The Effects of Social Behavior and its Relation to COVID-19 in the State of New York

A Practical use of Ordinary Differential Equations

Emily McNeil, Directed by Dr. Sedar Ngoma

SUNY Geneseo Mathematics (GREAT DAY)

Abstract

When COVID-19 first reached the United States the virus impacted the various states differently. By determining the initial rate of increase of the disease for each state, the basic reproduction number, can be used to determine how contagious the disease is. The basic reproduction number, denoted as $\mathcal{R}_0$, is the average number of secondary cases produced by one infectious individual in an entirely acceptable population. Using the $\mathcal{R}_0$ value determined from data collected from the state of New York, we construct SIR/SEIR models to quantify the effects of social behavior, like social distancing and wearing masks, and the relation to how the pandemic has evolved.

Introduction

In the field of epidemiology, ODE systems are frequently used to describe the spread of diseases. Different models can be used to represent different effects of the disease. The SEIR (Susceptible-Exposed-Infected-Recovered) epidemic model studies the disease transmission. Given the data collected from the state of New York, we are able to calculate the basic reproduction number, $\mathcal{R}_0$. The $\mathcal{R}_0$ reflects the diseases ability to spread from one individual to the next. With the value $\mathcal{R}_0$, curves can be created from equations concerning $\mathcal{R}_{eff}$. With these curves, the success of non-pharmaceutical interventions (NPI's) can be quantified.

Main Objectives

1. Identify incidence data when NY first imposed stay-at-home orders and plotting the incidence data.
2. Graph a linear regression of the incidence data points to determine the slope of ρ.
3. Using ρ, the the growth factor of the disease, $\mathcal{R}_0$, can be determined.
4. Using the value of $\mathcal{R}_0$ determined from the data collected from the state of New York, curves can be formed to conduct a visual analysis of the success of NPI's.

Methods

In order to perform our analysis, we use the pre-existing SEIR model, which assumes a homogeneously-mixed population and accounts for the fraction of the population that is susceptible, exposed, infected, or had recovered from a novel disease.

Mathematical Section

A SEIR model normalized to a population:

$$\frac{ds}{dt} = -\beta si, \qquad \frac{de}{dt} = \beta si - \sigma e$$
$$\frac{di}{dt} = \sigma e - \gamma i, \qquad \frac{dr}{dt} = \gamma i$$

with $s + e + i + r = 1$, β = rate of effective contacts, $\frac{1}{\sigma} = T_{lat}$ = mean latent period, and $\frac{1}{\gamma} = t_{inf}$ = mean duration of infectiousness.

We also have the equation for cumulative number of cases:

$$\frac{dc}{dt} = \sigma e \tag{1}$$

so that daily incidence on day i is:

$$inc_i = c_i - ci - 1 \tag{2}$$

The spread of an infectious disease can be halted if its effective reproduction number $\mathcal{R}_{eff} = \mathcal{R}_0 s < 1$. The effective reproduction number for both the SIR and SEIR compartmental disease transmission models is:

$$\mathcal{R}_{eff} = \frac{\beta}{\gamma}s \quad \text{and} \quad \mathcal{R}_0 = \frac{\beta}{\gamma} \tag{3}$$

.

In general when $s \approx 1$, the early growth of both i and inc is exponential:

$$i(t) = i_0 e^{\rho t}, inc(t) = inc_0 e^{\rho t} \tag{4}$$

.

In the SEIR model, one can express $\mathcal{R}_0$ in terms of ρ:

$$\mathcal{R}_{0SEIR} = \frac{(\rho_{SEIR} + \sigma)(\rho_{SEIR} + \gamma)}{\sigma\gamma} \tag{5}$$

.

Using the incidence data from March 3 to March 13, we are able to obtain an exponential plot known as figure 1. With equation (2) from our SEIR epidemic model, we can determine a log-linear plot of the incidence data shown in figure 2. With the use of the incidence data and a discrete approximation of the solution to the SEIR models, we obtain the equation:

$$ln\frac{i(t+1)}{i(t)} = \rho_t \tag{6}$$

.

With the above equation, we can make the assumption $\rho_{SEIR} \approx \rho_t$. Then using equation (9) and the equation $\mathcal{R}_{eff}(t) = \mathcal{R}_0(1 - c(t))$, we are able to obtain an equation for $\mathcal{R}_{eff}$:

$$\mathcal{R}_{eff} \approx \frac{(\rho_t + \sigma)(\rho_t + \gamma)}{\sigma\gamma}(1 - c(t)) \tag{7}$$

.

The above equation creates a curve (figure 3) containing the value of $\mathcal{R}_{eff}$. With the curve we found in figure 3, we can now use this curve and compare it to our incidence data. In Figure 4, we are able to estimate human behaviors factors, such as social distancing and mask compliance, to that of the $\mathcal{R}_{eff}$. With the curve created, we are then able to determine the success of the pandemics non-pharmaceutical interventions (NPI's).

Numerical Results

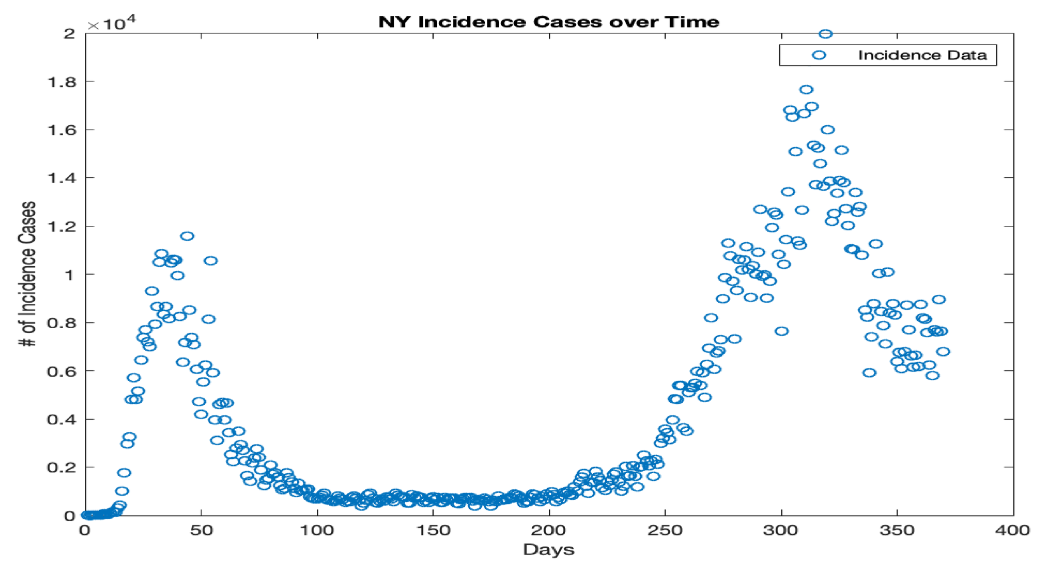

Figure 1: Daily COVID-19 incidence versus time from 3/3-3/24/2020.

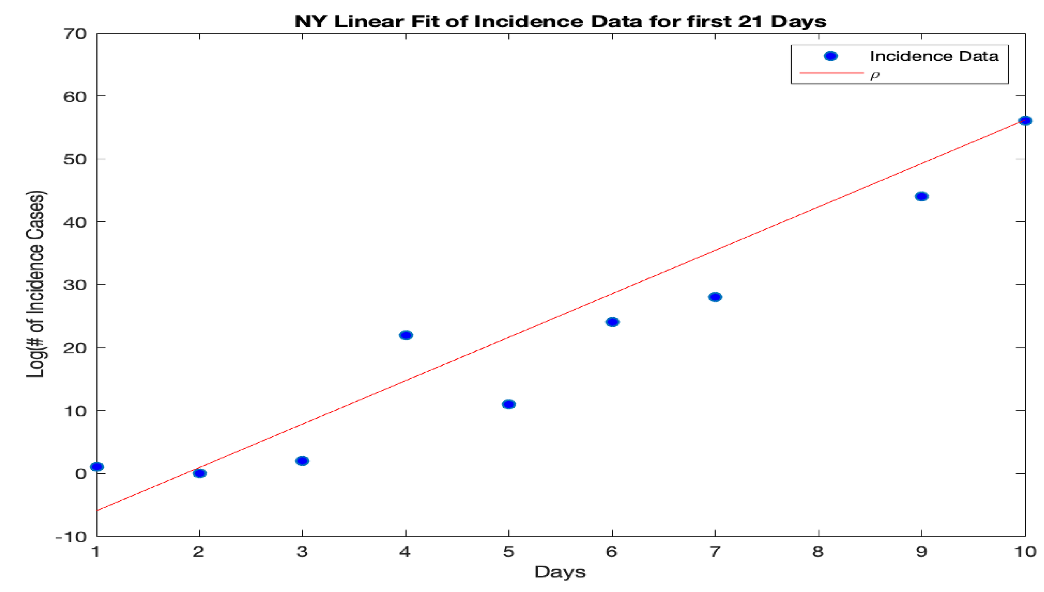

Figure 2: Log-linear plots of daily COVID-19 incidence versus time with a slope of ρ.

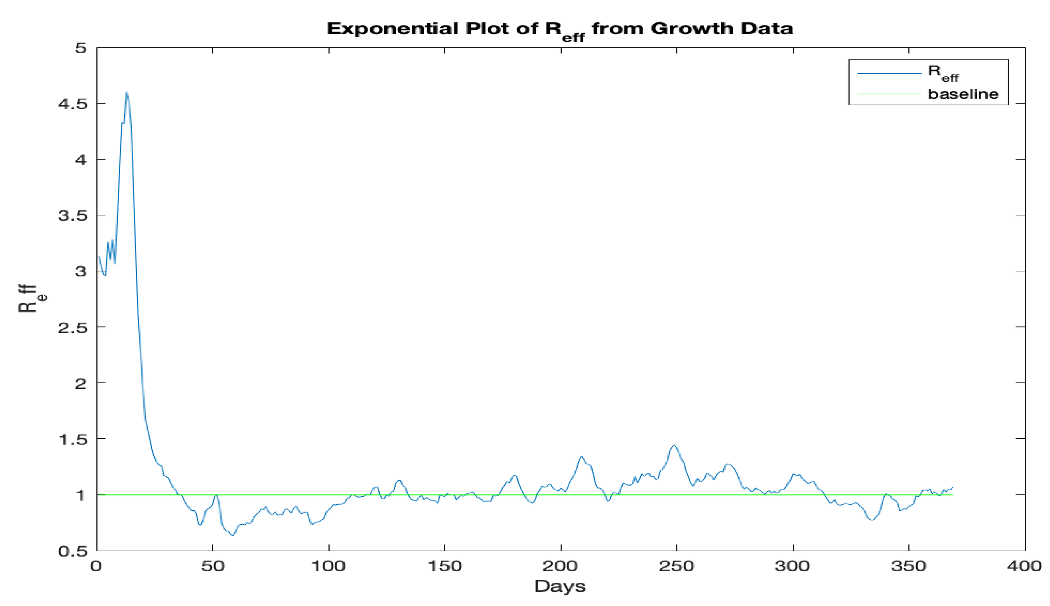

Figure 3: Exponential growth plot of the Incidence data containing the value of $\mathcal{R}_{eff}$.

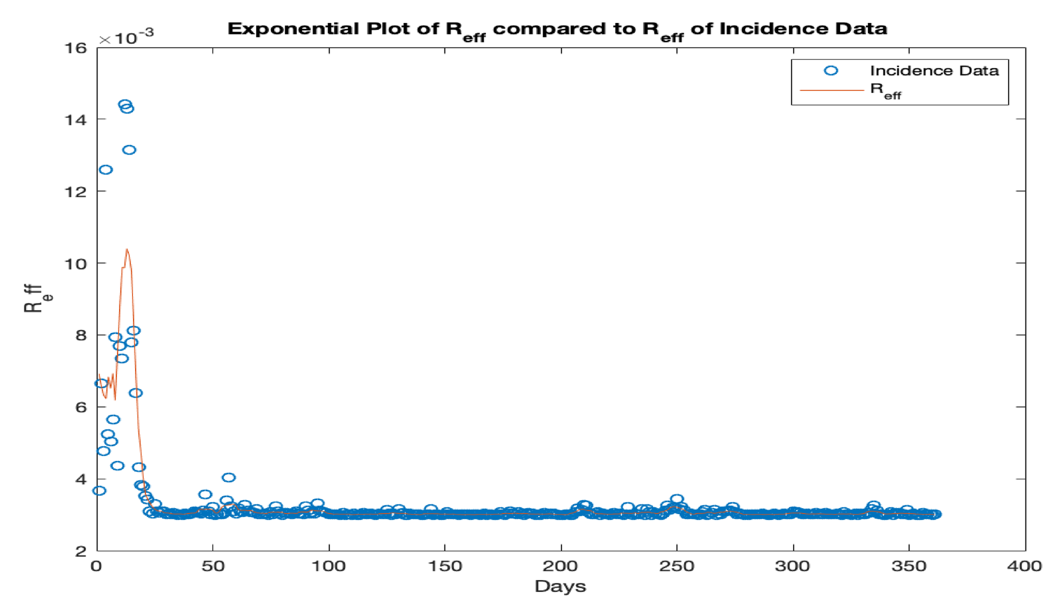

Figure 4: Comparing the value of $\mathcal{R}_{eff}$ determined to the $\mathcal{R}_{eff}$ of the Incidence data.

Conclusions

With the use of COVID-19 incidence data, different variables such as the reproduction number, $\mathcal{R}_0$, can be used to determine graphical analysis of human behaviors factors in the State of New York. These visual representations show us how successful the a region such as the state of New York can be successful with the pandemics non-pharmaceutical interventions (NPI's), such as social distancing and mask wearing. As we see in Figure 4, around the first 25 days before stay-at-home and mask compliance orders were placed, the disease, COVID-19, was more contagious. After stay-at-home orders were enforced, we can see that $\mathcal{R}_{eff} \approx 1$ which shows that the disease will be less contagious and less likely to cause an outbreak.

References

[1] Anastasopoulou, Cleo, et al. "Data-Based Analysis, Modelling and Forecasting of the COVID-19 Outbreak." PLOS ONE, Public Library of Science, Mar. 2020, journals.plos.org/plosone/article?id=10.1371

[2] "Data Download." The COVID Tracking Project, The Atlantic Monthly Group, 2021, covidtracking.com/data/download.

[3] Kermack William Ogilvy and McKendrick A. G., et al. "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, 1 Aug. 1927, royalsocietypublishing.org/doi/10.1098/rspa.1927.0118.

[4] Ramirez, Vanessa Bates. "What Is R0? Gauging Contagious Infections." Healthline, Healthline Media, 20 Apr. 2020, www.healthline.com/health/r-nought-reproduction-number.