Using Compartmental Models to Evaluate the Effectiveness of COVID-19 Interventions

by
Zane Reed

A thesis presented to the Honors College of Middle Tennessee State University in partial fulfillment of the requirements for graduation from the University Honors College

Fall 2021

Thesis Committee:

Yixiang Wu, Thesis Director

Ennio Piano, Thesis Committee Chair

Using Compartmental Models to Evaluate the Effectiveness of COVID-19 Interventions

by Zane Reed

APPROVED:

_____

Yixiang Wu, Thesis Director
Assistant Professor, Mathematics

_____

Ennio Piano, Thesis Committee Chair
Assistant Professor, Economics

Abstract

In this thesis, we propose a method for mathematically modeling the spread of COVID-19 with a compartmental model based on differential equations. Through the development of this model, we hope to be able to study the behavior of the virus so that information can be gathered about how to intervene in its spread. After computing some of the model's mathematical properties, we simulate the model using data from Rutherford County. From this, we can learn about the expected outcomes and the progression of an outbreak. The results show rapid growth of new cases without the presence of vaccination; with vaccination programs in place, the growth is considerably slower and can reflect the real data, but it depends on other factors such as the vaccine efficacy. As such, we conclude that the model is useful in the short-term and demonstrates the importance of vaccination programs.

Contents

List of Figures

List of Tables

1 Introduction

COVID-19 is the term for the novel strands of coronavirus which were first identified in Wuhan, China and continued to spread to the rest of the world [2]. Labeled as a pandemic by the World Health Organization (WHO) back in March 2020 [22], COVID-19 has since led to hundreds of millions of infections and millions of deaths globally [21]. Symptoms of COVID-19 patients vary from case to case, ranging from mild symptoms like coughing and a fever to more severe conditions like trouble breathing and persistent chest pain [20]; people with underlying medical conditions are at particularly high risk [19]. Since the pandemic has lasted long enough, new strains of the virus have also developed. Some of these strains are much more dangerous than the original; the Delta variant is currently one of the most contagious and widespread versions [10]. Considering the heavy cost of allowing the virus to spread unchecked, governments across the world have implemented various tactics to curtail its impact. This includes medical care for symptomatic individuals and vaccination programs as well as many nonpharmaceutical interventions (NPIs), such as lockdowns, mask usage, and social distancing.

In terms of pharmaceutical methods used to combat COVID-19, patients with critical conditions are referred to hospitalization when possible. The drug remdesivir was approved last year for treatment of the virus [14], and research on a variety of other potential treatments has been performed. As for vaccines, three have been approved by the CDC for use in the United States: Pfizer-BioNTech, Moderna, and Johnson & Johnson. There are also others undergoing clinical trials [11]. Research shows that these vaccines have been able to provide protection against COVID-19 in real-world conditions [9].

Given the severity of the situation, determining the effectiveness of different intervention tactics has been the primary focus of a multitude of scientific studies. Many such studies utilize ordinary differential equation compartmental mod-

els [1, 5, 16, 18, 23]. Differential equations are equations that includes variables and their derivatives; this allows for the study of how the rate of change of the variables responds to the values of those variables. For epidemiological purposes, people can study how a population changes over time by treating it as a group of connected compartments and investigating the interactions between them through a system of differential equations. People will then change their model through additional compartments and parameters in order to study the effects of a specific factor on the model.

In this paper, we will develop a compartmental model of COVID-19 within a population that incorporates medical intervention tactics of vaccination and hospitalization. Then, by analyzing the model's mathematical properties and running numerical simulations based on data, the model can judge the effectiveness of those programs in slowing the spread of COVID-19. Those judgements can then inform how to develop effective policies within a given area.

This paper is organized as follows. In Section 2, we present the models that will be used for modeling the spread of COVID-19. Section 3 contains analysis of the models with computation of important properties like the disease free equilibrium and basic reproduction. In Section 4, the model is tested through numerical simulations. Using data based on the presence of the disease in Rutherford County, Tennessee, values are assigned to the parameters and the model is used to estimate the outbreak over a short-term period. Lastly, Section 5 is a conclusion and summary of the findings of the paper.

2 The models

2.1 Model without vaccination

The compartmental model used in the analysis is partially based on a model used in analysis for the presence of the disease in Nigeria [16]. This model is distinguished from it primarily through the inclusion of a compartment for vaccinated individuals. It also features different parameters than their model to better suit the goal of judging the effectiveness of vaccination programs.

While the main model includes a compartment for vaccinated individuals, a version without it is used as well. Information can then be gleaned from comparisons between the results. The flow diagram of the model without vaccination compartment is shown in Figure 1.

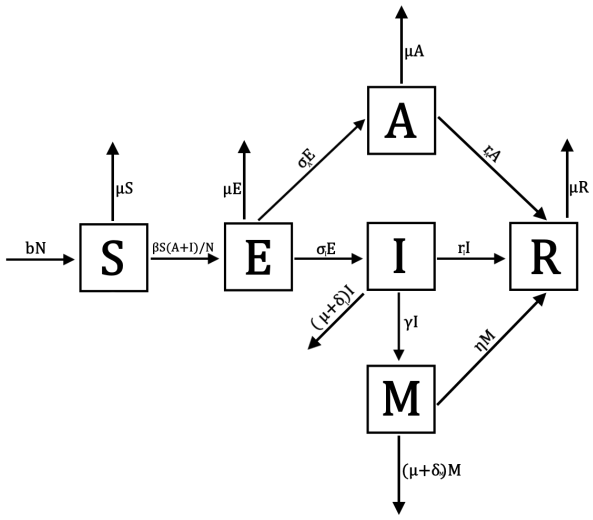

Figure 1: SEAIMR model diagram.

The model splits the population, N, into six compartments: susceptible (S); exposed, or infected but not yet infectious (E); asymptomatic infected (A); symptomatic infected (I); receiving medical care (M); and recovered (R). The model consists of a system of six differential equations:

$$\begin{cases} \dfrac{dS}{dt} = bN - \mu S - \beta S \dfrac{A+I}{N}, \\ \dfrac{dE}{dt} = \beta S \dfrac{A+I}{N} - \mu E - \sigma_A E - \sigma_I E, \\ \dfrac{dA}{dt} = \sigma_A E - \mu A - \tau_A A, \\ \dfrac{dI}{dt} = \sigma_I E - (\mu + \delta_I) I - \tau_I I - \gamma I, \\ \dfrac{dM}{dt} = \gamma I - (\mu + \delta_M) M - \eta M, \\ \dfrac{dR}{dt} = \eta M + \tau_I I + \tau_A A - \mu R. \end{cases} \tag{1}$$

The biological meaning of the parameters can be found in Table 1. In particular, we use standard incidence mechanism $\beta S(A+I)/N$ to describe the transmission of the disease, where β is the disease transmission rate.

Table 1: Parameters of the model.

Parameter	Description
b	Natural birth rate
μ	Natural death rate
β	Transmission rate
σ_A	Rate from E to A
σ_I	Rate from E to I
δ_I	Disease-related death rate (symptomatic)
δ_M	Disease-related death rate (hospitalized)
γ	Rate of hospitalization
η	Medical recovery rate
r_A	Recovery rate of asymptomatic
r_I	Recovery rate of symptomatic

2.2 Model with vaccination

Let V be the compartment for vaccinated individuals. We suppose that individuals in S are vaccinated at rate ρ and let $1-\epsilon$ be the protection rate of the vaccine. The flow diagram of the proposed model with vaccinations is given by Figure 2.

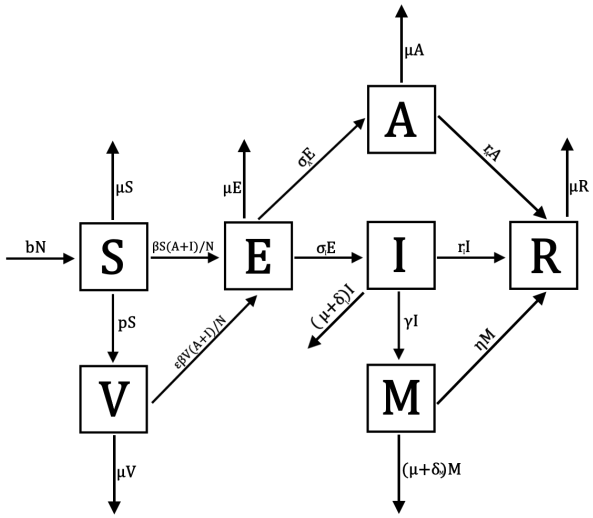

Figure 2: SVEAIMR model diagram.

Our model consists of a system of seven differential equations:

$$\begin{cases} \dfrac{dS}{dt} = bN - \mu S - \rho S - \beta S\dfrac{A+I}{N}, \\ \dfrac{dV}{dt} = \rho S - \mu V - \epsilon\beta V\dfrac{A+I}{N}, \\ \dfrac{dE}{dt} = \beta S\dfrac{A+I}{N} + \epsilon\beta V\dfrac{A+I}{N} - \mu E - \sigma_A E - \sigma_I E, \\ \dfrac{dA}{dt} = \sigma_A E - \mu A - \tau_A A, \\ \dfrac{dI}{dt} = \sigma_I E - (\mu+\delta_I)I - \tau_I I - \gamma I, \\ \dfrac{dM}{dt} = \gamma I - (\mu+\delta_M)M - \eta M, \\ \dfrac{dR}{dt} = \eta M + \tau_I I + \tau_A A - \mu R. \end{cases} \tag{2}$$

3 Analysis

Before calculating some of the mathematical properties of both models, the vectors for solutions are rearranged to have the infected states first. For both models, there are $m = 4$ infected states: E, A, I, and M. Thus, $\mathbf{x} = (x_E, x_A, x_I, x_M, x_S, x_R)^T$ for the SEAIMR model and $\mathbf{x}_V = (x_E, x_A, x_I, x_M, x_S, x_V, x_R)^T$ for the SVEAIMR model.

The disease free equilibrium (DFE) of the model is the steady solution to the model in the absence of the disease. For the model without vaccinations, there is only one compartment that contains individuals before infection. As such, it is trivial to calculate the DFE for the SEAIMR model which is $\mathbf{x}_0 = (0, 0, 0, 0, N, 0)^T$.

For the SVEAIMR model, the DFE is calculated by setting each differential equation to 0 and finding a solution. For the DFE, the infected states $E, A, I, M = 0$ which gives:

$$bN - \mu S - \rho S = 0 \text{ and } \rho S - \mu V = 0$$

Solving this simplified system for the values of S and V, the DFE of the SVEAIMR model is

$$\mathbf{x}_{0_V} = \left(0, 0, 0, 0, \frac{bN}{\mu + \rho}, \frac{\rho bN}{\mu(\mu + \rho)}, 0\right)^T.$$

Note if $b = \mu$, then $x_S + x_V = N$.

This paper uses the method outlined in [13] to calculate the basic reproduction number R_0 for both versions of the model. The epidemiological meaning of R_0 is the expected number of cases each new case will generate. When $R_0 < 1$, the DFE is locally asymptotically stable and the outbreak will eventually end. Otherwise, when $R_0 > 1$ the DFE is unstable and the disease will outbreak. As such, the basic reproduction value is useful in determining how contagious the disease is and whether the outbreak will go away on its own. As a result, the target of implementing various policies aimed at reducing infection is to reduce the magnitude of R_0 to below one.

We follow [13] to construct $\mathcal{F}$ and $\mathcal{V}$, where $\mathcal{F}$ contains the appearance of new infections and $\mathcal{V}$ contains other movement between compartments. Movement from E to A and I is treated as the progression of an already infected individual, so the SEAIMR model has the following:

$$\mathcal{F} = \begin{pmatrix} \beta S \frac{A+I}{N} \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{3}$$

and

$$\mathcal{V} = \begin{pmatrix} \mu E + \sigma_A E + \sigma_I E \\ \mu A + r_A A - \sigma_A E \\ (\mu + \delta_I) I + r_I I + \gamma I - \sigma_I E \\ (\mu + \delta_M) M + \eta M - \gamma I \\ \mu S - bN \\ \mu R - \eta M - r_I I - r_A A \end{pmatrix} \tag{4}$$

These matrices can then be used to construct F and V, defined by

$$F = [\frac{\partial \mathcal{F}_i}{\partial x_j}(x_0)] \quad \text{and} \quad V = [\frac{\partial \mathcal{V}_i}{\partial x_j}(x_0)].$$

Based on (3)-(4), the SEAIMR model has the following:

$$F = \begin{pmatrix} 0 & \beta & \beta & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} \mu + \sigma_A + \sigma_I & 0 & 0 & 0 \\ -\sigma_A & \mu + r_A & 0 & 0 \\ -\sigma_I & 0 & \mu + \delta_I + r_I + \gamma & 0 \\ 0 & 0 & -\gamma & \mu + \delta_M + \eta \end{pmatrix}.$$

This gives

$$V^{-1} = \begin{pmatrix} \frac{1}{\mu + \sigma_A + \sigma_I} & 0 & 0 & 0 \\ \frac{\sigma_A}{(\mu + \sigma_A + \sigma_I)(\mu + r_A)} & \frac{1}{\mu + r_A} & 0 & 0 \\ \frac{\sigma_I}{(\mu + \sigma_A + \sigma_I)(\mu + \delta_I + r_I + \gamma)} & 0 & \frac{1}{\mu + \delta_I + r_I + \gamma} & 0 \\ \frac{\gamma\sigma_I}{(\mu + \sigma_A + \sigma_I)(\mu + \delta_I + r_I + \gamma)} & 0 & \frac{\gamma}{(\mu + \delta_I + r_I + \gamma)(\mu + \delta_M + \eta)} & \frac{1}{\mu + \delta_M + \eta} \end{pmatrix}.$$

The basic reproduction number is equal to the spectral radius of FV^{-1}, i.e.,

$$R_0 = \beta \frac{\sigma_A(\mu + \delta_I + r_I + \gamma) + \sigma_I(\mu + r_A)}{(\mu + \sigma_A + \sigma_I)(\mu + r_A)(\mu + \delta_I + r_I + \gamma)}.$$

The same process can be applied to the SVEAIMR model. Applying the same logic to deciding what counts as a new infection, the model gives:

$$\mathcal{F}_V = \begin{pmatrix} \beta S \frac{A+I}{N} + \epsilon\beta V \frac{A+I}{N} \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{5}$$

and

$$\mathcal{V}_V = \begin{pmatrix} \mu E + \sigma_A E + \sigma_I E \\ \mu A + r_A A - \sigma_A E \\ (\mu + \delta_I) I + r_I I + \gamma I - \sigma_I E \\ (\mu + \delta_M) M + \eta M - \gamma I \\ \mu S + \rho S - bN \\ \mu V - \rho S \\ \mu R - \eta M - r_I I - r_A A \end{pmatrix}. \tag{6}$$

From this, we have:

$$F_V = \begin{pmatrix} 0 & \beta(\frac{b}{\mu+\rho} + \frac{\rho b}{\mu(\mu+\rho)}) & \beta(\frac{b}{\mu+\rho} + \frac{\rho b}{\mu(\mu+\rho)}) & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

and $V_V = V$. Therefore, the basic reproduction number for the model with vaccination is

$$R_{0_V} = \beta(\frac{\sigma_A(\frac{b}{\mu+\rho} + \frac{b\epsilon\rho}{\mu(\mu+\rho)})}{(\mu + r_A)(\mu + \sigma_A + \sigma_I)} + \frac{\sigma_I(\frac{b}{\mu+\rho} + \frac{b\epsilon\rho}{\mu(\mu+\rho)})}{(\mu + \delta_I + r_I + \gamma)(\mu + \sigma_A + \sigma_I)}).$$

4 Numerical simulations

4.1 Parametrization

The parametrization of the model is listed in Table 2.

Table 2: Parametrization of the model.

Parameter	Description	Value	Unit	Source
b	Natural birth rate	$\frac{1}{78 \cdot 365}$	$\frac{\text{person}}{\text{day}}$	[6]
μ	Natural death rate	$\frac{1}{78 \cdot 365}$	$\frac{1}{\text{day}}$	[6]
ρ	Vaccination rate	0.001	$\frac{1}{\text{day}}$	[7]
β	Transmission rate	-	$\frac{1}{\text{individual} \cdot \text{day}}$	-
ϵ	Vaccine efficacy	$50 - 90\%$	-	[8]
σ_A	Rate from E to A	$\frac{0.6}{5.1}$	$\frac{1}{\text{day}}$	[1]
σ_I	Rate from E to I	$\frac{0.4}{5.1}$	$\frac{1}{\text{day}}$	[1]
δ_I	Disease-related death rate (symptomatic)	$\frac{.013 \cdot r_I}{1-.013}$	$\frac{1}{\text{day}}$	[3]
δ_M	Disease-related death rate (hospitalized)	$\frac{.093 \cdot \eta}{1-.093}$	$\frac{1}{\text{day}}$	[15]
γ	Rate of hospitalization	0.083	$\frac{1}{\text{day}}$	[1]
η	Medical recovery rate	0.1	$\frac{1}{\text{day}}$	[1]
r_A	Recovery rate of asymptomatic	0.13978	$\frac{1}{\text{day}}$	[1]
r_I	Recovery rate of symptomatic	0.1	$\frac{1}{\text{day}}$	[1]

The death rate was calculated using the average lifespan for people in Rutherford County. The birth rate was set equal to the natural death rate. The vaccination rate was estimated by using data of Rutherford County to find the change in vaccinated individuals over a month. That was used to find the average number vaccinated per day which was then divided by the estimated total population of the county. The disease-related death rates were calculated using the following formulas:

$$\frac{\delta_I}{\delta_I + r_I} = .013 \qquad \frac{\delta_M}{\delta_M + \eta} = .093 \tag{7}$$

where .013 and .093 are the respective percentage of people that die as listed in the sources.

4.2 Model without vaccination

The numerical simulations were ran using MATLAB with the previously outlined system of differential equations. The initial values of the system assumed a small starting presence of the disease in the county. Although this does not perfectly reflect the current state of Rutherford County, the behavior of the model still provides useful information about how the presence of the disease might play out in the event of a surge after a lull in cases. The numerical values of the parameters were then plugged into the system to solve for the population of each compartment over a timespan of thirty days. The value of β is varied to see how it affects the model. The results are graphed in Figures 3-4.

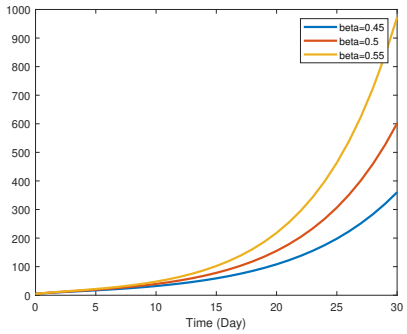

Figure 3: Newly Infected Cases for the model without vaccination.

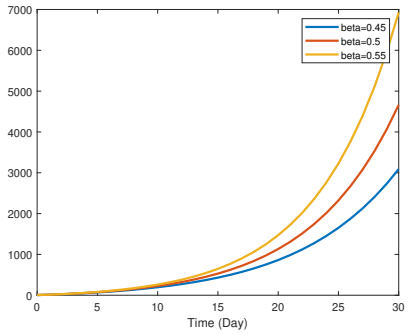

Figure 4: Accumulated Cases for the model without vaccination.

Note that these figures display the real number of cases based on the model. In real-world scenarios, not all cases are reported; some reports estimate up to 60% of cases go unreported in the United States [17]. What these figures show is that in the unvaccinated model of the county, new outbreaks will grow rapidly throughout the population. This is also shown when examining the corresponding values for R_0 which are presented in Table 3.

Table 3: R_0 for the model without vaccination.

β	R_0
0.45	2.9070
0.50	3.2300
0.55	3.5530

These values of R_0 are close to the confidence interval of $2.39 - 3.34$ given for the estimated value of the ancestral strain before intervention [4]. As such, the model without vaccinations acts as if there were little to no interventions in place. This suggests that, even assuming a modestly low rate of transmission, there is a need for more policies to control the spread in the absence of vaccinations. However, this would be offset somewhat when considering the R_0 would now be higher with increased presence of strains such as the Delta variant.

4.3 Model with vaccination

As with before, the simulations were run using MATLAB with the system of differential equations over a timespan of thirty days. Rather than varying the value of β, the value of ϵ is varied instead to judge how different levels of vaccine efficacy affect the simulation; $\beta = 0.55$ for the simulation. This simulation also used initial conditions assuming a small starting presence, but with the inclusion of how many people were vaccinated based on county data [7]. The starting point was selected to be August 1, and so the initial conditions were $\mathbf{y}_0 = (221811, 123089, 25, 25, 25, 25, 0)^T$ where the sum of all compartments is the estimated county population. The results are graphed in Figures 5-6.

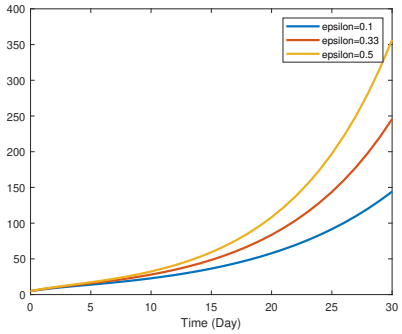

Figure 5: Newly Infected Cases for the model with vaccination.

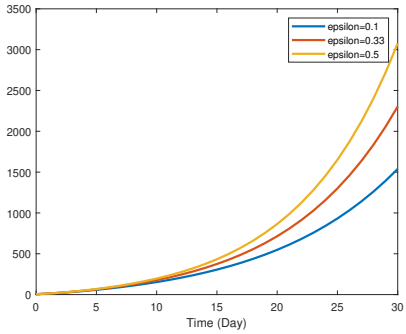

Figure 6: Accumulated Cases for the model with vaccination.

Although there is still large growth in cases over the given timespan, there are significantly fewer cases when compared to the SEAIMR model. The figures also visually demonstrate the importance of vaccine effectiveness; the cumulative cases for an assumed 90% effectiveness are about half of that in a situation with 50% effectiveness. The values of R_0 for each value of ϵ are presented in Table 4.

Table 4: R_0 for the model with vaccination.

ϵ	R_0
0.10	0.4638
0.33	1.2532
0.50	1.8368

Note that, in terms of the equation, a 90% vaccine effectiveness would correspond to $\epsilon = 1 - .9 = 0.10$, and so on. These estimations of R_0 are significantly lower than the estimations for the SEAIMR model under otherwise equivalent conditions. In fact, $R_0 < 1$ for $\epsilon = 0.10$, so the outbreak would be expected to die out in the long run for a 90% effectiveness scenario.

There is also data that lists the active cases, inactive cases, and hospitalizations for Rutherford County [12]. Using these values and assuming an equal proportion of asymptomatic and symptomatic cases, this gives a new vector of approximate initial values $\mathbf{y}_0 = (176208, 123089, 500, 250, 250, 1000, 43703)^T$. In addition, we can account

for the inclusion of unreported cases by multiplying the results by a factor $f = 0.4$ representing the estimated proportion of cases that are reported. The results of this simulation are graphed in Figures 7-8.

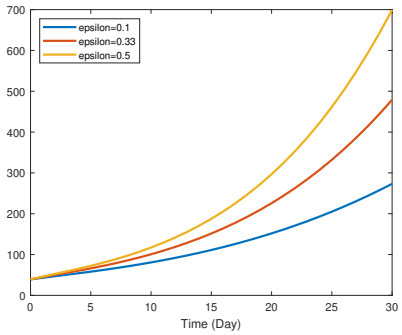

Figure 7: Reported Newly Infected Cases for the model with vaccination.

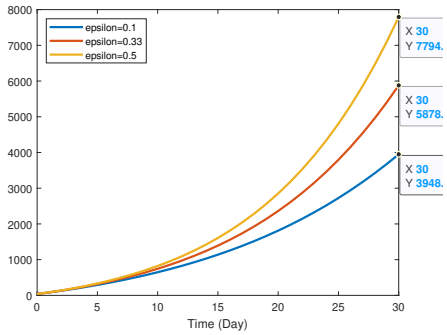

Figure 8: Reported Accumulated Cases for the model with vaccination.

Note that the values of the parameters were not changed, so the corresponding R_0 values are also unchanged. Based on the county data, there were a total of 6963 new cases reported over the time period of the model [12]. This number actually lies between the total reported cases for 50% and 66% vaccine effectiveness; this suggests the model is reflective of the real world data over this month for a vaccine effectiveness somewhere in that range.

5 Conclusion

In this paper, we proposed and analyzed the SEAIMR and SVEAIMR compartmental models of COVID-19 through computation of its mathematical properties and numerical simulations. The current model could be improved in the future through the utilization of the data to fit parameters like β; it is also partially limited in its long-term accuracy since a constant population was assumed. From the simulations, the SEAIMR model shows the number of cases in Rutherford County would potentially be much higher without the vaccination program in place. With a high enough

vaccine effectiveness, the SVEAIMR model will have a stable DFE in the county, but the numbers imply an efficacy too low for that. Since increasing vaccine effectiveness is infeasible at the local level, the county should consider additional intervention tactics to combat the disease, such as increasing the current vaccination program or implementing policies with other nonpharmaceutical interventions.

References

[1] D. Aldila, M. Ndii, and B. Samiadji. Optimal control on COVID-19 eradication program in Indonesia under the effect of community awareness. *Mathematical Biosciences and Engineering*, 17(4):6355–6389, 2020.

[2] Basics of COVID-19. `https://www.cdc.gov/coronavirus/2019-ncov/your-health/about-covid-19/basics-covid-19.html`. Accessed: 2021-05-21.

[3] A. Basu. Estimating the Infection Fatality Rate Among Symptomatic COVID-19 Cases in the United States. *Health Affaris*, 39(7), 2020.

[4] A. Billah, M. Miah, and N. Khan. Reproductive number of coronavirus: A systematic review and meta-analysis based on global level evidence. *PLoS One*, 15(11), 2020.

[5] S. Bugalia, V. Bajiya, J. 1 Tripathi, M. Li, and G. Sun. Mathematical modeling of COVID-19 transmission: the roles of intervention strategies and lockdown. *Mathematical Biosciences and Engineering*, 17(5):5961–5986, 2020.

[6] COUNTY PROFILE: Rutherford County, Tennessee. `http://www.healthdata.org/sites/default/files/files/county_profiles/US/2015/County_Report_Rutherford_County_Tennessee.pdf`. Accessed: 2021-10-07.

[7] COVID-19 Vaccinations in the United States,County. https://data.cdc.gov/Vaccinations/COVID-19-Vaccinations-in-the-United-States-County/8xkx-amqh. Accessed: 2021-09-16.

[8] COVID-19 Vaccine Effectiveness. https://covid.cdc.gov/covid-data-tracker/#vaccine-effectiveness. Accessed: 2021-10-07.

[9] COVID-19 Vaccines Work. https://www.cdc.gov/coronavirus/2019-ncov/vaccines/effectiveness/work.html. Accessed: 2021-10-19.

[10] Delta Variant: What We Know About the Science. https://www.cdc.gov/coronavirus/2019-ncov/variants/delta-variant.html. Accessed: 2021-10-18.

[11] Different COVID-19 Vaccines. https://www.cdc.gov/coronavirus/2019-ncov/vaccines/different-vaccines.html. Accessed: 2021-10-19.

[12] Downloadable Datasets, 'County New'. https://www.tn.gov/health/cedep/ncov/data/downloadable-datasets.html. Accessed: 2021-09-16.

[13] P. Driessche and J. Watmough. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences*, 180(1):29–48, 2002.

[14] FDA Approves First Treatment for COVID-19. https://www.fda.gov/news-events/press-announcements/fda-approves-first-treatment-covid-19. Accessed: 2021-05-21.

[15] L. Finelli, V. Gupta, T. Petigara, K. Yu, K. A. Bauer, and L. A. Puzniak. Mortality Among US Patients Hospitalized With SARS-CoV-2 Infection in 2020. *JAMA Network Open*, 4(4):e216556–e216556, 2021.

[16] E. Iboi, O. Sharomi, C. Ngonghala, and A. Gumel. Mathematical modeling and analysis of COVID-19 pandemic in Nigeria. *Mathematical Biosciences and Engineering*, 17(6):7192–7220, 2020.

[17] N. J. Irons and A. E. Raftery. Estimating SARS-CoV-2 infections from deaths, confirmed cases, tests, and random surveys. *Proceedings of the National Academy of Sciences*, 118(31), 2021.

[18] M. Santana-Cibrian, M. Acuña-Zegarra, and J. Velasco-Hernandez. Lifting mobility restrictions and the effect of superspreading events on the short-term dynamics of COVID-19. *Mathematical Biosciences and Engineering*, 17(5):6240–6258, 2020.

[19] Science Brief: Evidence used to update the list of underlying medical conditions that increase a person's risk of severe illness from COVID-19. `https://www.cdc.gov/coronavirus/2019-ncov/science/science-briefs/underlying-evidence-table.html`. Accessed: 2021-05-21.

[20] Symptoms of COVID-19. `https://www.cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html`. Accessed: 2021-05-21.

[21] WHO Coronavirus (COVID-19) Dashboard. `https://covid19.who.int/`. Accessed: 2021-10-14.

[22] WHO Director-General's opening remarks at the media briefing on COVID-19 - 11 March 2020. `https://www.who.int/director-general/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19---11-march-2020`. Accessed: 2021-05-21.

[23] H. Zhong and W. Wang. Mathematical analysis for COVID-19 resurgence in the contaminated environment. *Mathematical Biosciences and Engineering*, 17(6):6909–6927, 2020.