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Analysis of epidemic spread dynamics using a PDE model and COVID-19 data from Hamilton County OH USA

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Abstract: We study the spatiotemporal dynamics of an epidemic spread using a compartmentalized PDE model. The model is validated using COVID-19 data from Hamilton County, Ohio, USA. The model parameters are estimated using a month of recorded data and then used to forecast the infection spread over the next ten days. The model is able to accurately estimate the key dynamic characteristics of COVID-19 spread in the county. Additionally, a stability analysis indicates that the model is robust to disturbances and perturbations which, for instance, could be used to represent the effects of super spreader events. We also use the modeling framework to analyse and discuss the impact of Non-pharmaceutical interventions (NPIs) for mitigation of infection. Our results suggest that such models can yield useful short and medium term predictive characterization of an epidemic spread in a restricted geographical region and also help formulate effective NPIs for mitigation. The results also signify the importance of further research into the accurate analytical representation of specific NPIs and hence their dampening effects on an infection spread.

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Keywords: Control of Partial differential equations; stability of nonlinear systems; modeling; mathematical modeling; epidemiology; model validation.

1. INTRODUCTION

Developing pharmaceutical countermeasures for a pandemic caused by a novel virus is a time-consuming process; research, clinical trials and production planning are all essential before drugs and vaccines can be launched on a global scale with confidence. This can result in a time lag, sometimes of several years, between the emergence of a pandemic and the introduction of a vaccine. This delay could be at a significant cost, both in terms of human lives and the economy. At the onset of a pandemic, it is critical to curtail the spread of infection through carefully planned and implemented non-pharmaceutical interventions (NPIs). These measures may include complete lockdowns, restricted movement of population, social distancing, mask orders and so on.

COVID-19 has been the largest pandemic in over 100 years with 140 million cases and 3 million deaths worldwide over the past year. The NPI measures have been vital in helping to decrease the rapid spread of infection. NPIs have been the only defense against the spread of the virus before the launch of vaccines. It is a complex task to estimate when, where and to what extent an NPI measure has to be implemented. Wang and Yamamoto (2020) study the effectiveness of personal precautionary measures in countering a pandemic. In particular, two major modeling challenges here are: (1) analytical characterization of specific NPIs (2) accurate predictive dynamic models of infection spread that can also reliably predict the effects of specific NPIs on a spread.

Modeling and analysis of the dynamic characteristics of an epidemic mainly fall into two categories: mathematical and statistical. The ordinary differential equation (ODE) based compartmental model is a popular framework that has been used in a variety of contexts (see, for instance, Jang et al. (2020), Yang et al. (2014) and Mandal et al. (2020)). However, ODE models involve only a single spatial variable and hence are unable to represent an infection spread in a 2-D spatial domain. On the other hand, Partial Differential Equation (PDE) models involve functions of multiple spatial variables. These have been extensively used to model physical phenomena, for instance various reaction-diffusion systems (Lou and Zhao (2011), Wang et al. (2012), Deshpande et al. (2017)). The work in Adnaoui and El Alami Larroussi (2020) introduced a 2-dimensional spatio-temporal PDE model to investigate the
optimized strategy for vaccine distribution in a pandemic. Purely statistical and data-centric methods such as logistic regression in Goldstein et al. (2011) and deep learning based approaches in Pereira et al. (2020) and Wang et al. (2020) have also been used in epidemic modeling. However, these approaches have enjoyed only limited success in capturing the dynamics of a broad class of infection spreads.

In this paper, we discuss and evaluate a spatio-temporal PDE-based dynamic model, adapted from Li and Zou (2009), to simulate an epidemic spread. We also introduce a control parameter to simulate the effects of a NPI on this system. The model is then validated on empirical COVID-19 data obtained from the Department of Public Health, Hamilton County Ohio. For analysis, we select different windows of time to estimate the parameters of this PDE model. The model is then used to make predictions on the evolution of the infection for the subsequent 10 days, and the results are then compared with the true data. This is a continuation of our previous work Majid et al. (2021), which developed a similar model for the entire State of Ohio. In the light of our previous results, a particular focus here is the efficacy of the model on the smaller geographical scale of the county. Indeed, a finer grid can lead to better results since there is lesser accumulation of errors.

Section 2 discusses the mathematical model of the PDE system, the parameters that are estimated and the system rescaling. In section 3, we evaluate the model on the true data and analyze the results. We implement the NPI measures and discuss their effects on the evolution of the infection. In section 4 we mathematically evaluate the stability of the model and present numerical results that establish the robustness of the model under perturbations.

2. MATHEMATICAL MODELING

2.1 PDE model

We follow the compartmental modeling approach, whereby the total population in a domain is partitioned into the following compartments: Susceptible (S), Infected (I), and Recovered (R). The groups are disjoint and a transfer from R to I is not possible. The evolution of these compartments and the transfer of people from one group to the other is governed by a set of spatio-temporal differential equations. The pandemic ends when the infected population either approaches zero or an endemic equilibrium. This formulation can be traced to the seminal work of Kernack and McKendrick (1927).

Starting with this basis, more complexities are introduced into the model to better represent the actual infection dynamics. For instance, an infection typically has a time-delay $\tau$, which accounts for latencies in the infection spread. Hence, we add a Latent group L to the other three groups. We also note that the evolution of $S$, $I$, $R$ and $L$ is dependent on space and time, which allows for a realistic representation of the distribution of the population groups in a geographic area alongside the dynamics of the infection spread.

In mathematical terms, this model needs to be represented by PDEs rather than ODEs, since each component in the model including $S$, $I$, $R$ and $L$ has multi-variable dependencies. The use of PDEs, in this case, is also beneficial because they give a probabilistic interpretation of the infection dynamics which accounts for the unpreventable randomness in an infection spread. For instance, the random motion of individuals (both infected and susceptible) is a significant factor that influences the spread of infection and can be modeled using the diffusion terms in the PDE. A PDE model can naturally accommodate such diffusive processes. We, therefore, represent the dynamics of the $COVID-19$ spread with a coupled system of PDE:

$$\frac{\partial S}{\partial t} = \mu + D_S \nabla^2 S - dS - u(x,y,t)\tau R S,$$

$$\frac{\partial I}{\partial t} = D_I \nabla^2 I - \beta I - \gamma I + cu(x,y,t^*) \left( \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} r I(x,y,t^* - \tau) S^*(x,y,t^* - \tau) \right) f_u(x,y)dxdy ,$$

$$\frac{\partial R}{\partial t} = D_R \nabla^2 R - dR + \gamma I,$$

$$\frac{\partial L}{\partial t} = u(x,y,t^*) r I S^* - cu(x,y,t^*) \left( \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} r I(x,y,t^* - \tau) S^*(x,y,t^* - \tau) \right) f_u(x,y)dxdy.$$

Table 1 summarizes the parameters of our PDE model. Here, the population is grouped in partitions representing population densities of Susceptible ($S^*$), Infectious ($I^*$), Recovered ($R^*$) and Latent ($L^*$). Such epidemic models have been used in the past, dating back to the groundbreaking work in Kernack and McKendrick (1927). The use of PDEs characterizes such approaches as it enables the study of infection spread dynamics in a two-dimensional spatiotemporal setting. We, therefore, adopt a PDE-based dynamic model in Li and Zou (2009) as the basis in this work. Furthermore, we extend our model to include control parameters, (such as lockdown and mask mandates) to represent the NPIs. We also analyze the stability of the proposed dynamical system.

| Parameter Description | Description |
|-----------------------|-------------|
| $\mu$ | Birth-rate in the domain |
| $D_S$ | Diffusion coefficient representative of intensity of the random motion of the Susceptible population |
| $D_I$ | Diffusion coefficient representative of intensity of the random motion of the Infected population |
| $D_R$ | Diffusion coefficient representative of intensity of the random motion of the Recovered population |
| $d$ | Mortality rate due to natural deaths |
| $u(x,y,t^*)$ | The control parameter which is a function of space and time. This directly affects the rate of infection and mimics the implementation of an NPI in a certain location and time |
| $r$ | Infection rate |
| $\beta$ | Mortality rate due to $COVID-19$-19 deaths |
| $\gamma$ | Recovery rate from $COVID-19$ |
| $\epsilon$ | Fraction of the infected population that survive the latency period and enter the infected category |
| $f_u(x,y)$ | Gaussian kernel defining the extent of the mobility of the latent population |
| $\tau$ | Latency time of the model. For this paper, we assume it to be 15 days |
2.2 Non-dimensional model

Non-dimensional models are computationally and mathematically easier to analyze, and also provide deeper insights into the influence of the different parameters involved. This process reduces the number of parameters in the model by grouping them. Furthermore, this highlights the significance of parameters with respect to each other in any physical process. Non-dimensional equations are also applicable over multiple scales; for instance, a chemical reaction can be analyzed using a non-dimensional model, regardless of the size of the reaction vessel.

Here we define 3 parameters, viz., $l$ for the characteristic length which is the length of a single cell along $x$ or $y$ axis, $t$ representing the time after which we update the state variables. $N$ is considered as the total population of the county. Since it is significantly large as compared to the mortality and birth rate, this value is considered as a constant. The dataset that we use for model validation is updated daily. Therefore, we set $t$ to 1 day. Table 2 shows the non-dimensional parameter groupings derived using the scaling described above.

| Original Parameters | Non-dimensional Notation |
|---------------------|--------------------------|
| $\frac{\partial S}{\partial t}$ | $\lambda$ |
| $D_S \frac{\partial I}{\partial t}$ | $\eta_S$ |
| $D_R \frac{\partial R}{\partial t}$ | $\eta_R$ |
| $d \frac{\partial T}{\partial t}$ | $\theta$ |
| $r N \frac{\partial T}{\partial t}$ | $\phi$ |
| $(\beta + \gamma) \frac{\partial T}{\partial t}$ | $\delta$ |
| $\eta(\int_{-\infty}^{\infty} f(x, y, t-\tau) S(x, y, t-\tau) \ d x d y + \int_{-\infty}^{\infty} f(-x, y, t-\tau) S(-x, y, t-\tau) \ d x d y)$ | $\gamma_t$ |
| $\eta(\int_{-\infty}^{\infty} f(x, y, t-\tau) IS(x, y, t-\tau) \ d x d y + \int_{-\infty}^{\infty} f(-x, y, t-\tau) IS(-x, y, t-\tau) \ d x d y)$ | $\omega$ |

The equations (5)-(8) represent the non-dimensional PDE system derived using the reparameterization in Table 2. We use this non-dimensional model for further analysis in the remainder of this article.

For the simulation part, we take the entire map of the county and overlay a $60 \times 60$ cellular grid on the map. Each cell is assigned the following attributes; zip-code, boundary or no boundary and the initial value of $S$, $I$ and $R$. Our mesh size was equivalent to $0.63 \times 0.63$ sq. miles. The mesh size is determined keeping in mind the computational capacity and accuracy required. For $S$, we consider the total population in the zip code as the initial value, and for each day, we subtracted the number of cases reported. For each unique zip code, the values for $S$, $I$ and $R$ are equally divided among the number of cells that represent it.

We then discretize our non-dimensional model using the Euler’s forward method to obtain the following sets of equations:

$$I_{x,y}^{T+1} = \eta_I(I_{x,y}^T + I_{x+1,y}^T + I_{x,y+1}^T + I_{x-1,y}^T - I_{x,y}^T) + (1 - 4\eta_I - \delta)I_{x,y}^T + \epsilon u \frac{\phi}{N} \sigma_{x,y}^T,$$

$$R_{x,y}^{T+1} = \sigma_{x,y}^T(R_{x+1,y}^T + R_{x,y+1}^T + R_{x,y}^T) + (1 - 4\eta_R - \theta)R_{x,y}^T + \omega I_{x,y}^T,$$

$$S_{x,y}^{T+1} = N \lambda + \delta I_{x,y}^T + S_{x,y-1}^T + S_{x+1,y}^T + S_{x-1,y}^T + (1 - 4\eta_S - \theta - u \frac{\phi}{N} I_{x,y}^T) S_{x,y}^T,$$

$$I_{x,y}^T = u \frac{\phi}{N} I_{x,y}^T \sigma_{x,y}^T - \epsilon u \frac{\phi}{N} \sigma_{x,y}^T,$$

$$\sigma_{x,y}^{T+1} = \sum_{i=1}^{60} \sum_{j=1}^{60} I_{x,y}^{T-\tau} S_{x,y}^{T-\tau} f_{a}(x,y),$$

$$f_{a}(x,y) = \frac{1}{\sqrt{4\pi} \alpha} e^{-\frac{(x-x_o)^2 + (y-y_o)^2}{2\alpha}}.$$

Here $X_{x,y}^{T+1}$ represents the value of the state variable $X$ on day $T + 1$ in the cell $(x,y)$. $\alpha$ denotes the latent population for the entire time duration, throughout the county.

For our simulations, we consider a no-flux boundary condition, which treats the cells on the boundary as a solid wall, which the population cannot cross. Any attempt to cross the boundary will result in the individual being reflected to their nearest neighbouring cell which is present within the boundary. This allows us to maintain population conservation in the domain (apart from the deaths).

3. MODEL PARAMETER OPTIMIZING AND MODEL VALIDATION

In order to optimize our model parameters, we utilize the ground truth data from the month of April 2020. Our objective is to find the set of parameters such that a cost function is minimized. This cost function is given by
the infection parameter values that we have obtained and comparatively less than April, which is corroborated by

\[ L_m = \sqrt{\frac{1}{T} \sum_{n=1}^{N_c} \sum_{t=1}^{T} (X(n, t) - \hat{X}(n, t))^2}, \]  

(15)

where \( L_m \) is the model error (computed using a root-mean-square approach), \( N_c \) represents the total number of zip-codes considered (\( N_c = 66 \) in our case), \( T \) is the total number of days over which the simulation is executed (e.g., \( T = 30 \) days for the training phase), \( t \) is the time index and \( n \) is the zip-code index. The cost function is minimized while maintaining a physically reasonable range for the parameters. For instance, the birth rate and death rate are bounded between 0 and 1. After gaining an optimized set of parameters, the model is used to predict the infection evolution for the next 10 days and the results compared with the ground truth.

### 3.1 Model Validation

In the first experiment, after parameter estimation, we use the model which we trained with data from April 2020, to predict for the next 10 days. Figure 1 shows the corresponding results where the X-axis starts from April 01, 2020. The line in blue represents the time during which the model learns the parameters from the true data. The red line represents the prediction of the trajectory made using those parameters. The yellow dotted line is the ground truth. As observed from the graphs in Fig. 1, the proposed model captured the dynamics of the infection spread and closely followed the trend of the ground truth data.

Table 3 summarises the values of all the parameters learned from this experiment.

**Table 3. Optimized parameter values**

| Parameters | Optimized for April |
|------------|---------------------|
| \( \lambda \)   | 0.03802             |
| \( \eta_S \)   | 4.88 \times 10^{-5}        |
| \( \eta_R \)   | 2.89 \times 10^{-5}        |
| \( \eta_I \)   | 8.54 \times 10^{-6}        |
| \( \theta \)    | 5.23 \times 10^{-5}        |
| \( \phi \)      | 9.99 \times 10^{-4}        |
| \( \delta \)    | 0.0267                |
| \( \omega \)    | 0.0977                |
| \( e \)         | 0.1353                |
| \( \alpha \)    | 1.1                   |
| \( \hat{i} \)   | 1                     |

In the second experiment, we follow the same methodology, but use the data from a different time period. We train the model for the month of July 2020 and then predict for the next 10 days. However, we choose only selected parameters, namely \( \phi \) and \( \eta_I \) to be optimized. The remaining parameters are assumed the same. This is because during this time period, even though the social economic dynamics were different from that of April (when the first wave of COVID-19 occurred), the remaining parameters are not directly related to the change in infection dynamics. The values for \( \phi \) comes out to be \( 4.20 \times 10^{-4} \), and \( \eta_I \) comes out to be \( 1.5365 \times 10^{-5} \). In July, the infection spread was comparatively less than April, which is corroborated by the infection parameter values that we have obtained and which can be seen in figure 2. We again notice similar results and the model is clearly able to predict well, the system dynamics. We note that our assumption of uniformity of parameters throughout the spatial domain could likely explain the discrepancy between the ground truth and model output. However, in reality, these parameters change over time and space based on human behavior, local public health policy, and other environmental factors.

### 3.2 Control parameters

After validating the model to be able to adapt to the dynamics of the infection, we aim to control the spread of the infection. For this purpose, we change the value of \( u \) in the model. The main idea here is that enforcing an NPI measure will directly affect the infection rate. There are numerous possibilities that the \( u(x, y, t) \) function can take. In this study, we limit our analysis on a single value of \( u \) for the entire time duration, throughout the county. In real world, it would mean that a certain NPI had been in place in the county from the day of the first infection.

In figures 3 and 4, the blue trajectory represents the trajectory of the evolution of the infection spread, that would have had occurred if all the environmental and social conditions would have had remained the same as to when our model parameters were trained (i.e., month of April). Practically, however, that is not the case since different aspects have likely varied with time, including NPI measures, human behaviour, immunity of the population, environmental factors and so on. The red and yellow trajectories represent the cases where the infection rate was lowered using a certain NPI measure. This clearly indicates that
where $\psi$ is the frequency and $\beta$ the phase of the perturbation. Substituting equation 18 into equation 16, we obtain the following:

$$
\sin(\psi x + \beta) \frac{\partial f_i}{\partial t} = R(f_{eq} + \sin(\psi x + \beta) \nabla f) - \frac{D}{\beta^2} \sin(\psi x + \beta) \nabla f. \quad (19)
$$

The first term on the RHS of equation 19 can be linearized approximately as follows:

$$
R(f_{eq} + \sin(\psi x + \beta) \nabla f) \approx \sin(\psi x + \beta)J|_{f=f_{eq}} \nabla f, \quad (20)
$$

where $J$ represents the Jacobian of $R$ with respect to $f$ at $f_{eq}$. Substituting this term back in equation 19, we end up with the following expression

$$
\frac{\partial \nabla f}{\partial t} = (J - D\psi^2)|_{f=f_{eq}} \nabla f. \quad (21)
$$

Now in order to study the stability of the system, we need to find the eigenvalues of the matrix $J - D\psi^2$, where $D$ is a diagonal matrix with diffusion coefficients, and $\psi$ is the perturbation frequency, which we consider as a positive constant. Following Sayama (2020), for the system to be stable, the eigenvalues must all have negative real parts.

For our PDE model, the equilibrium states are:

$$
S_{eq} = \frac{\lambda_1}{\phi_0} \nabla f, \quad I_{eq} = \frac{\phi_0 \phi_1}{\delta} \nabla f, \quad R_{eq} = \frac{\phi_0 \phi_2}{\phi_1} \nabla f. \quad (22)
$$

It may be noted that $L$ is not considered for stability analysis since it does not directly interact with the other state variables. The expression $J - D\psi^2$ is evaluated as:

$$
J - D\psi^2 = \begin{pmatrix}
\theta - \phi I_{eq} - \eta_I \psi^2 & -\phi S_{eq} & 0 \\
0 & -\delta - \eta_R \psi^2 & 0 \\
0 & \omega & -\theta - \eta_R \psi^2
\end{pmatrix}. \quad (23)
$$

The eigenvalues for the above matrix are:

$$
\lambda_1 = (\theta - \phi I_{eq} - \eta_I \psi^2) \\
\lambda_2 = (-\delta - \eta_R \psi^2) \\
\lambda_3 = (-\theta - \eta_R \psi^2). \quad (24)
$$

By plugging in the parameters from table 3, the three eigenvalues are $-1.06 \times 10^{-6}, -0.0267$ and $-8.22 \times 10^{-5}$ respectively, given that $\psi$ is a constant, which in this case we assume to be 1. The negative eigenvalues establish that the PDE model is stable.

To validate our calculations, we trained the model using the data for April 2020 and simulated the evolution trajectory. As shown in figure 5 the infection spread hits a peak value and then starts to decrease and eventually dies out. Note, however, that the trajectory shown here is based on the assumption that all the environmental and social conditions remain invariant from when our model parameters were trained (i.e data of April 2020). In practice, this assumption cannot be expected to strictly hold. Indeed, factors such as NPI measures, human behavior, immunity of the population and environmental factors induce variations that require analysis using extensions of the present model.

We then validate the stability of the model by introducing perturbations in the trajectory. We increased the number of cases in the county by 50% on Day 50, 150 and 300 of the simulation. Interestingly, such disruptive perturbations may be viewed as consequences of super-spreader events such as large indoor gatherings. We see that the model...
is clearly indicated by the red trajectory in figure 5. This is clearly indicated by the red trajectory in figure 5.

5. CONCLUSION

Our goal here was to analyze a PDE model of epidemic spread and validate the predictive capability of the model using COVID-19 data from Hamilton County, Ohio. Given our previous results using the model for the entire state of Ohio (please see Majid et al. (2021)), of particular interest was the question of how the model would perform against data from the smaller region of the county and the results affirm that the model yields improved results in this case. The results show that the model was able to forecast accurately the actual COVID-19 county infection dynamics, upon being trained with data from a certain amount of time. Using the model to study the impact of NPI measures, our results also show quantitatively, the efficacy of NPIs for mitigation. Looking ahead, control-theoretic interventions as controls to mitigate the spread of epidemics: An analysis using a spatiotemporal pde model and covid–19 data. ISA Transactions. URL https://doi.org/10.1016/j.isatra.2021.02.038.

Mandal, M., Jana, S., Nandi, S.K., Khatua, A., Adak, S., and Kar, T. (2020). A model based study on the dynamics of COVID-19: Prediction and control. Chaos, Solitons & Fractals, 109889.

Pereira, I.G., Guerin, J.M., Silva Júnior, A.G., Garcia, G.S., Piscitelli, P., Miani, A., Distante, C., and Gonçalves, L.M.G. (2020). Forecasting covid-19 dynamics in brazil: A data driven approach. International Journal of Environmental Research and Public Health, 17(14). doi:10.3390/ijerph17145115. URL https://www.mdpi.com/1660-4601/17/14/5115.

Sayama, H. (2020). Linear Stability Analysis of Reaction-Diffusion Systems. URL https://chem.libretexts.org/@go/page/7853. [Online; accessed 2021-03-28].

Segel, L. and Jackson, J. (1972). Dissipative structure: an explanation and an ecological example. Journal of theoretical biology, 37 3, 545–59.

Wang, H. and Yamamoto, N. (2020). Using a partial differential equation with google mobility data to predict covid-19 in arizona. Mathematical Biosciences and Engineering, 17(5), 4891–4904. doi:10.3934/mbe.2020266. URL http://dx.doi.org/10.3934/mbe.2020266.

Wang, L., Chen, J., and Marathe, M. (2020). TDEFSI: Theory-guided Deep Learning-based Epidemic Forecasting with Synthetic Information. ACM Transactions on Spatial Algorithms and Systems (TSAS), 6(3), 1–39.

Wang, W., Cai, Y., Wu, M., Wang, K., and Li, Z. (2012). Complex dynamics of a reaction–diffusion epidemic model. Nonlinear Analysis: Real World Applications, 13(5), 2240 – 2258.

Yang, W., Karspeck, A., and Shaman, J. (2014). Comparison of Filtering Methods for the Modelling and Retrospective Forecasting of Influenza Epidemics. PLOS Computational Biology, 10(4), 1–15. doi:10.1371/journal.pcbi.1003583. URL https://doi.org/10.1371/journal.pcbi.1003583.

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REFERENCES

Adnaoui, K. and El Alami Laaroussi, A. (2020). An Optimal Control for a Two-Dimensional Spatiotemporal SEIR Epidemic Model. International Journal of Differential Equations, 2020.

Deshpande, A., Kumar, M., and Ramakrishnan, S. (2017). Robot swarm for efficient area coverage inspired by ant foraging: The case of adaptive switching between brownian motion and levy flight. In ASME 2017 Dynamic Systems and Control Conference. American Society of Mechanical Engineers Digital Collection.

Goldstein, E., Cobey, S., Takahashi, S., Miller, J.C., and Lipsitch, M. (2011). Predicting the Epidemic Sizes of Influenza A/H1N1, A/H3N2, and B: A Statistical Method. PLOS Medicine, 8.

Jang, J., Kwon, H.D., and Lee, J. (2020). Optimal control problem of an SIR reaction–diffusion model with inequality constraints. Mathematics and Computers in Simulation, 171, 136–151.

Kermack, W.O. and McKendrick, A.G. (1927). A contribution to the mathematical theory of epidemics. Proceedings of the Royal Society of London. Series A, Containing papers of a mathematical and physical character, 115(772), 700–721.

Li, J. and Zou, X. (2009). Modeling Spatial Spread of Infectious Diseases with a Fixed Latent Period in a Spatially Continuous Domain. Bulletin of Mathematical Biology, 71(8), 2048–2079. doi:10.1007/s11538-009-9457-z.

Lou, Y. and Zhao, X. (2011). A reaction-diffusion malaria model with incubation period in the vector population. Journal of Mathematical Biology, 62(4), 543–568. doi: 10.1007/s00285-010-0346-8.

Majid, F., Gray, M., Deshpande, A.M., Ramakrishnan, S., Kumar, M., and Ehrlich, S. (2021). Non-pharmaceutical interventions as controls to mitigate the spread of epidemics: An analysis using a spatiotemporal pde model and covid–19 data. ISA Transactions. URL https://doi.org/10.1016/j.isatra.2021.02.038.

Mandal, M., Jana, S., Nandi, S.K., Khatua, A., Adak, S., and Kar, T. (2020). A model based study on the dynamics of COVID-19: Prediction and control. Chaos, Solitons & Fractals, 109889.

Pereira, I.G., Guerin, J.M., Silva Júnior, A.G., Garcia, G.S., Piscitelli, P., Miani, A., Distante, C., and Gonçalves, L.M.G. (2020). Forecasting covid-19 dynamics in brazil: A data driven approach. International Journal of Environmental Research and Public Health, 17(14). doi:10.3390/ijerph17145115. URL https://www.mdpi.com/1660-4601/17/14/5115.

Sayama, H. (2020). Linear Stability Analysis of Reaction-Diffusion Systems. URL https://chem.libretexts.org/@go/page/7853. [Online; accessed 2021-03-28].

Segel, L. and Jackson, J. (1972). Dissipative structure: an explanation and an ecological example. Journal of theoretical biology, 37 3, 545–59.

Wang, H. and Yamamoto, N. (2020). Using a partial differential equation with google mobility data to predict covid-19 in arizona. Mathematical Biosciences and Engineering, 17(5), 4891–4904. doi:10.3934/mbe.2020266. URL http://dx.doi.org/10.3934/mbe.2020266.

Wang, L., Chen, J., and Marathe, M. (2020). TDEFSI: Theory-guided Deep Learning-based Epidemic Forecasting with Synthetic Information. ACM Transactions on Spatial Algorithms and Systems (TSAS), 6(3), 1–39.

Wang, W., Cai, Y., Wu, M., Wang, K., and Li, Z. (2012). Complex dynamics of a reaction–diffusion epidemic model. Nonlinear Analysis: Real World Applications, 13(5), 2240 – 2258.

Yang, W., Karspeck, A., and Shaman, J. (2014). Comparison of Filtering Methods for the Modelling and Retrospective Forecasting of Influenza Epidemics. PLOS Computational Biology, 10(4), 1–15. doi:10.1371/journal.pcbi.1003583. URL https://doi.org/10.1371/journal.pcbi.1003583.