Viral Basic Asymptomatic Spread and Impact of Social-Distance (V-BASIS)

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ABSTRACT

At the time of this writing, the debate over the origin, epidemiology, and policy regarding the novel coronavirus (COVID-19) is still intense across social media. One of the major sub-topics in the COVID-19 debate has been the surprise at the rapid and wide-spread community transmission on a global scale. The purpose of this paper is to present a basic model that visualizes the dynamics of community transmission of a novel disease and the effects that social distance has on a population. This paper will not delve into specifics of the COVID-19, nor try to project out impacts to real-world situations. This paper presents a model – Viral Basic Asymptomatic Spread and Impact of Social-Distance (V-BASIS) – that provides a simple graphic interface for researchers or interested parties can use to observe and analyze the results of community spread on different populations. The V-BASIS is an agent-based model implementation of the Susceptible-Exposed-Infected-Recovered (SEIR) framework and simulates random heterogenous agents (people) that move about a landscape. Two vignettes of the utility of the V-BASIS model to examine different epidemiologic characteristics and individual policy impacts to community transmission are presented.

1.0 Introduction

At the time of this writing, the debate over the origin, epidemiology, and policy regarding the novel coronavirus (COVID-19) is still intense across social media. One of the major sub-topics in the COVID-19 debate has been the surprise at the rapid and wide-spread community transmission on a global scale. While the origins and specific epidemiologic characteristics of the COVID-19 are undoubtedly being intensely investigated, the world has been quick to point fingers and make assumptions on the transmission parameters. This has been manifested in early shortages of medical personal protective equipment, cleaning supplies, and oddly enough, toilet paper. It has recently been revealed, however, that transmission of COVID-19 is likely occurring when little to no symptoms are being exhibited. (CDC 2020)

Another sub-topic focuses on the effectiveness of minimizing transmission rates by increasing the spatial distance between people and decreasing the probabilities of physical contact with infectious medium. This has been presented by the Center for Disease Control (CDC), which has recommended the need for "social distancing", staggered work shifts, downsizing operations, telework, and "other exposure-reducing measures". (OSHA 2019) While there are historical precedents of social distancing in the recent past, probably the most notorious was the Spanish Flu Pandemic of 1918. While over 102 years ago, the rapid spread of H1N1 caused widespread panic across the United States, with a mixed response of policy response from various cities. ("How Some Cities 'Flattened the Curve' during the 1918 Flu Pandemic" 2020) Regardless of historical precedence and scientific findings of the current pandemic,

it seems there is still some distrust in how mathematical models and resulting infection curves portray the situation.

The purpose of this paper is to present a basic model that visualizes the dynamics of community transmission of a novel disease and the effects that social distance has on a population. This paper will not delve into specifics of the COVID-19, nor try to project out impacts to real-world situations. This paper presents a model – Viral Basic Asymptomatic Spread and Impact of Social-Distance (V-BASIS) – that provides a simple graphic interface for researchers or interested parties can use to observe and analyze the results of community spread on different populations. The paper will illustrate how even a basic agent-based model can be used to address policy research. This paper addresses two research questions: firstly, what are the impacts of asymptomatic transmission compared with that of symptomatic transmission. Secondly, to what degree does social distancing impact the rate of community transmission.

2.0 Susceptible, Exposed, Infected, Removed (SEIR) Framework

This section presents a short overview of the Susceptible-Exposed-Infected-Recovered (SEIR) model that underpins the V-BASIS model presented below. The classical SEIR model divides a homogeneous population of a known size (N) into four categories: 1) those Susceptible (S) to the disease , 2) those that have been Exposed (E) to the disease, 3) those that were Infected (I) by the disease after exposure , and those that have Recovered (R) from the infection. Depending on the time scale, some models factor in additional known parameters such as birth, mortality, and vaccination rates. Interestingly, some researchers state that the SEIR is appropriate for diseases with a post-infection incubation period in which an exposed individual is not yet considered infectious. (Ameri and Cooper 2019) It is for these reasons that a SEIR model is used as a framework.

The SEIR model is often implemented as a systems dynamics model consisting of four main ordinary differential equations. (Ameri and Cooper 2019; "Analysis and Projections of Transmission Dynamics of NCoV in Wuhan" 2020; Schwartz and Smith 1983)
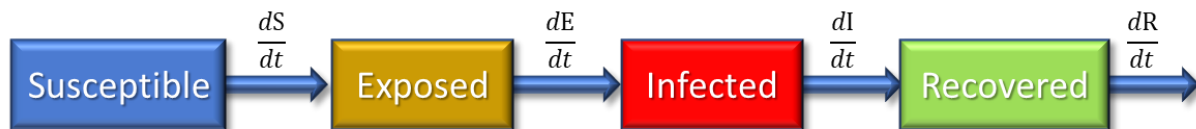

Figure 1 - SEIR Model

The susceptible (S) population changes are a function of the number of secondary infections each infected individual produces (C_0) and the infectious period (T_{inf}). As shown in equation 1 (eq1) the susceptible population decreases as the exposed and infected populations grow. This makes an important assumption that the Recovered (R) population is no longer susceptible to reinfection. In other words, once recovered the individual is immune, which is reflected in equation 4 (eq 4). The exposed population continues to grow at the expense of the susceptible population, but as the disease transitions from asymptomatic to symptomatic (incubation time (T_{inc})) progress, some of the exposed population transitions to the infected population (eq 3).

$$(Eq\ 1) \qquad \frac{dS}{dt} = -\frac{C_t}{T_{inf}} I\ S$$

$$(Eq\ 2) \qquad \frac{dE}{dt} = \frac{C_t}{T_{inf}} I\,S - T_{inc}^{-1}\,E$$

$$(Eq\ 3) \qquad \frac{dI}{dt} = T_{inc}^{-1}\,E - T_{inf}^{-1}I$$

$$(Eq\ 4) \qquad \frac{dR}{dt} = T_{inf}^{-1}\,I$$

3.0 The V-BASIS Agent-Based Model

In section 1, it was stated that the purpose of this paper is to present a basic model that visualizes the dynamics of community transmission of a novel disease and the effects that social distance has on a population. While the SEIR model as presented in section 2 could be implemented as a systems dynamic model or microsimulation model to solve for the total population N over a specified time t, using real-world epidemiological statistics, it would not meet the intent of this paper. A systems dynamics (SD) assumes a homogenous population (where all are equally susceptible, healthy, etc.) and takes a system-wide view of the process, abstracting minutiae such as spatial distancing. While a microsimulation model could better represent a target population, the movement and interaction between such population would not be modeled. For this reason, an agent-based model (ABM) of the SEIR is introduced.

Agent-based modeling is a computational modeling approach that employs individual agents to describe processes, phenomena, and situations in complex systems. (Wilensky and Rand 2015) The agents are often heterogenous and interact with their environment, as well as other agents, according to a set of rules. These interactions aggregate to allow for a bottom-up dynamics and analysis of non-linear systems. (Gilbert and Troitzsch 2005; Axtell 2000) ABM are well suited to emulate potential disease transmission, such as the SEIR model, since they allow the researcher to control population, infection rates, social habits, and the landscape and iterate over large populations multiple times. (Jacobsen et al. 2016)

3.1 V-BASIS

The V-BASIS ABM is a simple agent-based model that models a susceptible population of agents (people) with a certain percentage of people starting off infected and steps through the SEIR model over time, allowing the researcher to visualize the spread. The model is implemented in NetLogo and provides the user with several controls to instantiate the model, set epidemiological parameters, policy response, and visualizations to analyze the transmission over time and space.
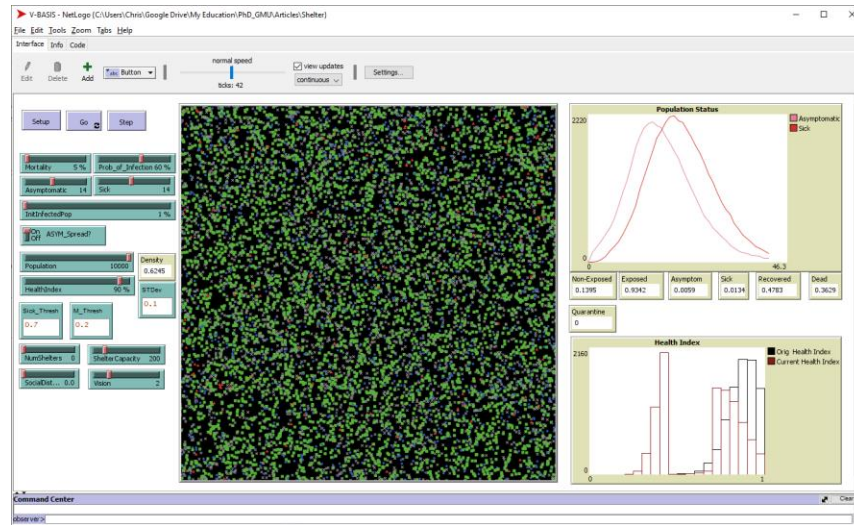
Figure 2 - V-BASIS Interface

3.1.1 Landscape

The initial landscape in the basic model is a toroidal grid of homogenous patches (landscape) of 101 x 101 (a total of 10201 patches). While there is no specific spatial geography, the model is stylized for each patch to represent a 6 foot by 6 foot square (36 square feet). Based on the classical concept of proxemics (Hall et al. 1968), space within this landscape is based on an arbitrary unit distance that is then apportioned into intimate, personal, and social spaces. Intimate space is generally anything within 0-2 feet, personal from 2-4 feet, and social from 4-10; after 10 feet, the space is regarded as public and
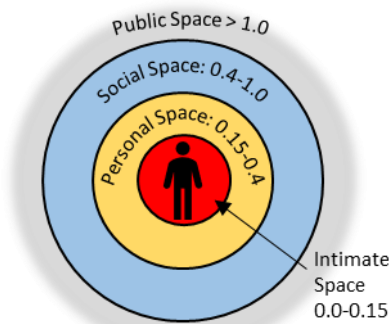

Figure 3 - Social Space (Proxemics) Dervied from Hall et. al., 1968

of no consequence to agents. Each patch is 6 x 6 pixels, yielding a 1 pixel : 1 foot scale. Based on CDC guidance (OSHA 2019), a sneeze has the ability to propel droplets up to 6 feet from the host, therefore any agent that falls within a 0.0-0.6 unit distance from another turtle is considered to be within the intimate to close-social zone and susceptible to physical or aerial contact.

3.1.2 Agents

People. The primary agent in this model is the Person (People). Each person is instantiated with an original health index falling in a normal distribution controlled by the HEALTHINDEX and STDEV controls. The model currently allows for up to 10000 agents (N = 10000), which allows for a population density of 0.999. As agents traverse the landscape, they come into contact with agents in their immediate distance, which is defined as being in within the intimate to close-social range (section XX). If an

exposed/infected individual is in the same proximity of another susceptible (non-exposed) person, then that person has Pi probability of being infected. If infected, that person transitions to being asymptomatic for T_{inc}. As time progress, the likelihood of the individual becoming symptomatic increases. Once symptomatic, the individual's health degrades rapidly, and those with already compromised systems (lower health index) have a greater chance of succumbing to the disease.

orig_health	Starting health of individual
health	Current health of patient
status	Current state of the agent
statchange	Time of last status change
exposed?	Has this agent been exposed to the virus?
infected?	Has this agent been infected?
recovered?	Has the agent recovered... assuming immunity.
quarantined?	Is this agent current under quarantine?

Figure 4- People State Variables

Quarantine Shelters. Quarantine Shelters are an optional agent in this model which simulate shelters such as hospitals or quarantine shelters. These agents aggregate infected people in their field of regard and transport them to the center. Once within a shelter, the agent's health degrades at a slower rate. If recovered, the agent is checked out of quarantine and moves about the landscape. Quarantine shelters have predefined capacity, which cannot be exceeded. Once at 100%, the shelter will stop aggregating agents and will only accept newly infected once current agents are recovered or succumb to the infection.

3.1.3 Model Execution

The model execution randomly activates every agent each time period t. Each time period is stylized as a day where each agent moves across the landscape (walk) and interacts with individuals. If the Quarantine Shelters are activated, the agents are Quarantined based on their current health status. The model then has each agent update their state of health according to figure 5, which is adapted from the SEIR model described in section 2.0.
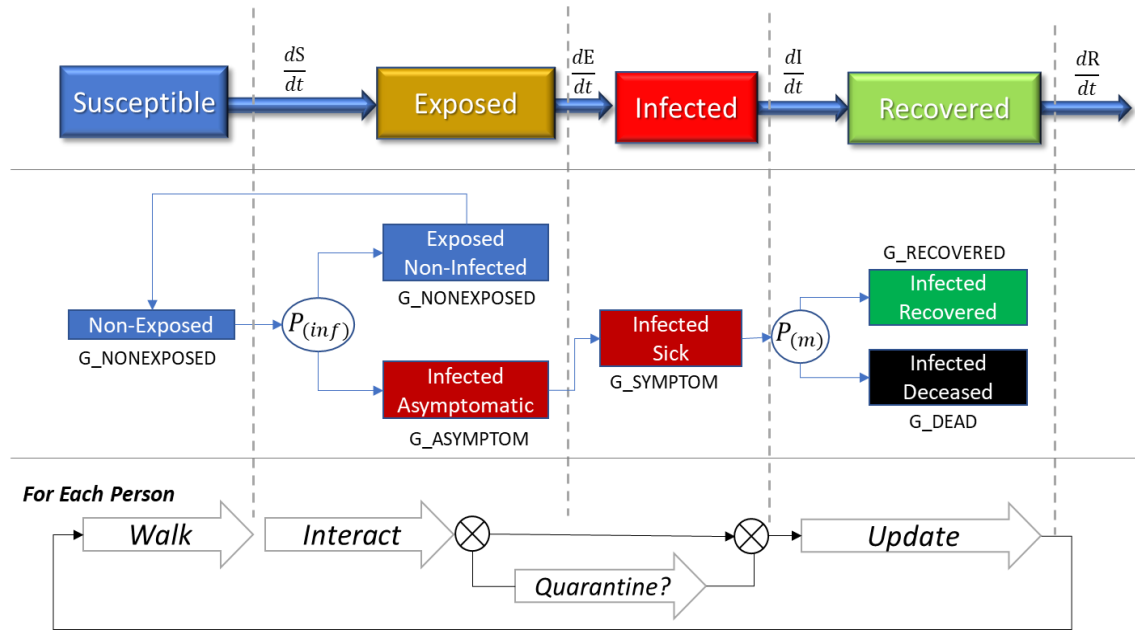
Figure 5 - Model Execution

4.0 Research

4.1 Methodology

To demonstrate the ability of using V-BASIS to model community spread and explore different policy implications, the model was verified using unit testing and code walk throughs. The validation was pattern-based using real world data provided by the Johns Hopkins and the European. For each test, the model was randomly instantiated and run 100 times for each parameter set. The results were aggregated to average out statistical outliers and abstract spatial stochasticity. The results below were derived using Python and associated packages (pandas, numpy, scipy, matplotlib, and seaborn).

4.2 Impacts of Symptomatic vs. Asymptomatic

In section 1, the subtopic of symptomatic versus asymptomatic spread was briefly presented as a sub-topic of the current COVID-19 discussions. Specifically, can an agent-based model visualize the spread of an asymptomatic virus and, if so, what are the impacts of asymptomatic transmission compared with that of symptomatic transmission. When considering diseases such as Ebola that have high probabilities of infection and high mortality rates, but minimal observed asymptomatic transmission, infections tend to die out quickly if they are able be localized. This was the case in the 2014 PHEIC EVD in West Africa. Conversely, it has been established that COVID is transmitted without symptoms being present, which has significant challenges. Running the model 1000 times over the same range of parameters, but varying the asymptomatic period (T_{inc}) from 0 (no asymptomatic transmission) to 21-days, results in the following plot:

Total Infected Population
(Asymptomatic + Symptomatic + Sick)

Figure 6 - Asymptomatic Plots
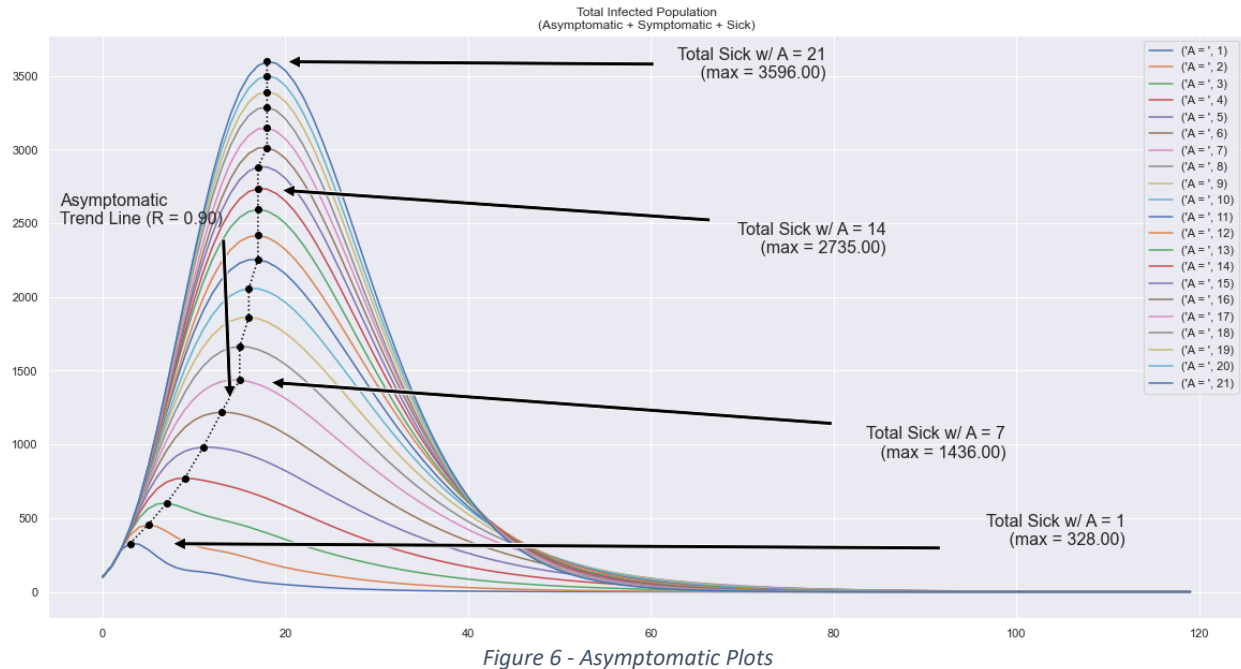
Compared to current data obtained through the Johns Hopkin's University, the modeled results are similar in shape and follow a general logistic and exponential growth pattern. While the data plotted

Figure 7 - Real-World vs. Model Results
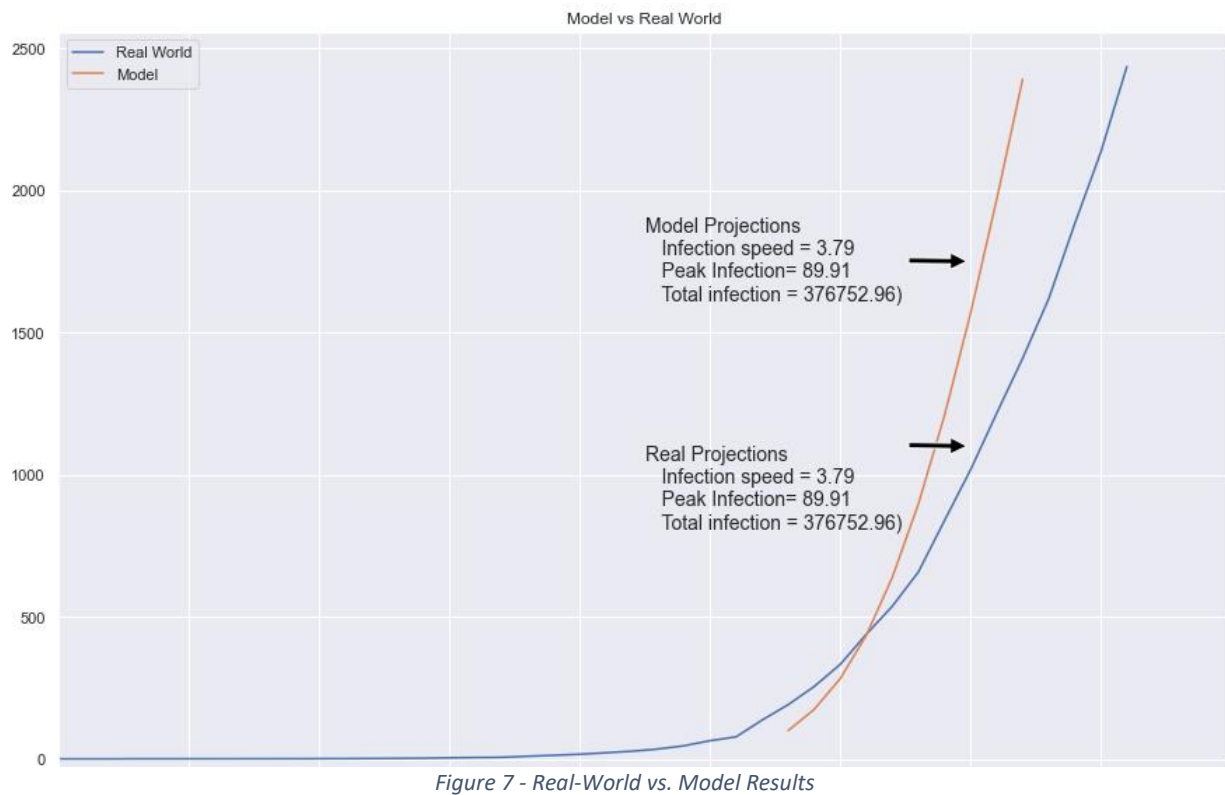
below are from the US Aggregate dataset, it may be interesting to plot the model results against city-level data, calibrating the landscape to match density and population.

4.3 Social Distance

The V-BASIS ABM is able to examine different policy impacts at the individual level, whereas more traditional SEIR models cannot. Specifically, to what degree does social distancing impact the rate of community transmission? Similarly, to the Asymptomatic test, running the model 1000 times over the same range of parameters, but toggling on Social Distance from 0.0 to 1.0 as described in Section 3.1.1. The following plot illustrates the impacts of social distancing on transmission rates.
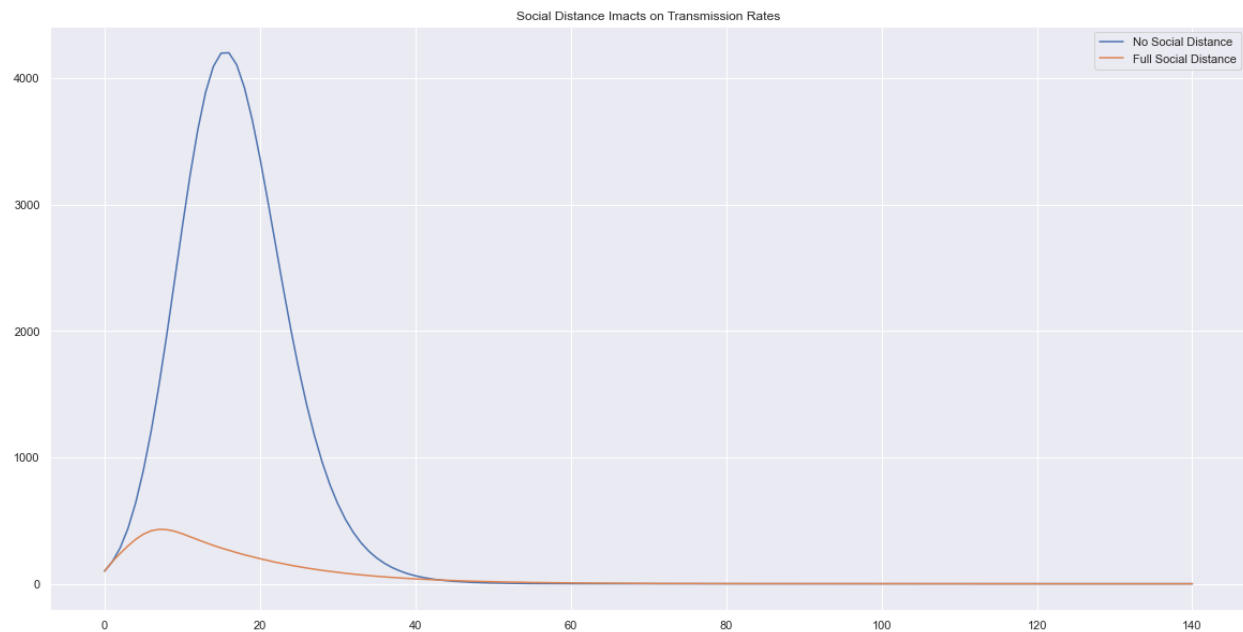

Figure 8 - Social Distance vs. No Social Distance

5.0 Conclusion

The purpose of this paper was to present a basic model that visualizes the dynamics of community transmission of a novel disease and the effects that social distance has on a population. The Viral Basic Asymptomatic Spread and Impact of Social-Distance (V-BASIS) model provides a simple graphic interface to observe and analyze the results of community spread on different populations. The paper described the model concept, structure, and presented a quick analysis of the impacts of asymptomatic transmission compared with that of symptomatic transmission. Secondly, the paper illustrated the ability to examine aggregate impacts of individual policies, such as social distancing, and their impact the rate of community transmission. Recommended future uses of this model could be to incorporate heterogenous landscape (down to a building level), alternate movement (shifts), and incorporate social networks. The V-BASIS Model can be found at https://github.com/boychrisparrett/V-BASIS.

Acknowledgements

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