

Covid Spread Using Agent-Based Modeling

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I. INTRODUCTION

The COVID-19 pandemic has brought to the forefront the importance of understanding and managing infectious disease outbreaks. One way to achieve this is through simulations that can accurately predict the spread of a virus under different environmental conditions. In this report, we will explore the simulation of virus spread under various parameter variables such as population size/density, infection probability, and infection radius.

Simulations can provide valuable insights into the potential impact of a virus and the effectiveness of different measures or protocols that can be implemented to prevent its spread. With the use of sophisticated algorithms and models, we can simulate the spread of a virus in a virtual environment, making it possible to explore different scenarios and test different interventions.

We will consider the effects of population density on the rate of virus spread, as more densely populated areas typically present greater challenges in containing a virus. We will also examine the impact of infection probability, which is the likelihood of an individual getting infected by coming into contact with an infected person. Furthermore, we will explore the role of infection radius, which refers to the distance over which the virus can spread from an infected individual.

By understanding how different variables affect the spread of a virus, we can gain valuable insights into the measures or protocols that should be taken under various environmental conditions to effectively contain and manage a virus outbreak. This report will provide a comprehensive analysis of the simulation of virus spread, and the findings will have implications for public health policy and practice.

All the code for this project is available on our [GitHub](#). Including the necessary Python libraries and working environment to run the code.

II. APPLICATION

A. Model Description

This model simulates the spread of COVID-19 in a population based on certain parameters such as initial population, initial COVID-19 rate, catching COVID-19 probability, fertility factor, and mortality factor. The initial COVID-19 rate is a proportion of the population that is considered infected on day zero of the simulation. The "catching COVID-19 probability" is a float number between 0 and 1, the fertility factor is a scalar multiple that is used to increase the pregnancy rate of females in the population, and the mortality rate works similarly to the pregnancy rate but for covid-related deaths. A woman can only give birth when uninfected and deaths only occur when someone is infected. The population is represented by individuals who can move in random directions on a two-dimensional grid with the width and height specified by the user. Each person has a unique identifier, location, age, gender vaccination status and infection status. The model is designed to track the number of healthy and infected people, as well as the number of births and deaths over time.

The model starts by initializing the population and assigning COVID-19 to a certain number of people based on the initial COVID-19 rate. Then, the model runs through each day, updating the population by checking whether each person catches COVID-19 based on their proximity to infected individuals and the

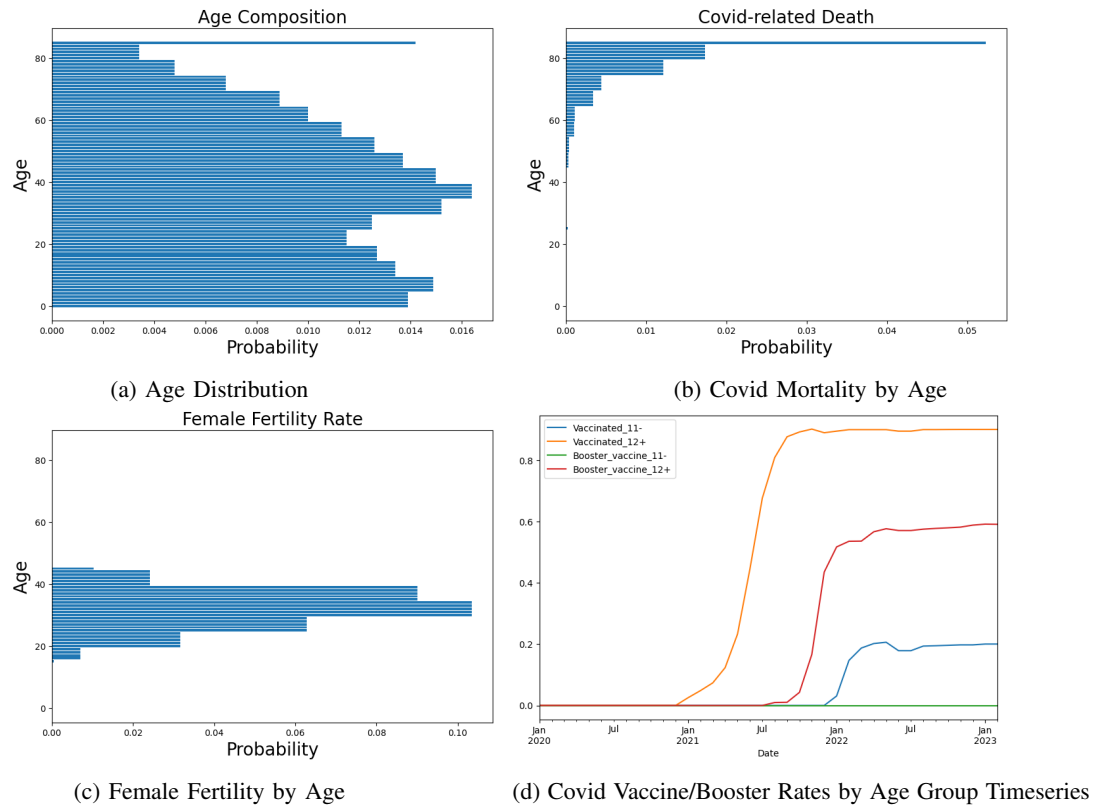


Figure 1: Irish Population Statistics

catching COVID-19 probability. Infected individuals have a chance of dying based on the mortality factor. A healthy woman can give birth based on fertility factor.

The model also allows for the simulation of vaccinations, with the start date of the vaccination campaign set by the user. In our model, the date reflects the actual release of the COVID-19 vaccine in Ireland. The model tracks the number of vaccinated individuals and updates the population dynamics accordingly.

The model outputs plots of the population contained within a two-dimensional grid, as well as the number of healthy and infected individuals, births and deaths over time and the relationship between the number of infected and healthy people. The simulation can be saved to a directory if specified by the user. The model design is based on a realistic representation of population dynamics, and the inclusion of various parameters allows for the simulation of different scenarios.

B. Data Collection and Processing

We decided to base our agents on real statistics about the Irish population to create a realistic ABM. This includes assigning the agent a random age and sex based on the Irish age and sex composition found from the 2016 CSO census¹, we assigned females a fertility rate based on the 2020 CSO birth records² and assigned agents a mortality rate by age based on covid related deaths from the HSPC 2020-2023 Covid report³. We also included realistic vaccination data based on covid vaccination and booster data starting in 2020 up until 2023⁴. The processed data for age, sex, mortality and fertility can be found in the JSON file [person_probabilities.json](#) while the vaccine and booster time series data is stored in the CSV file [vaccination_stats.csv](#)

In [Figure 1](#), we present three bar graphs based on the statistics mentioned above, these are the distributions

¹Census

²Birth Data

³Covid Deaths

⁴Vaccine Data

used to create our agents. The first figure (1a), shows the age distribution of the Irish population, with age on the y-axis and their corresponding population percentage on the x-axis. In Figure 1b we illustrate the Covid-related mortality rate by age followed by Figure 1c, which presents the probability of a female giving birth depending on their age. Due to the way that CSO shares their data, certain ages have the same statistics, for example, in the age composition graph (1a) the percentage of people who are 0 years old is the same as people who are 1,2,3 and 4 years old. While the statistics for anyone over the age of 85 are grouped into one, this is why the graphs 1a and 1b contain a large spike for the age of 85. The final graph, Figure 1d is a time series plot of the percentage of the population who are vaccinated or has one booster, this is split into two age categories, the first includes people who are 11 years old or younger and then the second group includes the remaining people. Since our model is based on real statistics we decided to start our model on the same date that is used in the vaccination data, which is the first of January 2020. That is the reason why the agents in our model can not get vaccinated until the first of January 2021, the month that the Irish population began to get vaccinated.

During the initialisation of the ABM, the `model.py` script imports the population characteristics from `person_probabilities.json` and uses the Person class from `Person.py` to randomly assign each person their age and sex based on the statistics collected such that the expected population distribution should match the real data.

C. Model Interface

To run the simulation, follow the steps outlined in the README.md file. Once the necessary environment is correctly set up and you have run the `model.py` script, the simulation and the control panel will open in a new window. The control panel includes four sections but the two that we believe are the most important to understand are the sections titled "Run" and "Parameters". These two sections can be broken down further as seen in Figure 2.

- Run
 - 1) **Continue Run/Pause:** This function is used to continue the simulation when you have paused it and to pause it when it is running.
 - 2) **Step Once:** This allows you to simulate one time step at a time before pausing the simulation again.
 - 3) **Reset:** This resets the ABM back to the original values at step 0.
- Parameters
 - 1) **Population:** This is a positive integer which allows the user to adjust the initial population of the ABM.
 - 2) **StartingCovidRate:** This is a positive float number between 0 and 1 which is used to randomly assign Covid to a proportion of the population. The expected number of covid cases on day zero is equal to $Population \times StartingCovidRate$
 - 3) **MortalityFactor:** This is a positive scalar number used to increase/decrease the probability of an infected agent dying of Covid. When this value is set to 1.0, the death rate is modelled by the death statistics found from the real Irish population.
 - 4) **FertilityFactor:** This follows the same principles as MortalityFactor but is instead used to increase/decrease the probability of a healthy female agent giving birth
 - 5) **CatchingCovidProbability:** This is a positive float number between 0 and 1, the user can use this parameter to set the probability of a healthy agent catching covid if they are with the InfectionRadius of an infected agent.
 - 6) **InfectionRadius:** This is the aforementioned InfectionRadius, this variable is used to change the maximum distance that someone can catch covid from.
 - 7) **SaveModelData:** The final parameter is a boolean variable which can either be True or False, it does not have any impact on the simulation's outcome but it is instead used to save various statistics about the model to a text file inside the data directory.

III. EXPERIMENTS

We aimed to investigate the impact of two crucial parameters on the spread of a virus in a population: infection radius and infection probability. Specifically, we examined the effect of these parameters in two distinct population densities, namely low and high. Furthermore, we explored the conditions that led to a

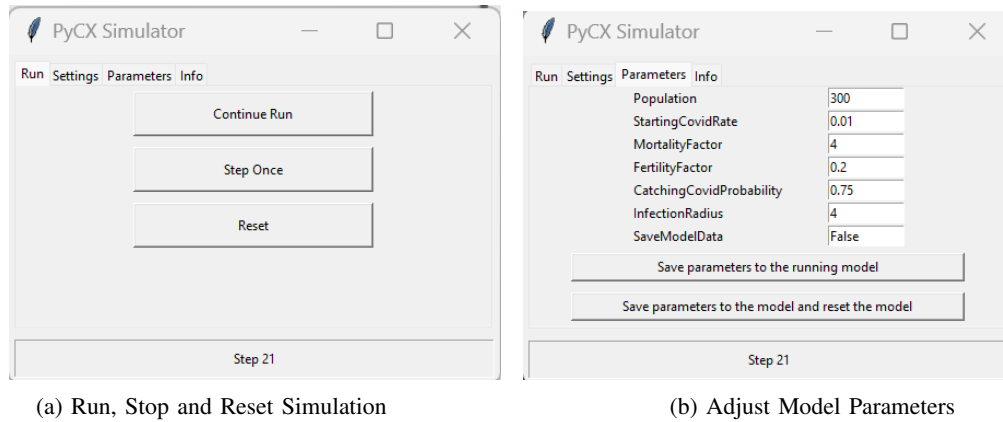


Figure 2: The GUI of the ABM

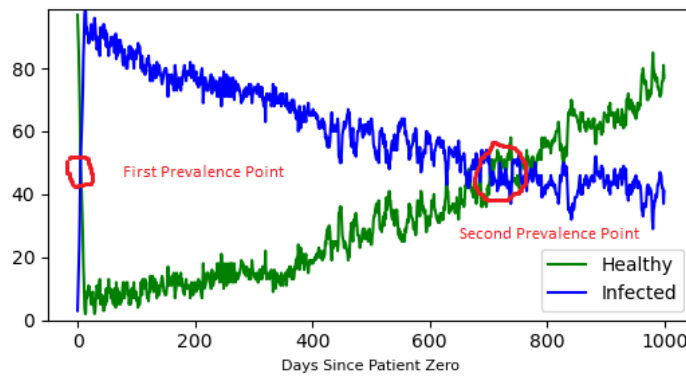


Figure 3: Prevalence Points

catastrophic outbreak of the virus resulting in a complete wipeout of the population. On the other hand, we also analyzed scenarios where rapid vaccination strategies were implemented, and their impact on the spread of the virus was evaluated. Our experimental investigations may provide insights into the dynamics of virus spread and could assist policymakers in devising effective strategies to contain outbreaks and safeguard populations.

A. Assumptions

During the model design and experiment implementation, a number of assumptions were taken into consideration. These assumptions aimed to capture the key insights gleaned from our data analysis in the hopes to streamline the simulation process. Specifically, we made the following assumptions:

- The likelihood of mortality decreases with age.
- Women exclusively give birth when they are healthy.
- Infection is the only cause of death.

B. Experiments

Twelve experiments were conducted over a period of 1000 days, varying across different conditions to simulate and assess the impact of different outbreak types. To distinguish between outbreak types, the first two prevalence points were identified, where a prevalence point signifies the day when the infection rate surpasses 50% of the population. In Figure 3, the prevalence points are depicted as the intersection between the healthy and infected populations. Slight outbreaks have no prevalence points and therefore never exceed a 50% infection rate. Moderate outbreaks, on the other hand, have two prevalence points where the infection rate rises, reaches a peak, and eventually falls. Severe outbreaks, however, have only one prevalence point where the infection rate remains above 50% throughout the entire simulation period.

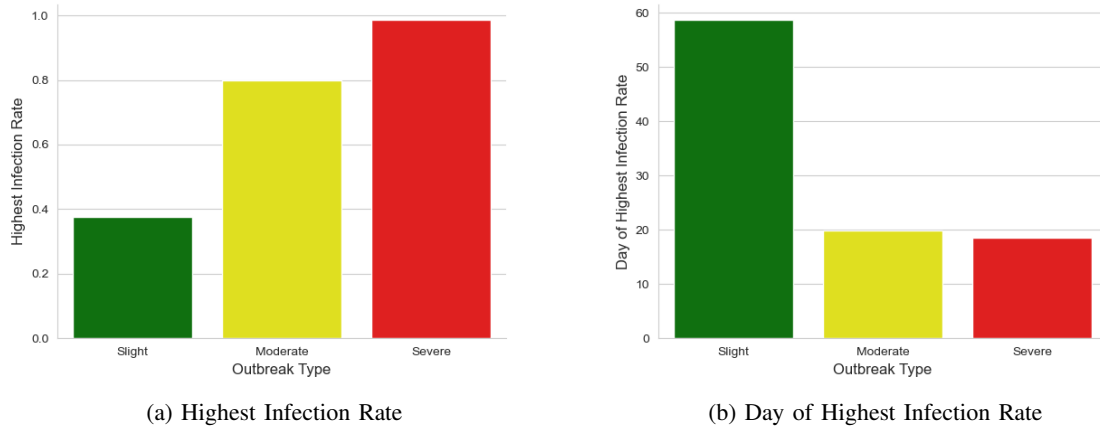


Figure 4: Comparison of Slight, Moderate and Severe Outbreaks based on Key Metrics

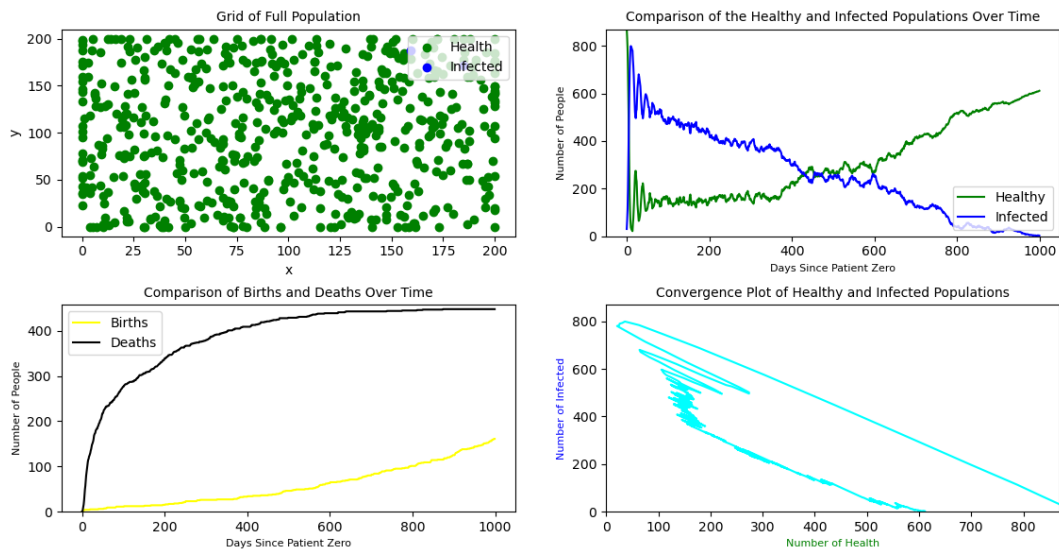


Figure 5: High Density Population Simulation

To compare the different outbreak types, Figure 4 was generated, where Figure 4a represents the proportion (ranging between 0 and 1) of the population that is infected and shows that more severe outbreaks are associated with higher infection rates. Figure 4b, on the other hand, demonstrates that more severe outbreaks reach their peak faster than less severe ones, as it compares the average day that each outbreak type reaches its peak.

C. Low Density vs. High Density Population

Population density played a crucial role in each simulation. We tested the effects of low and high-density populations on the spread of a virus.

The results of the high-density population simulation are shown in Figure 5. In this simulation, there were 900 agents in the grid with an infection rate of 0.99. The top left plot displays the 2-D grid of each agent, with all agents healthy by the end of the simulation. The top right plot compares the number of healthy and infected individuals at each point in the simulation. The bottom left plot compares the birth and death rates for each day of the simulation. The bottom right plot is a phase space of the number of healthy and infected people.

We observed an initial rapid spike in cases, leading to a high number of deaths. As the population decreased,

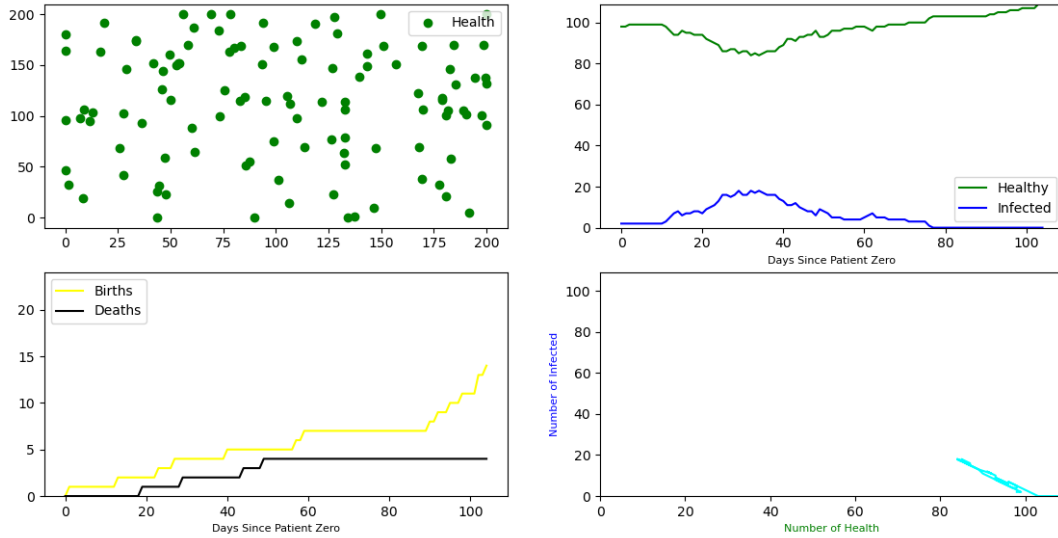


Figure 6: Low Density Population Simulation

the number of cases and deaths also decreased. This represented a negative feedback loop in the model. The virus is dependent on people to be transmitted. As the virus spreads, more people die and therefore there is less chance of the virus being transmitted. Around day 370, there was a clear change in the trajectory toward a healthier population, which we attribute to the rollout of vaccines. Vaccines had a significant impact on the spread of the virus by improving immunity in people. These findings were supported by the phase space plot, where the population first tended toward the infected but then swung back to the healthier side. In the end, there were only 600 individuals, a net decrease of 300 people in the population. As the number of COVID cases decreased, the number of births increased due to women being able to give birth.

In [Figure 6](#), we investigated the effects of low infection radius on a low-density population. We observed an initial spike at around the thirty-day mark, but the curve was flattened, and things went back to normal. This was reflected in the lack of deaths and change of movement in the phase space plot in the bottom right.

Infection radius is an essential factor that controls a virus's ability to spread. The contrast between high and low-density populations clearly demonstrates these effects.

D. Survivor Analysis

Through analysis of survival rates during a virus outbreak, we can better prepare for future occurrences by prioritizing vulnerable populations. Age and gender are two crucial factors that we examined. Our investigation enabled us to generate population pyramids, which are presented in [Figure 7](#). The simulation produced high death and infection rates, leading to a significant decrease in the number of births. The impact of the outbreak was most pronounced in older age groups. While apparent differences in gender were observed among younger individuals, we attribute these results to randomness, as they were not statistically significant.

This data was gathered from a simulation with high population density, and mortality and infection rates. We can see that the older population were most vulnerable to virus attack. The simulation ended on day 152. This is before any vaccine was rolled out. Therefore, everyone who died was unvaccinated. This is a common theme across all simulations. Most deaths occur in the early part of the simulation. [Figure 8](#) illustrates how more severe viruses transmit through the population more rapidly than slight outbreaks. Within a few days, the severe viruses had been transmitted through over 95% of the population.

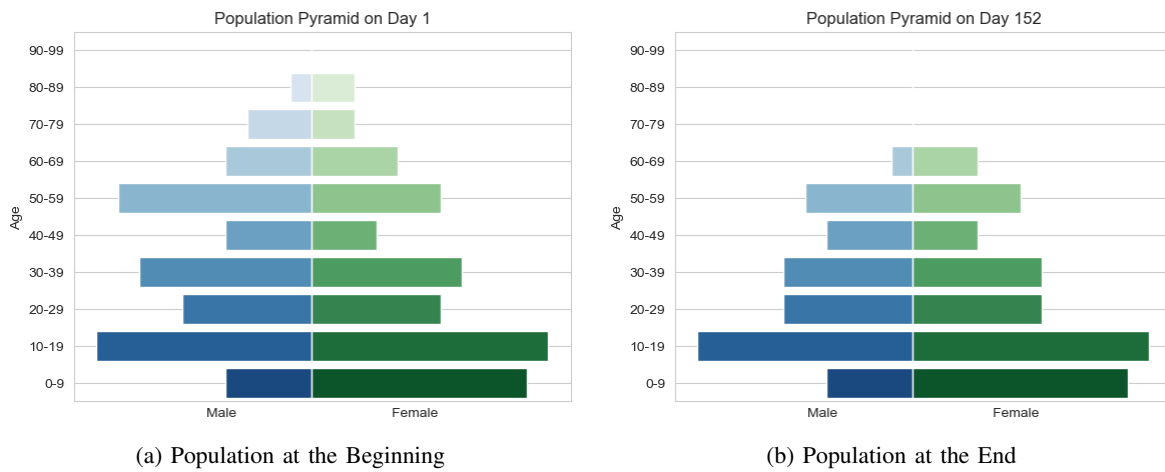
IV. CONCLUSION

Based on the experiments conducted in Section III, it is clear that the spread of a virus is affected by several variables, including population density, infection probability, and infection radius. The simulations revealed that higher population densities led to more rapid and widespread virus transmission, highlighting the

importance of implementing effective control measures in densely populated areas. Moreover, the infection probability also played a critical role, with a higher probability leading to a faster spread of the virus.

The experiments also demonstrated that vaccination campaigns can have a significant impact on reducing the number of infections and deaths. The simulations showed that a well-executed vaccination campaign can lead to a substantial reduction in the number of infections, especially if implemented early enough. Furthermore, the simulations showed that vaccine hesitancy could hinder the effectiveness of a vaccination campaign, highlighting the importance of public education campaigns to encourage vaccine uptake.

In conclusion, the agent-based model presented in this report has shown that simulations can provide valuable insights into the potential impact of a virus and the effectiveness of different measures or protocols that can be implemented to prevent its spread. The findings of the experiments conducted in this report have implications for public health policy and practice, highlighting the importance of effective control measures, early implementation of vaccination campaigns, and public education campaigns to encourage vaccine uptake. Overall, this report demonstrates the potential of agent-based modelling to inform decision-making during infectious disease outbreaks.



(a) Population at the Beginning (b) Population at the End
Figure 7: Comparison of Population Age and Gender Before and After Outbreak

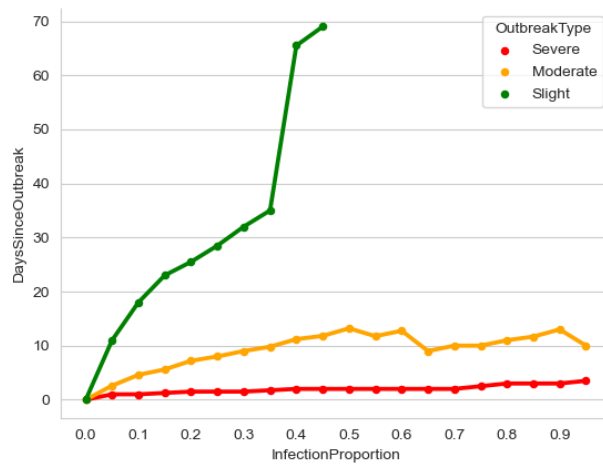


Figure 8: Rate of Virus Transmission for Outbreak Type