estimate the diffusion term and we solve the system using the *lsodes* method from the package *deSolve* in R.

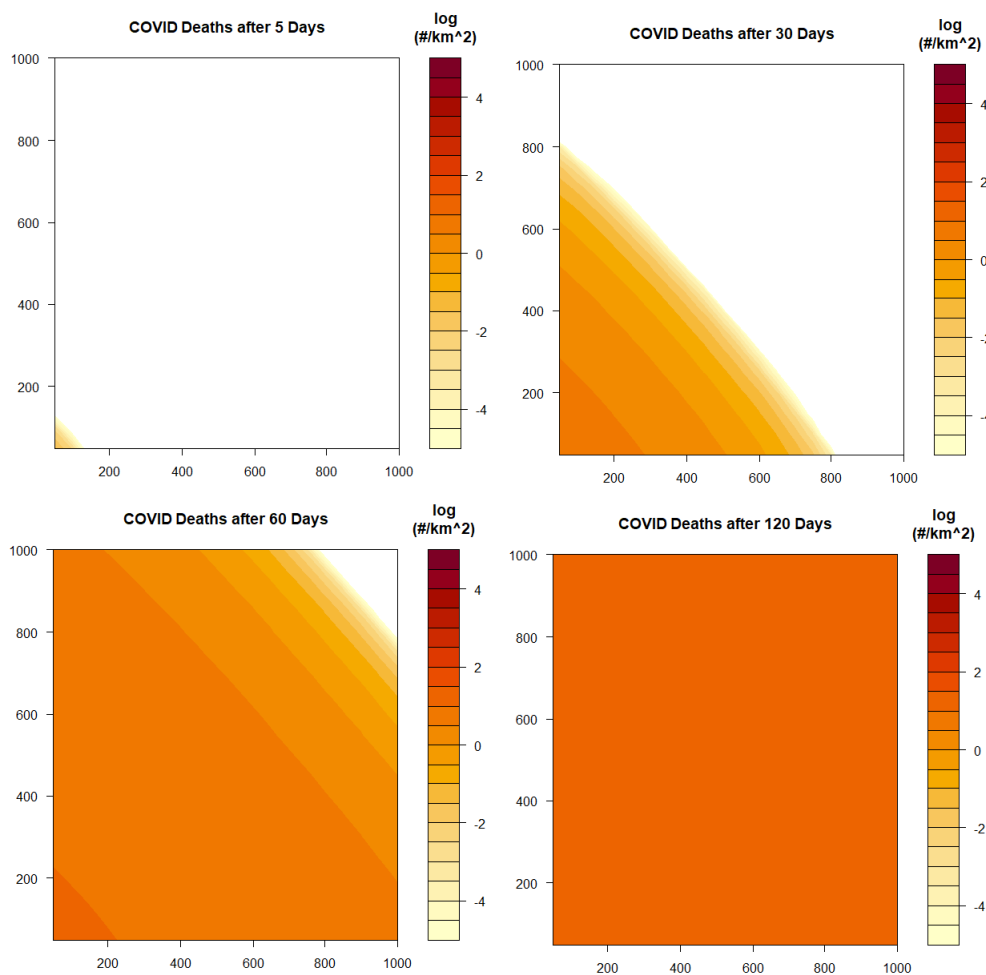
For the base analysis, we will set the following parameters. For this relatively short time span, we will assume insignificant births and non-COVID deaths ( $\alpha, \mu = 0$ ). We will set  $\delta = 1/7 \text{ days}^{-1}$ ,  $\phi_e = 1/6 \text{ days}^{-1}$ ,  $\phi_r = 1/24 \text{ days}^{-1}$ ,  $\beta_e = \beta_i = 0.00005 \text{ persons}^{-1}\text{days}^{-1}$ ,  $\phi_d = 1/160 \text{ days}^{-1}$ , and  $A = 1000$  people. For diffusion constants, we will let  $D_s = 0.02 \frac{\text{km}^2}{\text{day}}$ ,  $D_e = 0.01 \frac{\text{km}^2}{\text{day}}$ ,  $D_i = 0.00001 \frac{\text{km}^2}{\text{day}}$ , and  $D_r = 0.01 \frac{\text{km}^2}{\text{day}}$ . For the boundary conditions, we will assume an isolated region (net zero flux at the boundary).

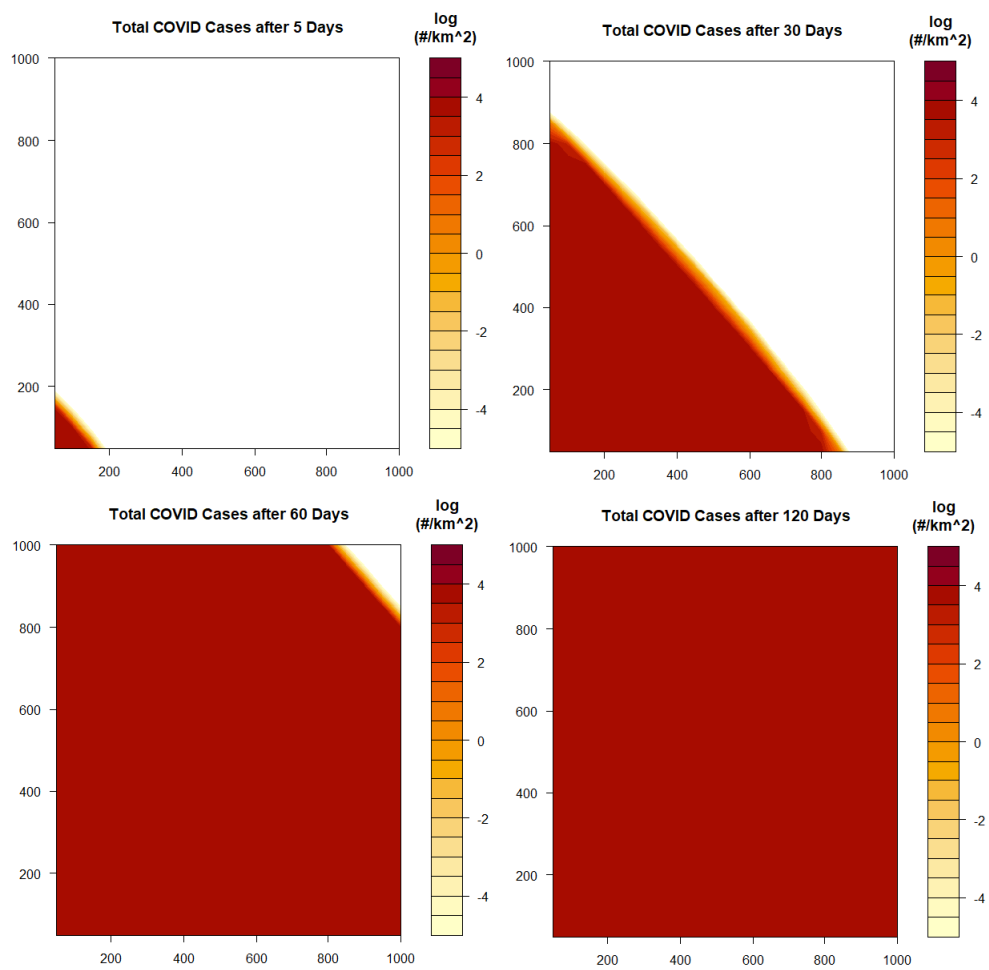
Now, we will showcase the model forecast with two different initial conditions. Note that the scale is a (natural) logarithmic scale denoting the number of people per unit area. We denote active cases to include both exposed and infected individuals and we denote total cases to include active, recovered, and dead individuals.

#### Scenario 1:

In this scenario, we assume an initial uniform population with a population density of 50 people per square km. Initially, we will have the outbreak start at the bottom left corner of the region with 0.5% of that population being infected.

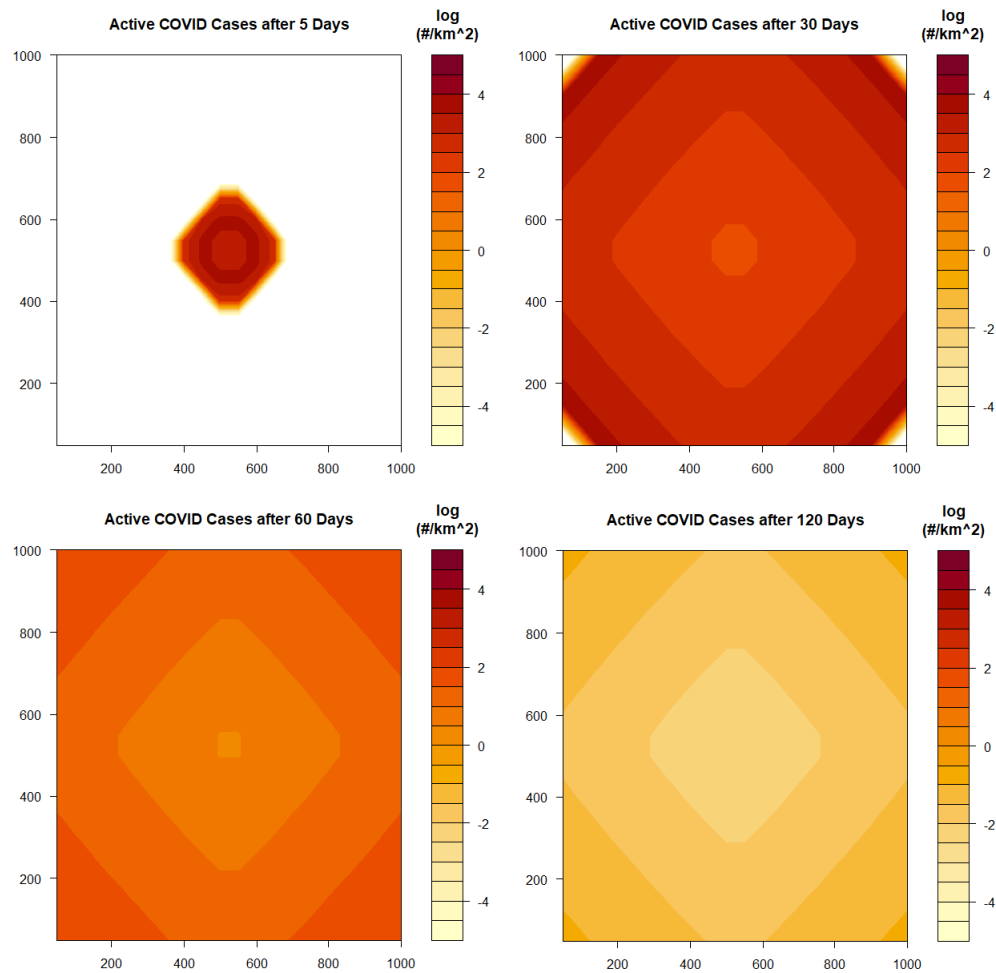


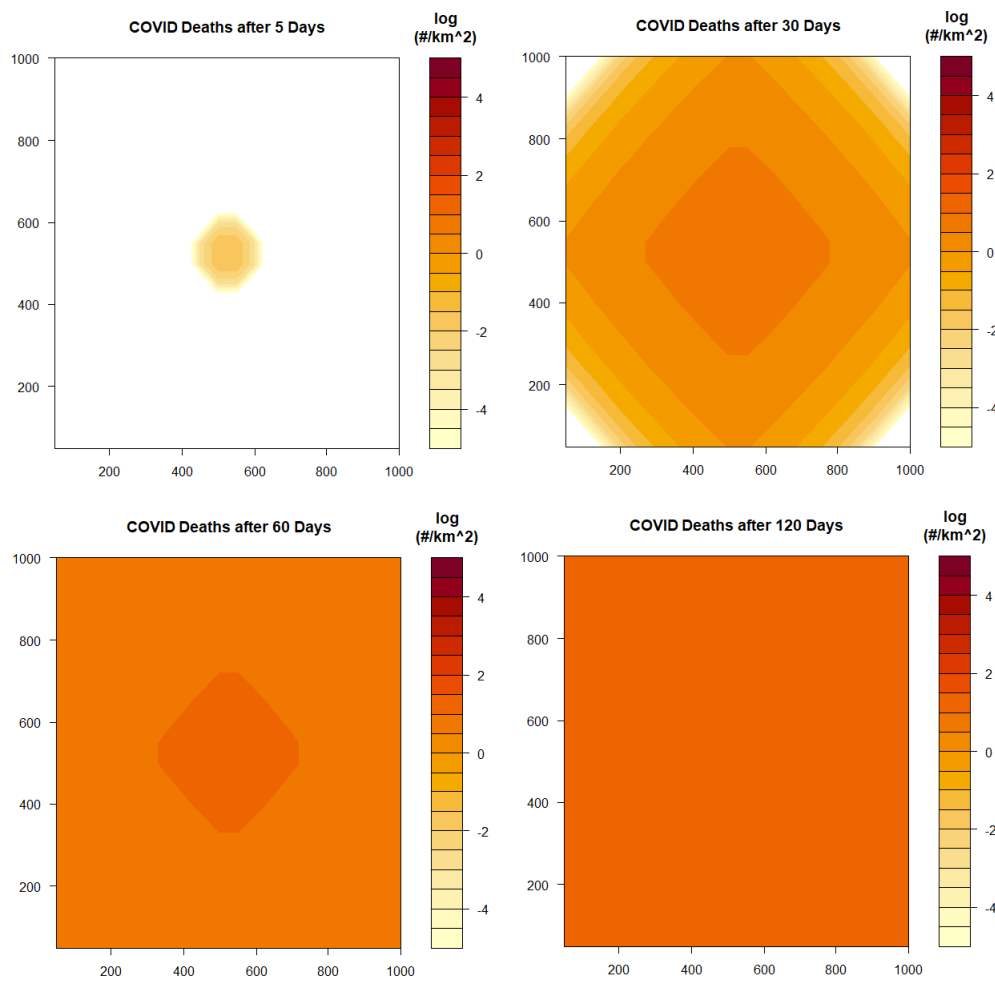




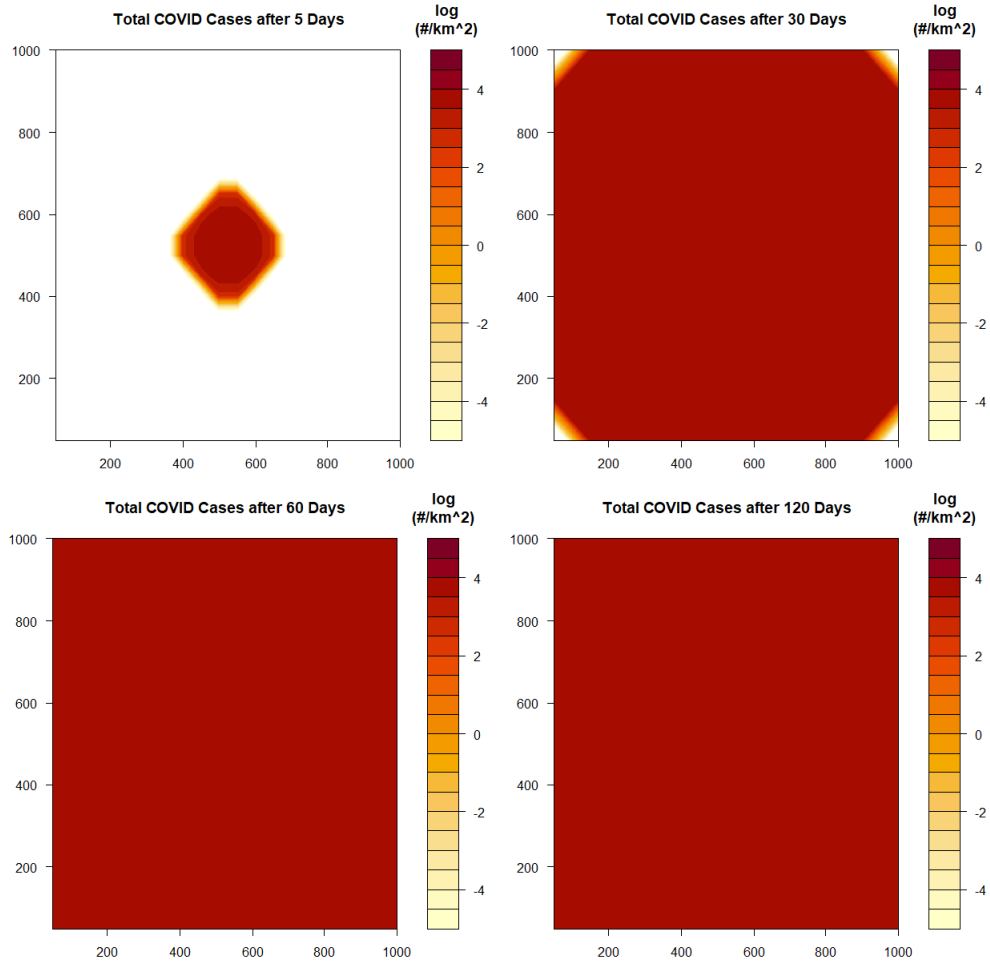
## Scenario 2

Here, we also assume an initial uniform population with a population density of 50 people per square km. This time, the outbreak will be initially in the center region with 0.1% of that population being infected.









## Analysis

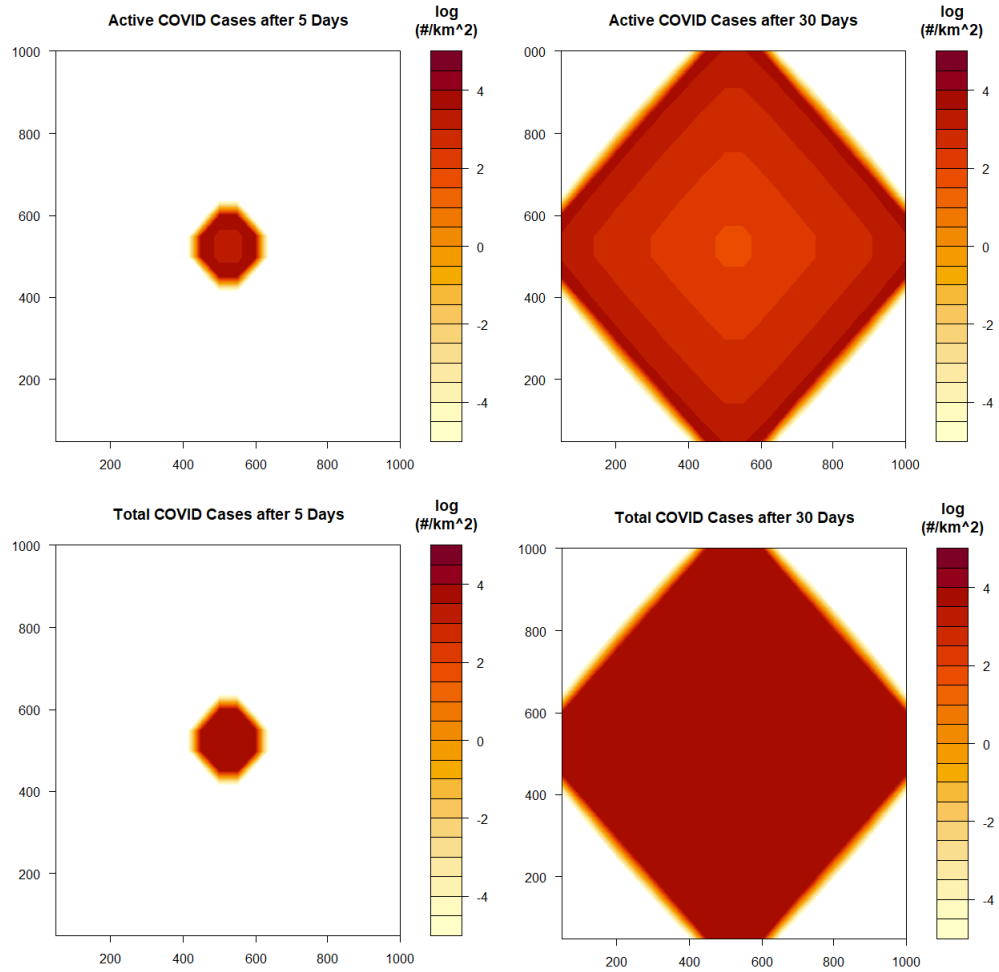
With these parameters, we see that at five days, the spread of the virus has already begun. After 30 days, the virus has spread across most parts of the region, and we see that previously affected regions have already begun the process of recovery. Between 60 and 120 days, the virus has affected everyone in the entire region. It seems that the epidemic wave ceases some time after four months, with the active cases dwindling down. There are clear limitations with this model and the parameter settings, as realistically, after the epidemic is finished, there should still be some susceptible individuals remaining.

## 4 Parameter Effects

Due to new information and data pertaining to the virus and its spread, new state and government restrictions, or change in the public's behavior, model parameters change over the course of a pandemic. Next, we will look at how changing different parameter settings affects the model's forecast. For comparison, we will be using Scenario 2's initial conditions (initial outbreak in the center).

### 4.1 Diffusivity

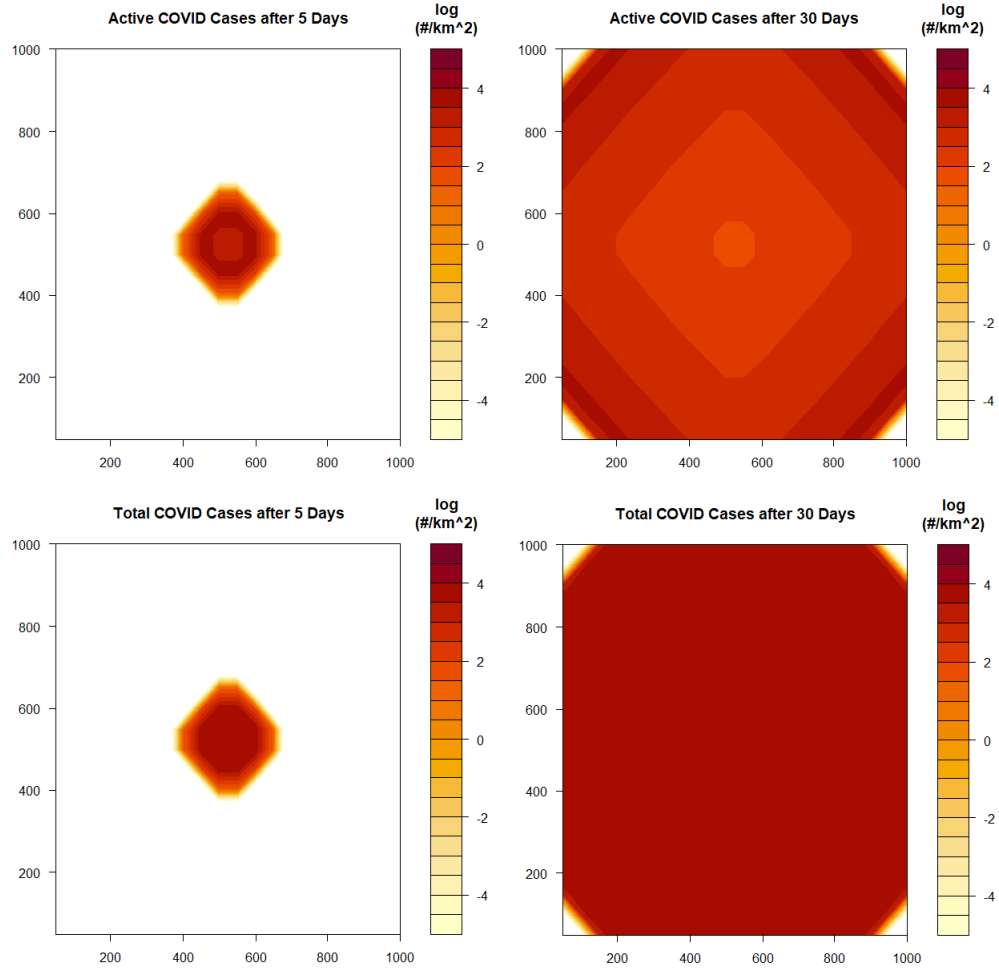
We will set  $D_e = 0.00002$ . This reflects a region with contact tracing and testing where individuals who are asymptomatic but likely (or do) have the virus are advised to not travel much away from their homes.



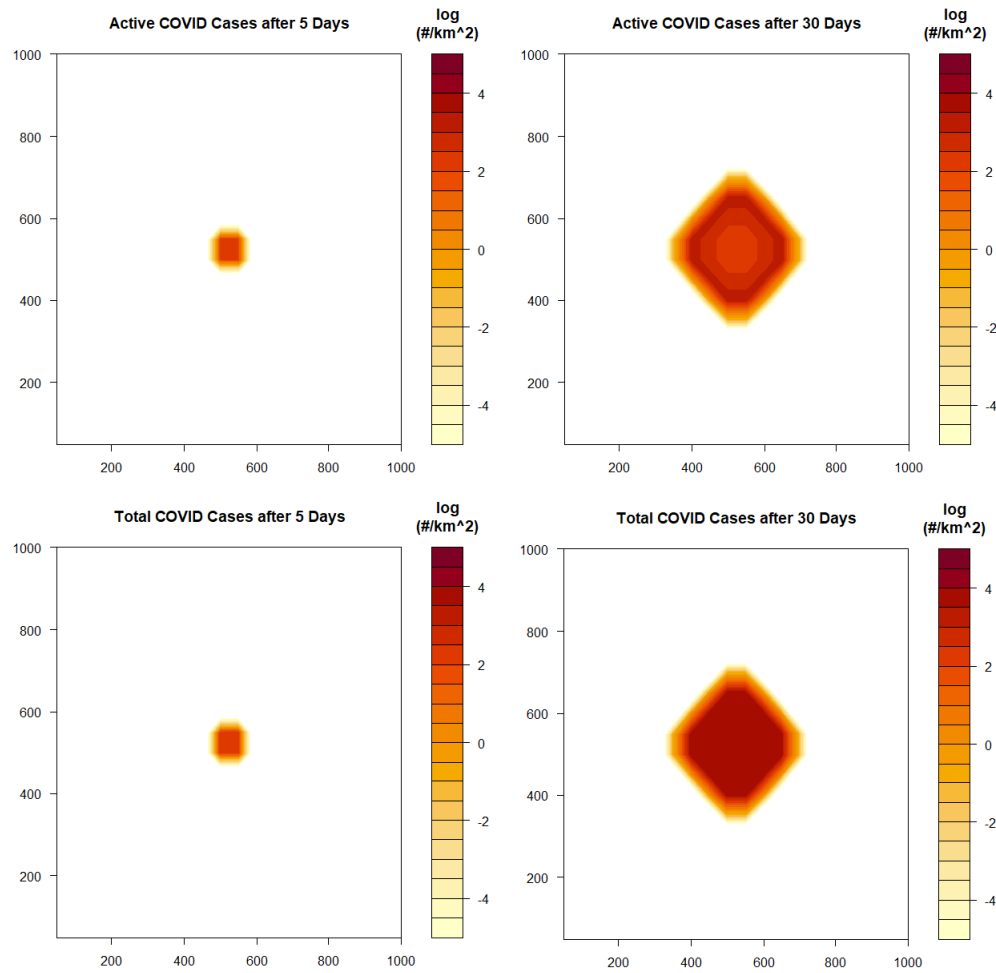
We see that the geographic spread of the virus has significantly slowed down. With these current parameters, setting  $D_s = 0.00002$ , limiting the spatial diffusion amongst susceptible individuals, actually has negligible influence on the geographic spread of the disease, mainly due to the fact that 1) the initial population distribution is uniform, and 2) the contact rate of the virus is more significant to the spread of the disease, which we will see in the next section.

## 4.2 Contact Rate

We will reset our model back to that of Scenario 2. This time, we will assume the diffusion stays the same, but the contact rate of the virus significantly goes down, which would likely be due to a combination of masks, social distancing, improvement in personal hygiene, and quarantining. First, we will only decrease the symptomatic contact rate down to  $0.00001 \text{ persons}^{-1}\text{days}^{-1}$ .



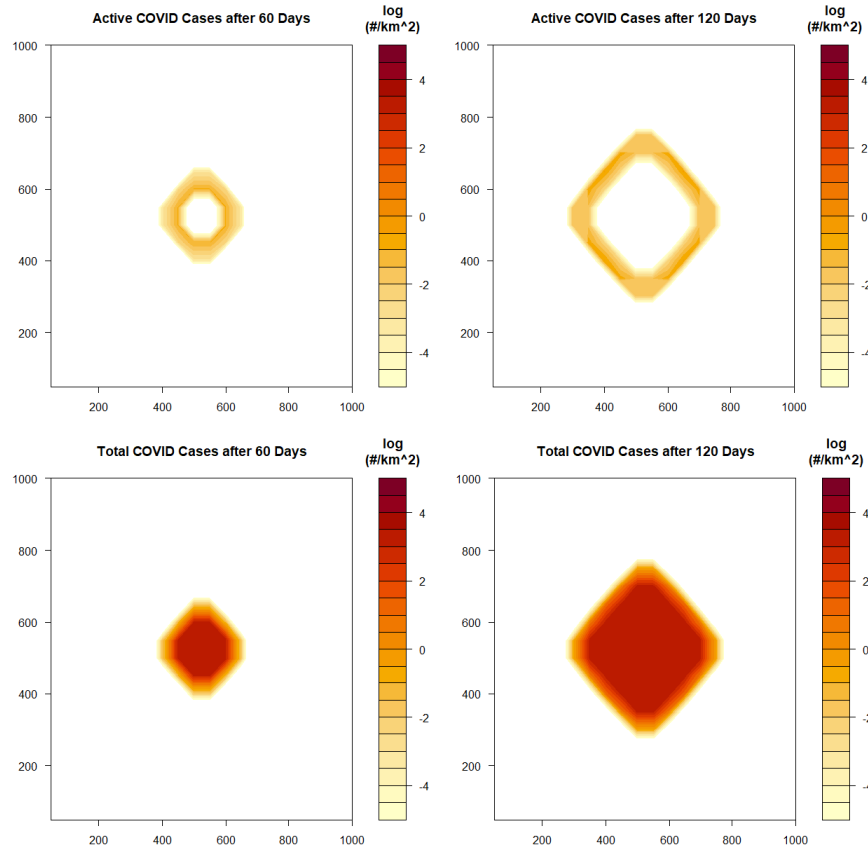
Surprisingly, the spread of the virus was not slowed in any meaningful way. Now, we will decrease the asymptomatic contact rate down to  $0.00001$ , which would indicate overall stricter measures in an effort to contain the virus rather than simply quarantining those with visible symptoms.



With these restrictions, we observe that the spread of the virus has slowed down significantly, highlighting the importance of limiting contact even for those who may not visibly have the virus.

### 4.3 Other Parameters

There are many more parameters that we can look at in detail, but diffusivity and contact rate are the ones that are most controllable by governments and the public. Increasing the rate of recovery would, in general, decrease the amount of deaths and decrease the amount of total cases (due to less opportunity for viral transmission). If combined with a low enough contact rate, this could lead to more of the population remaining unaffected by the virus after the pandemic wave is finished. As an example, here are the model calculations with the contact rates set to those in the previous section, as well as the asymptomatic recovery period set to 1 day and the symptomatic recovery period set to 2 days:



Increasing the mortality rate of the virus would both increase the proportion of deaths for those affected and decrease the amount of total cases (again, less opportunity for viral transmission). In a more pertinent model projecting the long term, the effect of birth rates and non-disease deaths may also be discussed.

## 5 Steady State

The steady state of the model was calculated using the *runsteady* function from the *rootSolve* package. With homogeneous Neumann boundary conditions, the spatial model looks rather uninteresting. The population in each compartment is uniformly distributed across the entire region. Thus, analysis in the steady state can be simplified to that of an ODE compartmental model, with later uniform distributing. Much like in the previous section, the parameters having the greatest effect on the steady state will be the contact rates, recovery rates, and infected mortality rate, which all contribute to the infection's basic reproduction number,  $R_0$ .

## 6 Discussion

This document showcases a primitive PDE model for the geographic spread of an infectious disease in a bounded rectangular region. We looked at how different parameters affected the spread of the disease and concluded that the most effective practical way to slow and quell the disease's spread is to decrease the rate of contact with both infected and exposed individuals.

One potential scenario that this model could look at is nonhomogeneous flux boundary conditions for different compartments, indicating some sort of travel to and from the region across its boundary. We could look at various different initial conditions, including a more realistic population distribution and initial outbreak. If projecting the long term, we may factor in new births and non-disease related deaths, as well as finding a different PDE solver method to account for nonlinear diffusion that may depend on both time and location.

Other new additions may include modeling the epidemic with both previous and ongoing vaccinations and potential reinfections. To model reinfections, we would simply add a term  $\gamma r$ , where  $\gamma$  represents the reinfection rate, that is removed from the recovered compartment and added back into the susceptible compartment. For vaccinations, if we were to model vaccinations along with reinfections, we would create a new compartment, called  $V$  for vaccinated/immune, and some proportion of the susceptible population would move to the vaccinated group per time step. Previously vaccinated individuals would simply be placed into the vaccinated compartment when defining the initial conditions.

If this project were to continue, future steps would include taking the above into account as well as gathering real life data and using statistical methods to fit proper parameters and initial/boundary conditions into the model in order to produce an accurate forecast of an ongoing epidemic like COVID-19.