ADVANCED "COVID-6644" PANDEMIC SPREAD SIMULATION USING A SEIR MODEL

A Project
Presented to
The Academic Faculty of ISYE 6644

By

Juan Raul de la Guardia
Pong-Ravee Halelamien
Ethan Maluhia Roberts
Anna Zhu

For ISYE 6644 Simulation and Modeling
in the Master of Science in Analytics Program
H. Milton Stewart School of Industrial and Systems Engineering
College of Engineering

Georgia Institute of Technology

Dec 2023

TABLE OF CONTENTS

Abstract

The SEIR model is a widely used mathematical model for describing the dynamics of infectious diseases. It divides the population into Susceptible, Exposed, Infectious, and Recovered. The model assumes that individuals move from category to category at certain rates, depending on the characteristics of the disease and interventions applied. In this project, we aimed to simulate a pandemic based on the SEIR model in Python, using real-world data and parameters from the COVID-19 pandemic.

We explored how different disease and social factors affected the spread and severity of the pandemic. We ran 4 different variations of the same population and compared the increased infectivity and death toll of increased population density and limiting access to a viable vaccine to the base case on sparsely populated locations with access to a working vaccine. The project is aimed to provide insights on what relieves and what exacerbates a large-scale contagion.

CHAPTER 1

BACKGROUND & DESCRIPTION OF THE PROBLEM

1.1 Background

The COVID-19 pandemic was responsible for millions of deaths and an economic downturn around the world that is still in effect today. Our goal was to simulate a similar type of infection, starting with five infected people entering a susceptible population. Epidemic simulations and SEIR models are common, and there are many epidemiological phenomena that affect how contagious a disease is. Ideally, a successful simulation will help us further understand the spread of disease, but this is not meant to be a formal study of a real disease [1].

There are several important values to track with disease [2], but the most common is the basic reproductive number, R_0, which is "the expected number of secondary cases produced by a single (typical) infection in a completely susceptible population" [3]. We expect the R_0 to be between 1.8 and 2.2, which is similar to theR_0value for COVID-19 [4]. We expect the total deaths (fatality rate) to be about 4% of the total population, based on COVID-19 values [5]. The disease is expected to be more infectious without vaccination and with fewer locations where people can gather because they will be more concentrated. It is expected to be less severe with vaccination and with more locations because this reduces the number of "super spreader" events.

The simulation expands on the Susceptible-Exposed-Infectious-Removed (SEIR) model for infectious diseases. It reflects real-life COVID-19 and SARS statistics for a population similar to a small town. These include population statistics (total population results), virus behavior (incubation times, contagious duration, infectivity), immunity-boosting events (recovery from infection, vaccination), and vaccine supply chain (time until development, development duration, supply). We have included a location data structure that simulates travel to common locations such as one's home, grocery stores, workplaces, or hospitals and how that affects the spread of disease.

A Jupyter notebook was used to simulate the infectious disease. A variety of scenarios were tested with several replications each as Monte Carlo simulations. Simulation progress is recorded in a pandas dataframe.

1.2 The SEIR Model

Our primary model tool is the SEIR model [6]. It divides the population into the four groups previously mentioned, Susceptible, Exposed, Infectious, and Removed. In our model, a person who recovered from an infection can be re-infected and a person who is removed is dead. Each person is generated with two probabilities; a base health called $recoverHealth$ and a threshold called $deathHealth$. Both of these probabilities are generated from a triangular distribution and are used to see if the person will become infected and if they would die if infected. In our simulation, all starting members of the population except for five infected are Susceptible.

Our triangular distribution for base health is described as (0.97, 0.98, 0.99), as seen in Figure 1.1. This assumes on average a 2% chance of being infected on contact with a contagious person. This is in order to simulate a similar change of infection for all our population.

In this model, when an infected person enters a location with susceptible people, all susceptible people are guaranteed to interact with a certain amount of contagious people. The amount of contagious people a susceptible person interacts with is defined by a triangular distribution which is defined as TRIA(0, half the contagious population capped at 20, all the contagious population capped at 50). This is in order to simulate a random amount of potential exposures for each susceptible person.

However, whether people actually get sick is represented by a series of Bernoulli [7] trials against their health value, represented by a Binomial distribution that is defined as (number of contacts, $1 - Health$ where Health is their base health plus any bonuses due to antibodies or vaccinations. For each exposed individual, we calculate a Binomial distribution based on the above values and consider the individual infected if the calculation obtains at least one success. Continuing the example above, an individual with 98 Health would run the Bernoulli trials with a

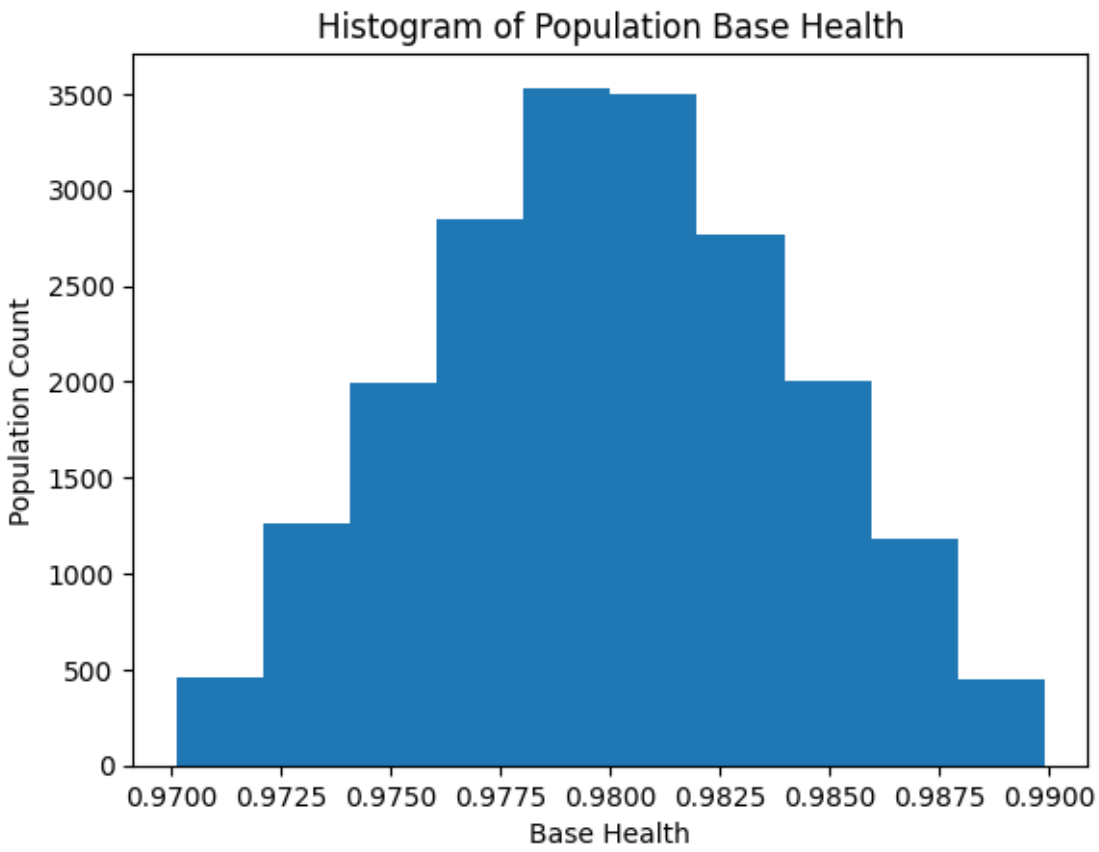

Figure 1.1: Histogram of Population Health.

success probability of 0.02. Additionally, for infected individuals we also calculate a probability of death, based on a similar series of Bernoulli trials.

Infected individuals have an incubation time before becoming contagious, and then will continue the course of their infection for the entire duration. At the end of their contagious period, they will become non-contagious or die. Assuming they did not die, at the end of their total sickness period, they will recover. Length of infection, length of contagious period, and total length of sickness are all modeled on normal distributions.

Recovered individuals are tracked with a status when they recover from the infection. After an individual recovers from infection, they are assigned a Bonus Health variable, which is obtained with a triangular distribution which is defined as (0.4, 0.6, 0.8). This Bonus Health is added to their base health amount when performing the infection checks, which effectively means that these individuals have a 0% chance of being infected. This Bonus Health decays daily by an amount ob-

tained by a triangular distribution defined as (0.01, 0.015, 0.02), representing an immunity period that on average will last about 40 days.

In addition, we can also simulate the distribution of a vaccine in our population. We begin vaccine preparations after a certain population ratio of sick to healthy individuals is exceeded, confirm vaccine ready for distribution after a certain amount of time has passed (modeled by a normal distribution), and increase our vaccine supply based on an exponential function, up to a maximum daily availability of 2% of the total population. In the United States, vaccinations per day accounting for all 3 major manufacturers peaked at 1.96% of the total population in 2022, so we consider our assumption adequate [8].

After each simulation run, statistics such as the growth ratio (a simplified version of R_0), total deaths, peak infection population, and pandemic duration were recorded in a dataframe for visualization. With these results, we were able to compile several reports on how populations react to widespread infection.

This simulation is designed to help forecast possible scenarios to support decision-making should we face another pandemic.

In the planning of this simulation, the following flow chart Figure 1.2 was created to visualize the different components and interactions to consider.

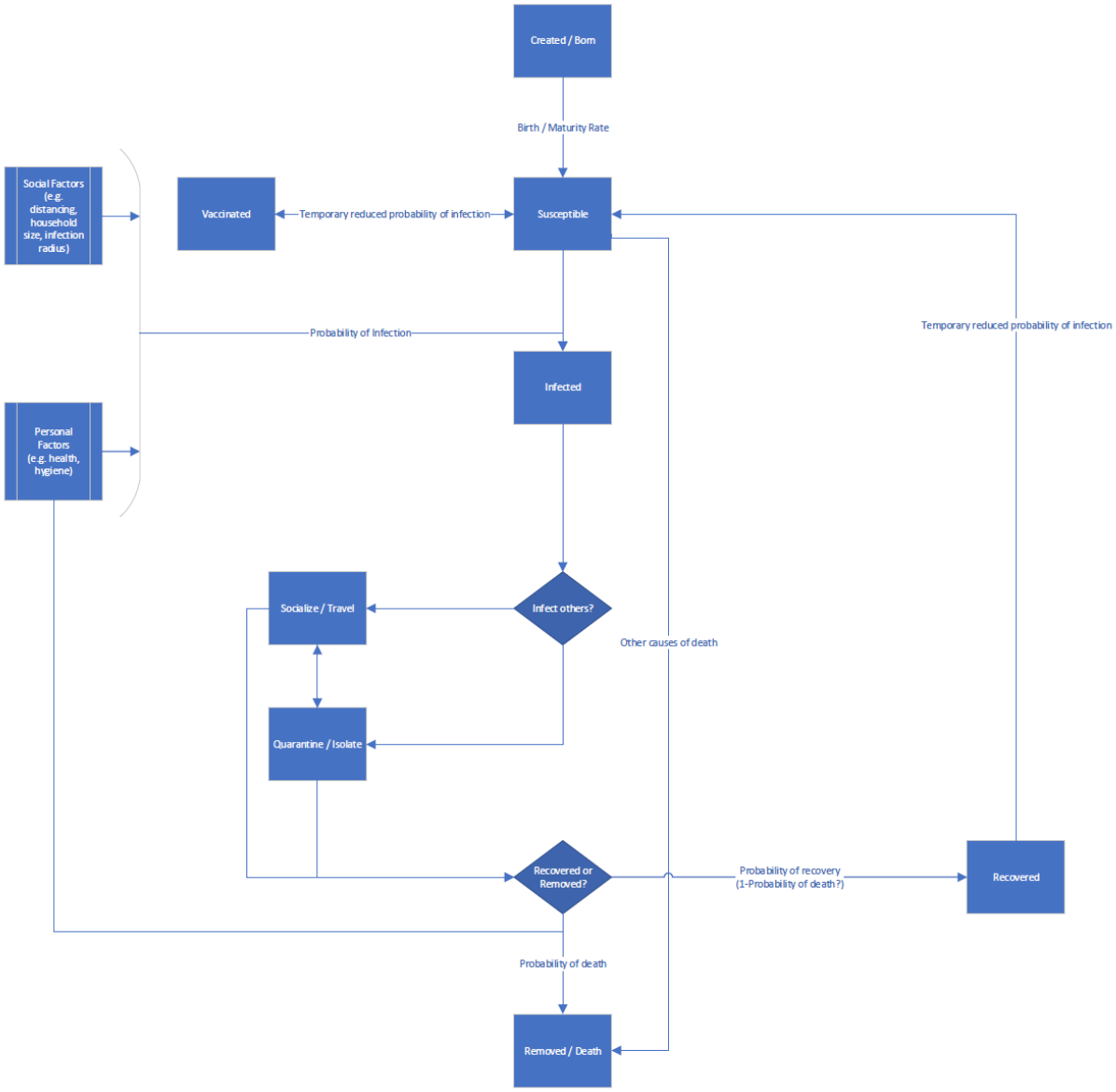

Figure 1.2: SEIR Model Flow Chart

CHAPTER 2
SIMULATION DESCRIPTION

This simulation model for a pandemic flu spread has several components, all of which have unique attributes that are either real reference numbers or created for this model.

2.1 Random Number Generating and Tuning Functions

Several functions are specifically made for tuning to obtain realistic results. For now, many follow a triangular or a normal distribution, but future studies can use real data and distributions as an input for this model. Health functions define the likelihood that someone will recover or die from disease. Vaccines and post/sickness recovery provide immunity as a "bonus health" value, which will decay over time.

A travel function defines the travel behavior of each individual. For this model, all individuals in the population live alone and do not actively quarantine when they become ill. Their most likely location is home, and they are considered as isolating when at home and thus not checked for exposure. The distribution of travel plans for each person was generated with a geometric distribution where each person had a probability generated from a uniform distribution.

2.2 System Functions

The system functions define the parameters of the environment. They include creating the total population, the number of locations for people to travel to, and initializing a vaccine. They also set the system time and seed for the run, if required. Additionally, it allows for multiple replications of the simulation that re-initializes each run.

Because this is a discrete-event simulation, there is also a function for incrementing time and a function for ending the simulation based on specific end conditions. The model runs until it

reaches a maximum number of time units, or until there are no unhealthy people left, whether by eradication of all infected people before spreading, or by vaccination of the susceptible population.

Data structures to record statistical information about the model are also initialized at this point.

2.3 Population and Population Count Functions

These functions define each person's attributes, which will change during the course of the simulation. They include the following categories:

- Status: indicates health status of the individual. Everyone starts the simulation healthy, susceptible to the disease, and alive. As the disease progresses, people may become infected but not contagious, infected and contagious, recovered from disease, vaccinated, or dead. Dead people do not interact with the living population, are not contagious, and cannot change their status. There is also a boolean to indicate if someone will die from an infection.

- Contagious: whether an individual is infected and contagious or not. We also track the progression of disease in each individual, such as the incubation period, recovery time, and contagious period.

- Health: each person has a baseline health value which follows a triangular distribution. People can acquire additional immunity from recovering from infection or vaccination. They also have a unique threshold for recovering or dying from infection. Both of these follow a triangular distribution, which was arbitrarily picked because we do not have enough information about this attribute.

There are additional population functions that count the number of people that satisfy a certain criteria. These functions include getting the number of people alive, the number of sick people, the number of contagious people, and more.

2.4 Location Functions

Using the travel function defined above, which produces a data structure of each person's location at any given time in the simulation, these functions will move the population to their corresponding locations.

Once at a location of interest, every susceptible person in that location is exposed to any contagious people in the location, up to a maximum amount of potential exposures.

2.5 Disease Functions

Each individual in the population starts with a unique base health. When exposed, each individual has a series of Bernoulli trials [7], representing the probability of not getting sick and the amount of contagious people they were exposed to. If there is at least one success in the Bernoulli trials, the person gets infected.. Vaccines and post-sickness recovery immunity add to the base health, further protecting the individual.

The contagious duration for each infected person is calculated upon infection. Every day that passes, duration is decreased until the individual is no longer infected. This also triggers health status changes for each individual.

We used real data from the COVID and SARS viruses to obtain our initial assumptions and then to simulate how likely someone is to become infected, how long it takes for the virus to incubate in a person, how long they are contagious, and how long their symptoms last.

2.6 Vaccine Functions

Vaccinations add health to the individual according to a triangular distribution. An individual with 0.98 health would see a vaccine health benefit added to their original 0.98, bringing them to an example total of 1.58, functionally representing immunity to the disease. Vaccine "bonus health" isn't permanent, just as in real life. It decays according to a triangular distribution until it reaches zero, so the individual is left with just their base health.

Vaccine development begins when a specific proportion of the population falls ill, which we have set to 5%. Development time is randomly assigned according to a normal distribution.

Once the vaccine is completed, the daily vaccine supply will vary to simulate production based on an exponential function which simulates demand and the supply chain.

2.7 Result Functions

The results functions capture the daily results, create graphs, and calculate replication results. This is also where the statistical analyses are done.

The following equations were used to calculate statistical results [9]: Denote the sample mean from replication i by

$$Z_i \equiv \frac{1}{m}\sum_{j=1}^{m} Y_{i,j}$$

where $Y_{i,j}$ is observation $j = 1, 2, ..., m$ from replication $i = 1, 2, ..., r$ Define the grand sample mean as $\bar{Z}_r \equiv \frac{1}{r}\sum_{i=1}^{r} Z_i$, where the point estimator for $Var(\bar{Y}_m) = Var(Z_i)$ is the sample variance of the Z_i's. Denote the sample variance of the Z_i's by

$$S_Z^2 \equiv \frac{1}{r-1}\sum_{i=1}^{r}(Z_i - Z_r)^2$$

With enough observations per replication, then the sample means are approximately i.i.d. Nor$\theta, Var(Z_1)$ and

$$S_Z^2 \approx \frac{Var(Z_1)\chi^2(r-1)}{r-1}$$

The approximate IR $100(1-\alpha)\%$ two-side confidence interval for θ is

$$\theta \in \bar{Z}_r \pm t_{\alpha/2,r-1}\sqrt{S_Z^2/r}$$

The R_0 is calculated as the transmission rate of the disease multiplied by the average duration of the contagious period [3]. In this model, we calculated an approximation on R_0 using the growth rate of the pandemic, comparing the amount of people infected each day to the amount of people

infected the day before. This lets us find the peak growth rate of the disease.

For a more in-depth explanation of the code written to simulate the disease, additional information can also be found within the docstring of each function and comments within the Jupyter notebook.

CHAPTER 3

RUNNING THE SIMULATION

The $runSimulation$ function, located on the bottom of the notebook, takes the following inputs:

- $numPeople$: Number of people in the simulation (integer)
- $numLocations$: Number of locations that people can travel to (where location 0 is defined as each person's "home") (integer)
- $maxRepLength$: Maximum replication length, which defines the maximum number of days that a replication can run for (integer)
- $seedRun$: Seed run, to give the option of setting a specific seed for the run (boolean)
- $vaccineDevelopmentIndicator$: Vaccine development to easily turn the vaccine functions on and off (boolean)
- $numRepetitions$: Number of repetitions, which is the number of independent replications for the simulation (integer)

We assign the required variables to the runSimulation function, and then run the entire notebook. For example, in order to run the first simulator scenario, in which we have a population size of 20000, a location count of 300, a maximum replication time of 365 days, without initializing the RNG seed, accounting for vaccine development, and running for 30 replications, we would assign the following variables to the function call:

$$runSimulation(numPeople = 20000, numLocations = 300, maxRepLength = 365,$$
$$seedRun = False, [vaccineDevelopmentIndicator = True, numRepetitions = 30)$$

Results are calculated and displayed at the end of the run.

Because people were likely to stay home, when the disease started with a single infected individual there was a significant number of simulation runs where the disease spread very little or not at all. Although that is good for the population, it skewed the results towards short disease durations, so these runs all start with multiple "patient zeros" to ensure a full pandemic every run.

CHAPTER 4

RESULTS

For the following inputs:

- # of people = 20000
- # of locations for the “Many Locations” condition = 300
- # of locations for the “Few Locations” condition = 100
- Max rep length = 365 days
- Seed Run = False
- Vaccine Development Indicator for the “No Vaccine” condition = False
- Vaccine Development Indicator for the “Vaccine” condition = True
- # of repetitions = 30

The results are shown below.

Scenario	Epidemiological Parameters	Sample Mean	Sample Variance	95% Confidence Interval
Vaccine Many Locations (this is the control)	Peak Growth Rate	1.56	0.03	(1.491, 1.623)
	# of Total Deaths	2023.57	2824.81	(2003.72, 2043.41)
	Pandemic Duration	183.60	530.46	(175.00, 192.20)
	Peak Infected Population	9425.33	19824.64	(9372.76, 9477.91)
Vaccine Few Locations	Peak Growth Rate	1.95	0.09	(1.842, 2.067)
	# of Total Deaths	4868.60	15251.01	(4822.49, 4914.7)
	Pandemic Duration	104.13	1413.29	(90.10, 118.17)
	Peak Infected Population	15413.97	7520.93	(15381.58, 15446.35)
No Vaccine Many Locations	Peak Growth Rate	1.53	0.03	(1.46, 1.59)
	# of Total Deaths	4841.17	7365.52	(4809.12, 4873.21)
	Pandemic Duration	365	N/A	N/A
	Peak Infected Population	9374.47	13763.36	(9330.66, 9418.27)
No Vaccine Few Locations	Peak Growth Rate	2.00	0.22	(1.82, 2.17)
	# of Total Deaths	9474.13	7870816.33	(8426.54, 10521.72)
	Pandemic Duration	273.80	14812.65	(228.35, 319.25)
	Peak Infected Population	15403.93	6095.86	(15374.78, 15433.09)

Table 4.1: Simulation Results

4.1 Scenario 1: Vaccine, Many Locations

While our goal was not to recreate the COVID-19 pandemic, we did use it to help create our epidemic. That said, we expected similar results. We hypothesized that the control infection's peak growth rate would be between 1.8 and 2.2 with a death toll of about 4% of the population, or 800 people.This means we were expecting each sick individual to infect about 2 healthy people at the height of the infection. That initial hypothesis was a little high, with the actual peak growth rate of the infection ranging between 1.491 and 1.623. Our original death hypothesis was also less than half of the reality, with between 2003 and 2043 people dying, 10.01-10.21% of the total population. In total, just under half the population was infected at least once.

As individuals become susceptible again past day 100, following the end of their immunity period, we can see the infection start to restart its cycle. Susceptibility rises, and we can see a slight resurgence of the infection between days 125 and 150, which is significantly lower due to the effects of the vaccine on population immunity. The virus wasn't necessarily programmed to do this, but it does model the reality of the situation, that people can become reinfected, and that large scale contagions are cyclical, taking advantage of reduced vigilance in susceptible populations.

The last infected individual either recovered or died just after day 175, marking the end of the simulation.

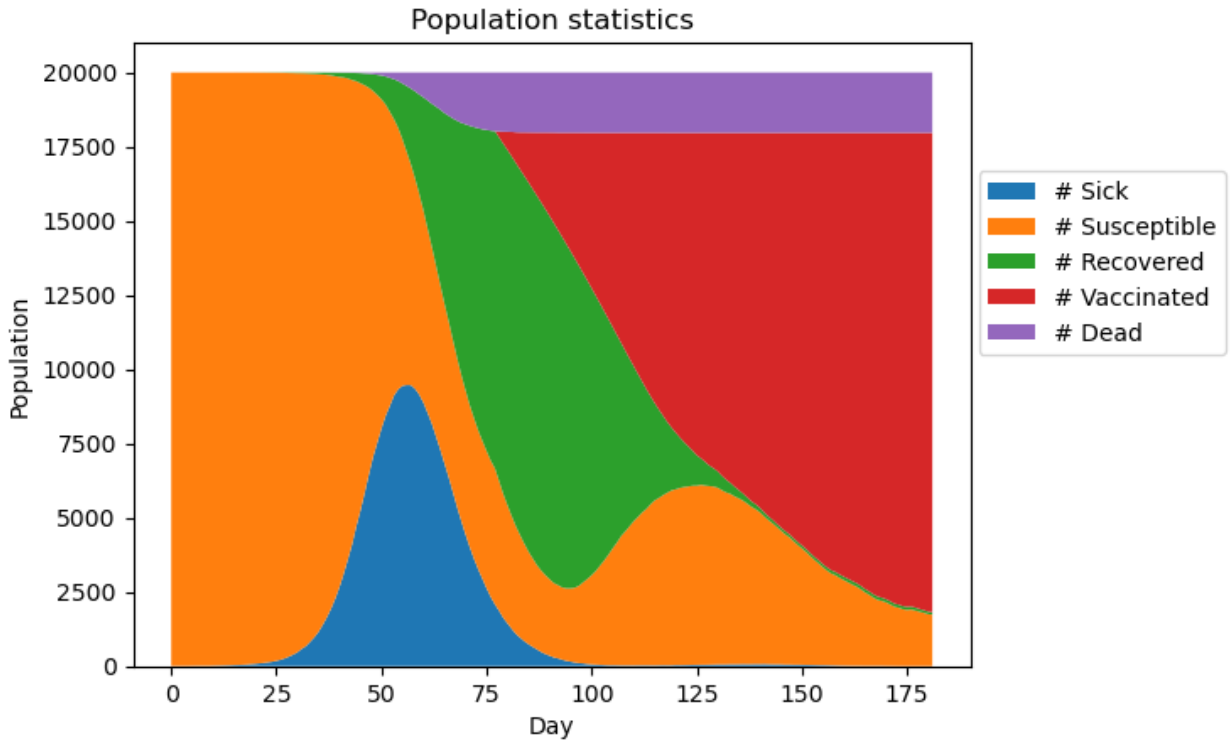

Figure 4.1: Sample timeline of the pandemic with a vaccine and many locations.

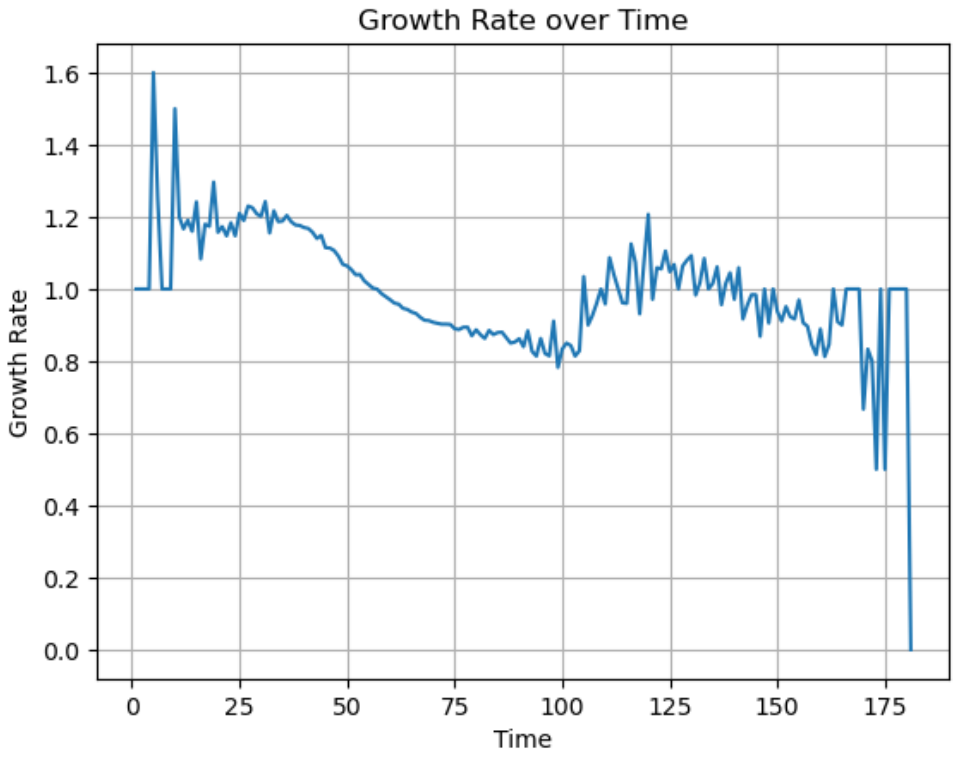

Figure 4.2: Sample timeline of the growth rate of the pandemic with a vaccine and many locations.

4.2 Scenario 2: Vaccine, Few Locations

We had mixed hypotheses when lowering locations. Some of us expected the lower number of locations to mean a higher probability of people staying home, resulting in less infections, while others hypothesized that the lower locations would just concentrate the sick individuals, making infection much more likely. Clearly, the latter rationale was more accurate. Dropping the available locations by 33% resulted in a 25% increase in peak infection growth rate, 141% increase in total deaths, and a 64% increase in total number of people infected at least once. This difference between the control and fewer locations supports what happened in reality; as more people visit high-concentration locations, they are more likely to be infected and die from infection.

This pandemic was much shorter than the control, ending in just under half the time. This is likely due to the disease infecting so many people at first that it did not leave many people to infect while the initial population benefited from their post-illness immunity. There was another resurgence, similar to the control, but at a smaller growth rate. The control resurgence was on the path to regrow with a growth rate of 1.2 people getting sick each day. In this scenario, the disease comeback only reached 1.0, or maintenance level. At the time people started to lose their immunity, the vaccine was released, and we can see the amount of susceptible population drops even further starting at day 60. Even though the susceptible population starts growing, the combined effect of immunity due to the vaccine and a large recovering population ensure the pandemic ends before infection rates can rise again.

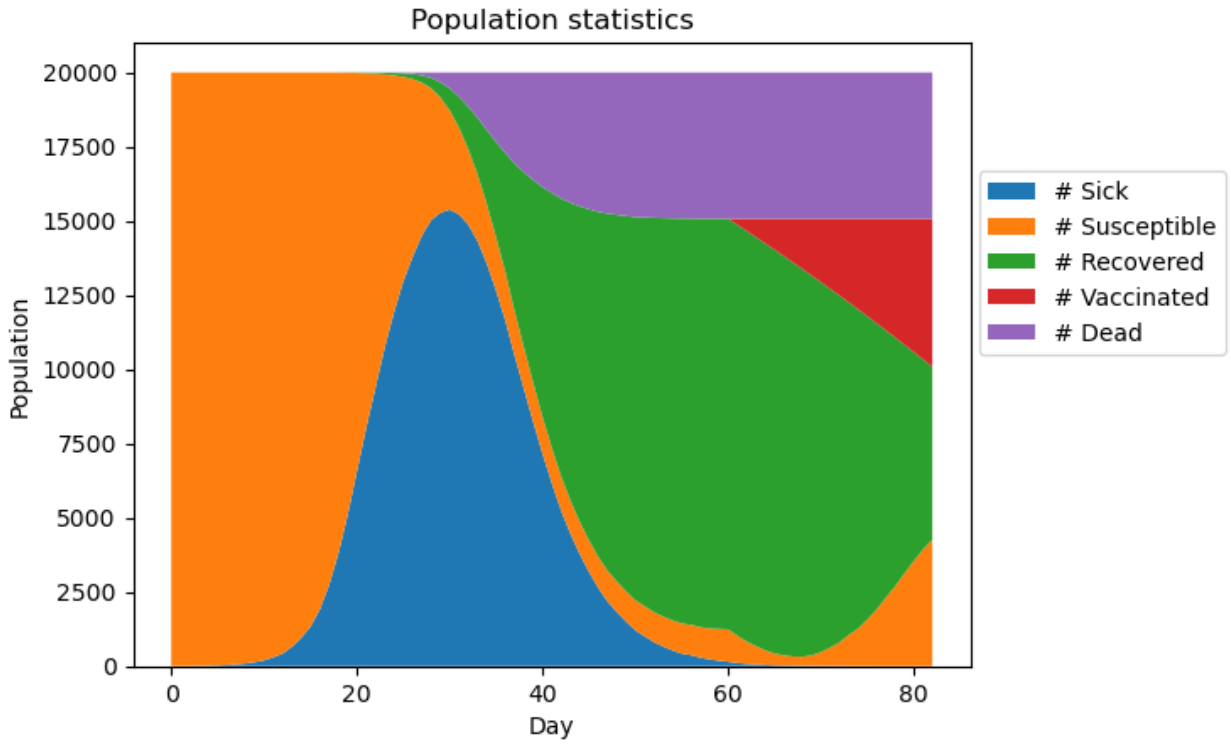

Figure 4.3: Sample timeline of the pandemic with a vaccine and few locations.

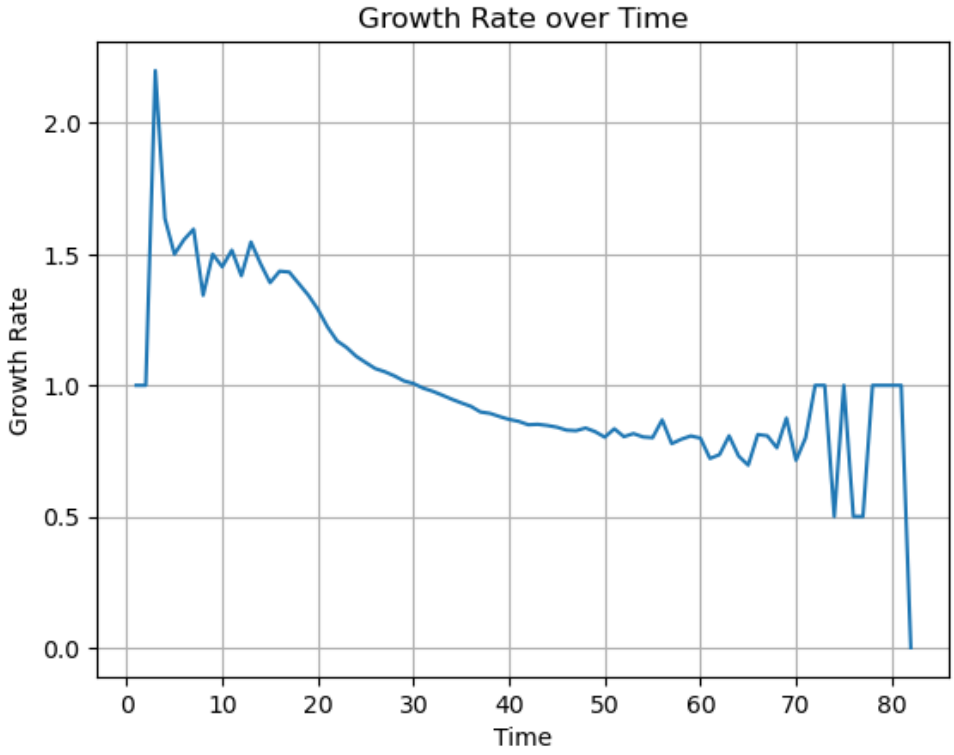

Figure 4.4: Sample timeline of the growth rate of the pandemic with a vaccine and few locations.

4.3 Scenario 3: No Vaccine, Many Locations

This is our first simulation without a vaccine. Each replication ran the maximum 365 days, as opposed to the previously vaccinated simulations, where the disease was immunized out. Our limit was 365 days, meaning the simulation ended early rather than the virus dying out in one year. Compared to our control, the peak growth rate was almost identical, which is not surprising, since the peaks in both occurred with full populations, were uninhibited by vaccines, and made use of 300 locations. The back half of the simulation where we don't have a vaccine is of course where this run differs from the control.

Our hypothesis for this scenario was a similar beginning peak to the control, but with a more obvious cyclical infection pattern that would only end after humanity was killed. We couldn't run this scenario to burnout because of computation constraints, but we can see that even though the peaks of the sick population shrink over time, it is because of the total population shrinking with every cycle, not because of any added immunity. We believe that our hypothesis holds, that this scenario will end in total population eradication.

Without a vaccination present, the total death toll is 139 of the control, while the peak infected population is about the same as the control.

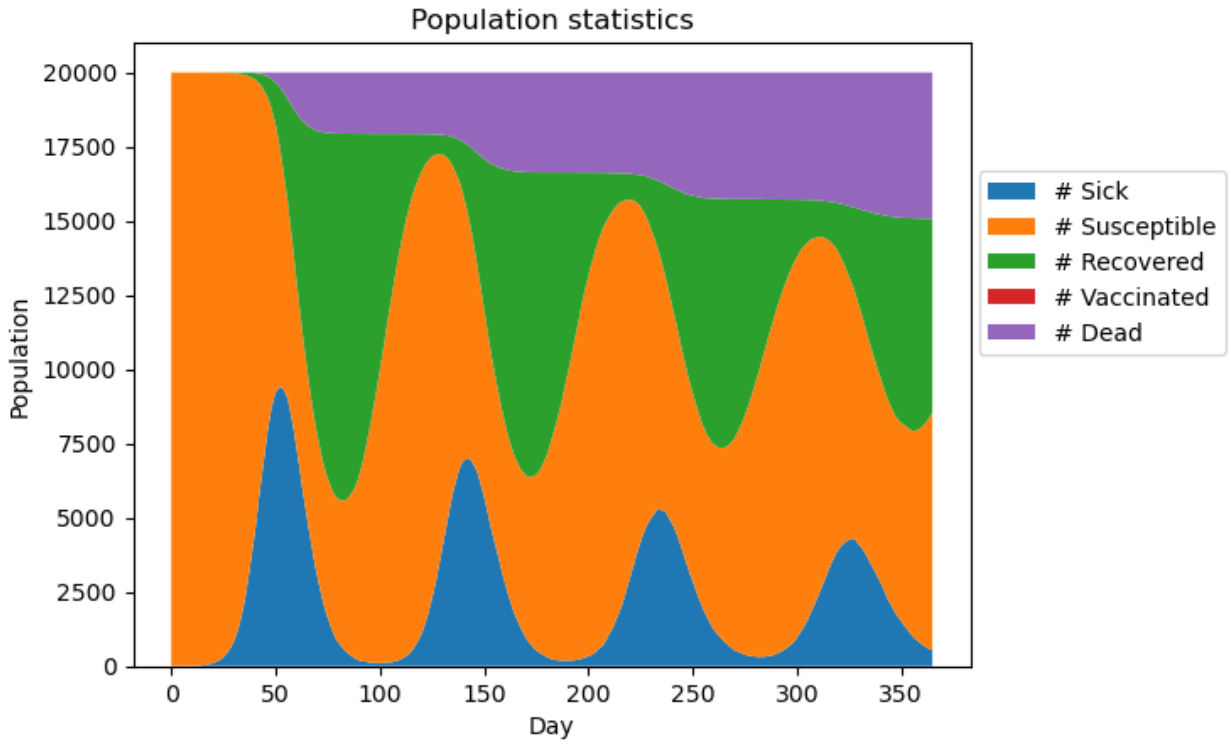

Figure 4.5: Sample timeline of the pandemic with no vaccine and many locations.

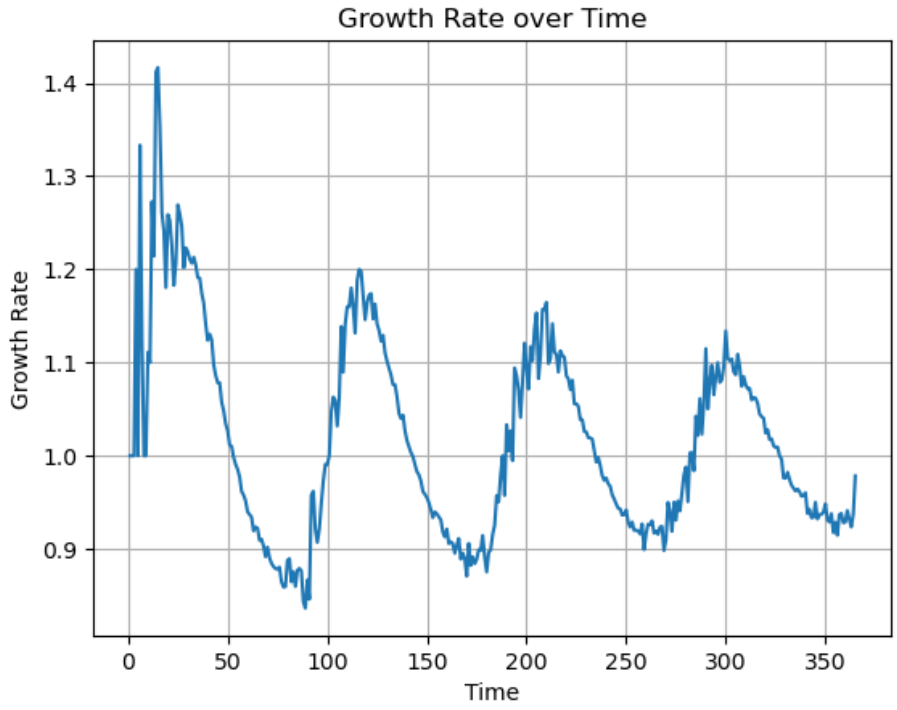

Figure 4.6: Sample timeline of the growth rate of the pandemic with no vaccine and many locations.

4.4 Scenario 4: No Vaccine, Few Locations

This final scenario is the most variable of the four. We decreased the locations by 33% and removed the vaccine. Our hypothesis for this scenario was that it would look similar to a combination of the second and third scenarios: that the disease would concentrate itself in the fewer locations, infect the majority of the population and almost burn itself out like scenario 2, cycle again like scenario 3 but with more intense peaks and wider troughs, and end with total population death. That was the result for about half the runs. The other half followed the image below, where the disease swept through the population with such intensity that it was initially too strong to maintain itself long-term in the rapidly dwindling susceptible population of super healthy individuals.

Compared to our control, this simulation's peak growth rate increased 28%, the total number of deaths increased 368%, lasted 49% longer, and peaked at 63% more infected individuals. Some of these runs lasted the entire 365 days, and some lasted only 80 days, as shown.

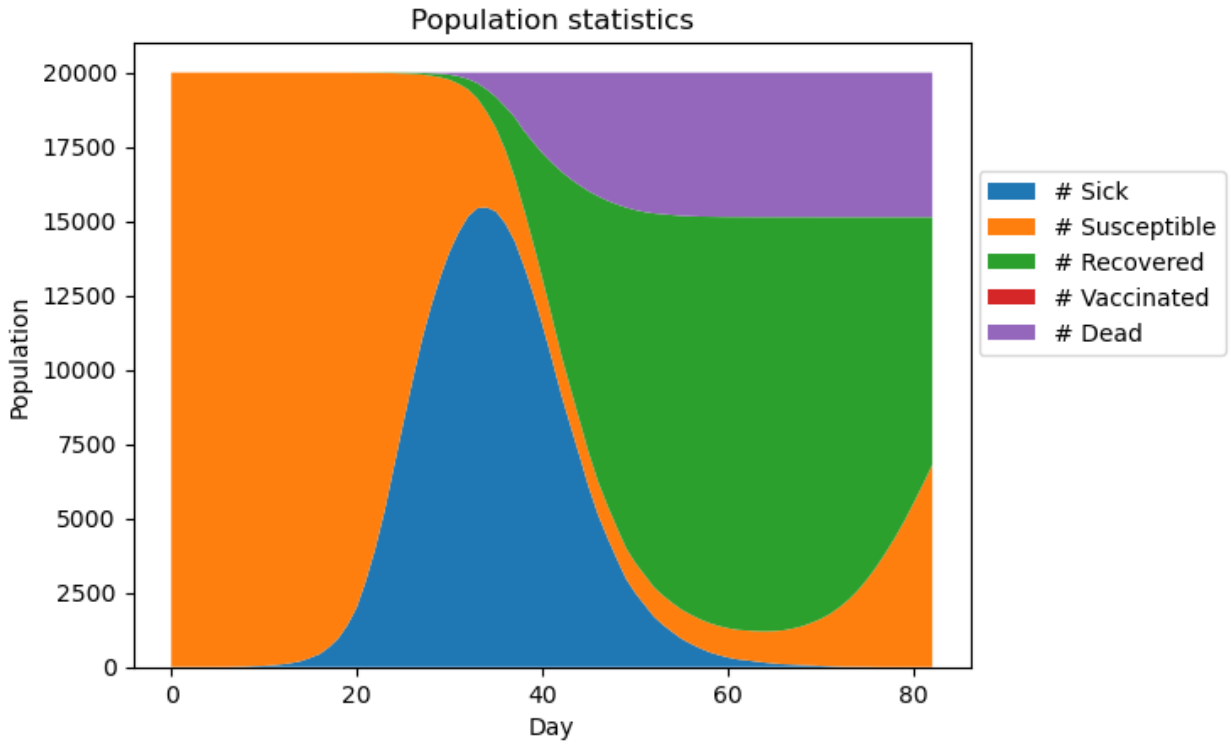

Figure 4.7: Sample timeline of the pandemic with no vaccine and many locations.

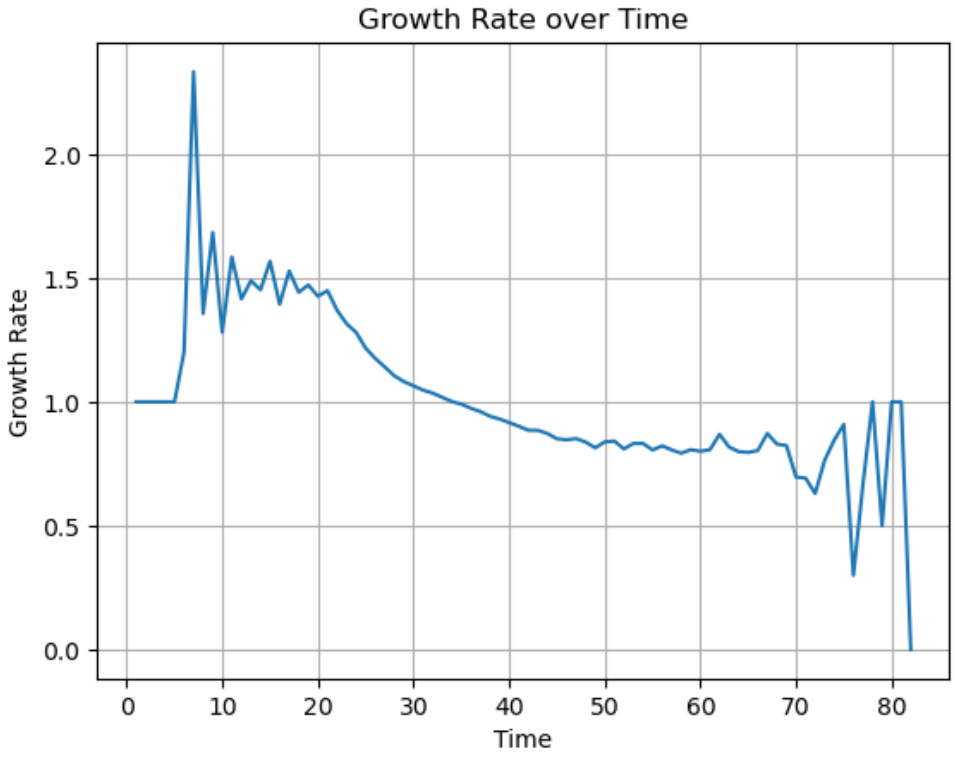

Figure 4.8: Sample timeline of the growth rate of the pandemic with no vaccine and many locations.

4.5 Comparing Systems

We can compare the differences of the obtained parameters using Paired Confidence intervals for the difference between two means [9]. Comparing the pandemic duration of scenarios 1 and 2, we can apply the approximate CI to obtain a value of 79.47 ± 13.50, indicating that a more concentrated pandemic would be expected to last between 66 and 92 days less than a more spread out pandemic. We can also apply approximate CI to compare the growth rates and obtain a value of 0.39 ± 0.11, indicating that a more concentrated pandemic will be between 0.28 and 0.50 times more infectious. The vaccine effectiveness in reducing pandemic duration is shown in comparing scenarios 1 and 3 (where scenario 3 never ended since not enough of the population was immune to the virus) and scenarios 2 and 4 (where using the approximate CI results in a value of 169.7 ± 38.34, indicating that the vaccine can reduce the duration of the pandemic by 131 to as much as 207 days.

For the approximate confidence intervals, if the X's and Y's are independent but with arbitrary unknown variances, then the CI for the difference in means is

$$\mu_X - \mu_Y \in \bar{X} - \bar{Y} \pm t_{\alpha/2,\nu}\sqrt{\frac{S_X^2}{n} + \frac{S_Y^2}{m}}$$

using the *approximate* degrees of freedom

$$\nu \equiv \frac{(\frac{S_X^2}{n} + \frac{S_Y^2}{m})^2}{\frac{(S_X^2/n)^2}{n+1} + \frac{(S_Y^2/m)^2}{m+1}} - 2$$

CHAPTER 5
CONCLUSION

In this simulation, we found that many runs with only a single infected individual ended very quickly, and no runs ran for a very long time. For COVID-19 to become a worldwide pandemic and still persist more than 3 years may mean that the initial spread of the disease was from a highly concentrated location where a large population was exposed to a significant infection event, such as tainted food in a busy restaurant or grocery store, instead of a singular mutated illness. This may also show that some diseases are quickly eradicated or die off before they're really noticed.

The vaccine development assumes a rather simple and efficient supply chain, but that is unrealistic. A model could be built to simulate the supply chain to different locations, including severe delays which are common in real life, or accounting for the scenario where two doses of the vaccine are required for immunity. Variations in the immunity duration provided by the vaccine (or by recovering naturally) also affect many of the key parameters.

Due to computational limitations, this population is closed and does not change beyond deaths from the disease. Future research can integrate demographic trends to increase or decrease population size independent of the pandemic. Future projects can model travel between systems. Some people choose to isolate themselves completely when they are sick, but that is not represented in this scenario. Many people live with others, which we did not model in this simulation. Future work can analyze the effect of multi-person households on disease propagation.

This model also assumes uniform exposure to all the people in one location, but in fact the level of exposure is a function of proximity to the infected individual, the duration of time spent in proximity, the location itself (e.g. an open windy beach has much less transmissibility than a closed meeting room), and the behaviors of the people (imagine a classroom full of kindergarteners) that can vastly affect exposure. Future work can expand on these location-based and human behavior-based nuances.

None of the pandemics achieved a steady-state where the cycle maintained its amplitude over the long-term. This is primarily due to the deaths that occur during each cycle of renewed infection rate without introducing new members of the population. This makes sense for the closed population that we created, but for a population that can renew itself, either with births or immigration and emigration, steady state infection and recovery is most likely under the third scenario; infected individuals are not as concentrated, and a vaccine is not introduced to remove susceptible individuals from the virus's path.

Appendices

APPENDIX A

SCENARIO 1: VACCINE, MANY LOCATIONS

These are additional graphs from each scenario run.

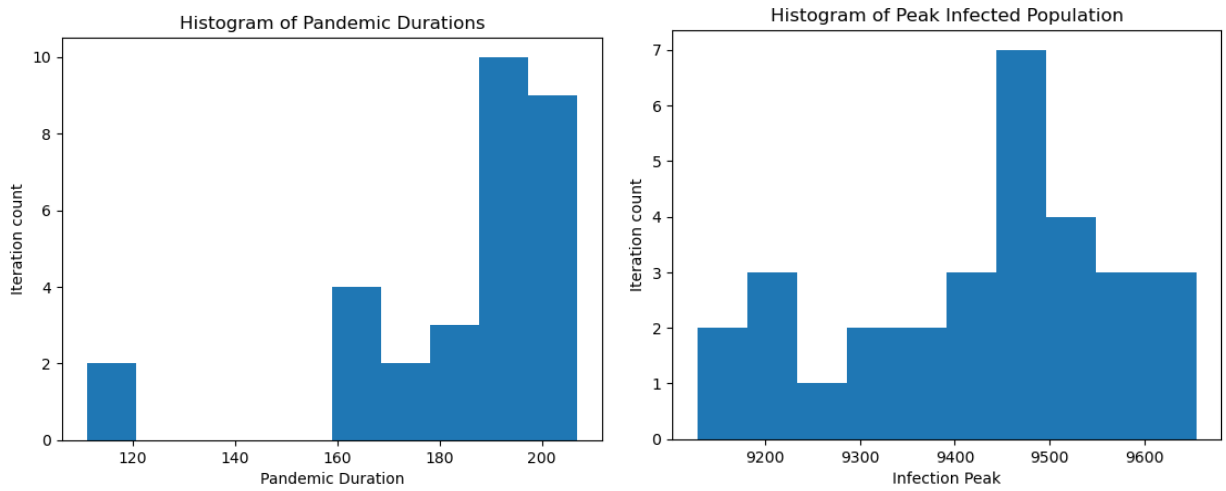

Figure A.1: Histograms of pandemic duration and peak infected populations with a vaccine and many locations.

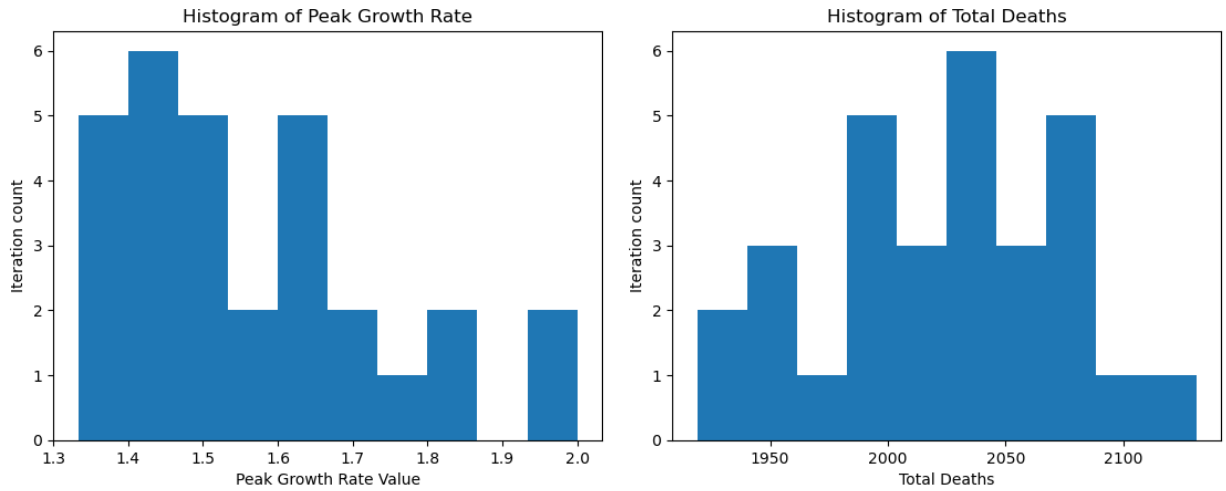

Figure A.2: Histograms of peak growth rate and total deaths with a vaccine and many locations.

APPENDIX B

SCENARIO 2: VACCINE, FEW LOCATIONS

These are additional graphs from each scenario run.

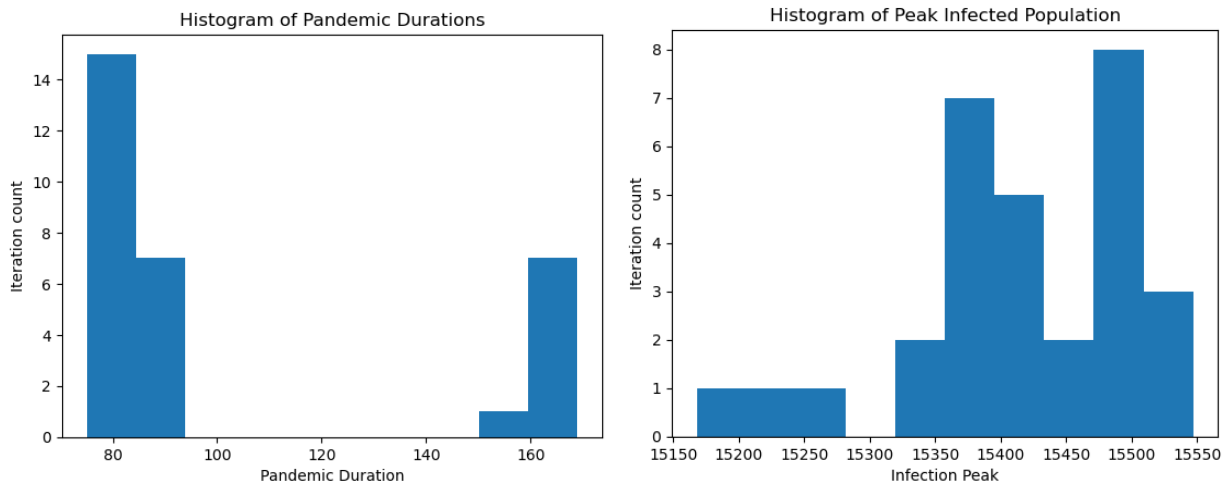

Figure B.1: Histograms of pandemic duration and peak infected populations with a vaccine and few locations.

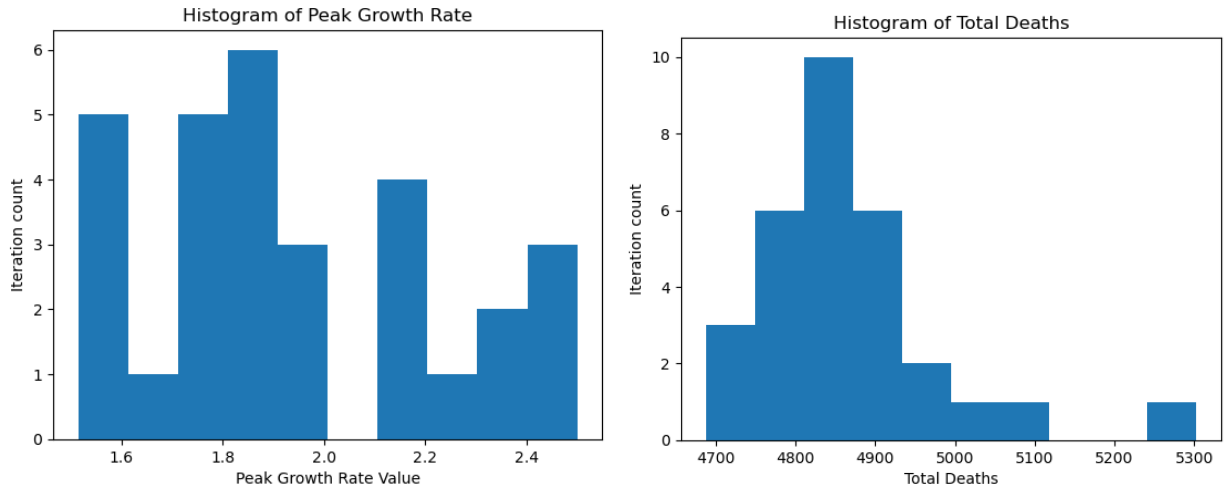

Figure B.2: Histograms of peak growth rate and total deaths with a vaccine and few locations.

APPENDIX C

SCENARIO 3: NO VACCINE, MANY LOCATIONS

These are additional graphs from each scenario run.

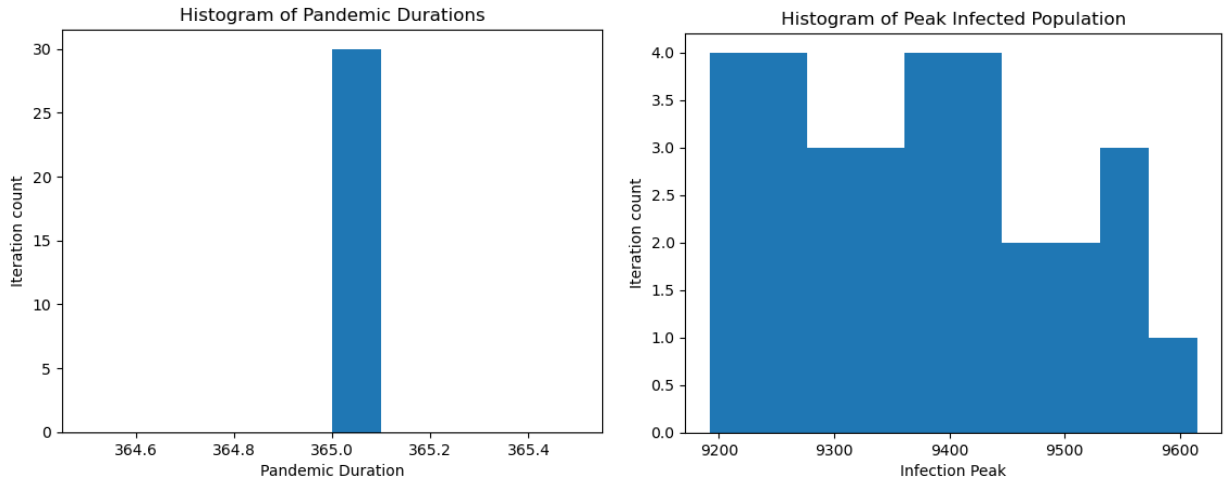

Figure C.1: Histograms of pandemic duration and peak infected populations with no vaccine and many locations.

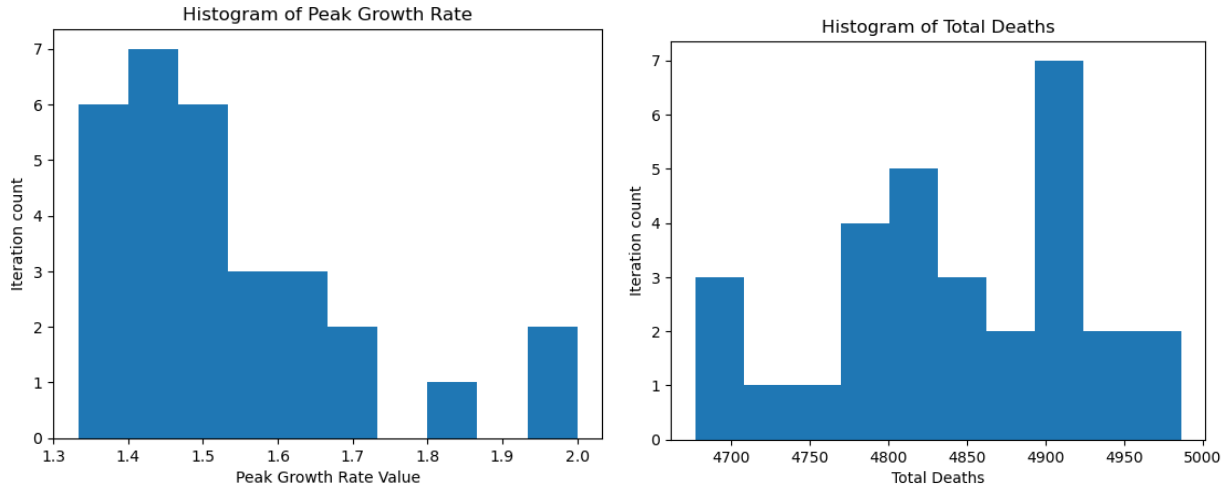

Figure C.2: Histograms of peak growth rate and total deaths with no vaccine and many locations.

APPENDIX D

SCENARIO 4: NO VACCINE, FEW LOCATIONS

These are additional graphs from each scenario run.

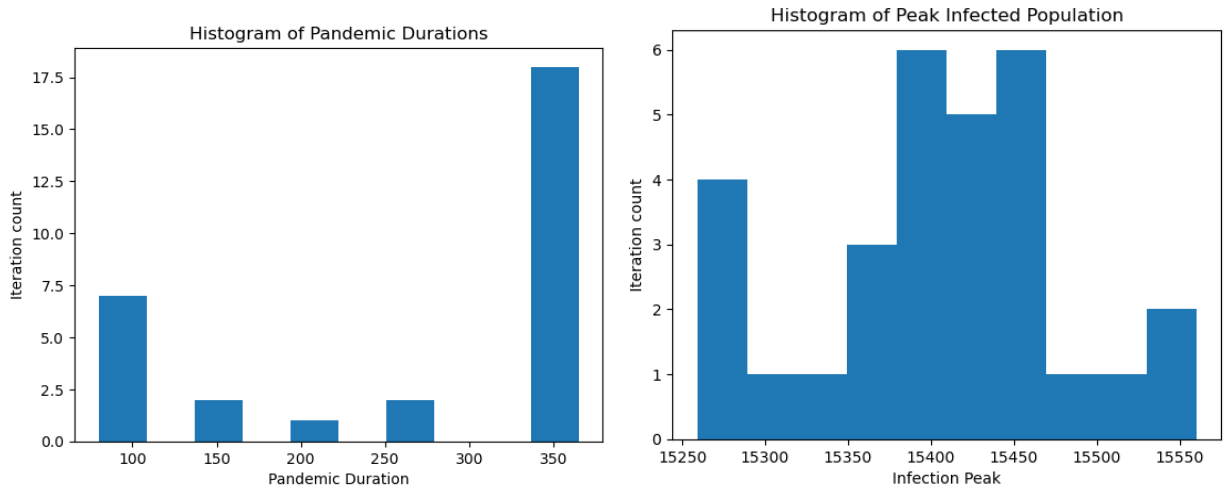

Figure D.1: Histograms of pandemic duration and peak infected populations with no vaccine and few locations.

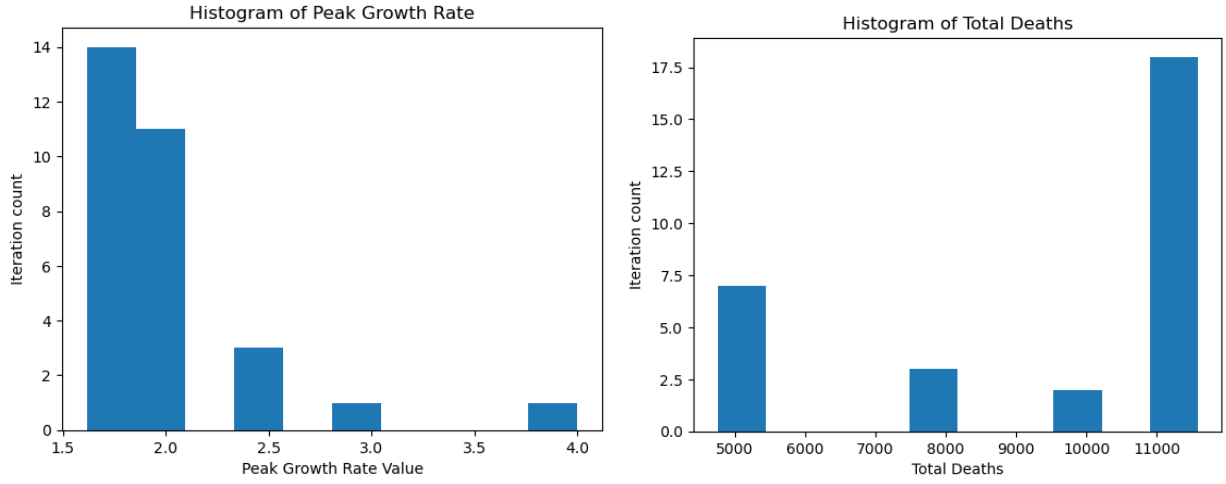

Figure D.2: Histograms of peak growth rate and total deaths with no vaccine and few locations.

REFERENCES

[1] G. Sanderson, "Simulating an epidemic," *YouTube*, 2023, https://www.youtube.com/watch?v=gxAaO2rsdIs [Accessed: (Sep. 25, 2023)].

[2] L. G. G. et al., "Ten epidemiological parameters of covid-19: Use of rapid literature review to inform predictive models during the pandemic," *Frontiers in Public Health*, vol. 8, 2020, doi:10.3389/fpubh.2020.598547.

[3] J. H. Jones, "Notes on r0," *Stanford.edu*, 2023, https://web.stanford.edu/~jhj1/teachingdocs/Jones-on-R0.pdf [Accessed: (Nov. 19, 2023)].

[4] "Basic reproduction number," *Wikipedia*, 2023, https://en.wikipedia.org/wiki/Basic_reproduction_number [Accessed: (Nov. 12, 2023)].

[5] J. Elflein, "Topic: Coronavirus (covid-19) in the u.s.," *Statista*, 2023, https://www.statista.com/topics/6084/coronavirus-covid-19-in-the-us/ [Accessed: (Nov. 10, 2023)].

[6] S. M. et al., "Seir model for covid-19 dynamics incorporating the environment and social distancing," *BMC Research Notes*, vol. 13, no. 1, 2011, doi:10.1186/s13104-020-05192-1.

[7] N. Developers, "Numpy.random.binomial," *NumPy v1.26 Manual*, 2023, https://numpy.org/doc/stable/reference/random/generated/numpy.random.binomial.html [Accessed: (Nov. 13, 2023)].

[8] "Covid-19 vaccine doses administered by manufacturer," *Our World in Data*, 2023, https://ourworldindata.org/grapher/covid-vaccine-doses-by-manufacturer [Accessed: (Dec. 3, 2023)].

[9] D. Goldsman, "Computer simulation module 9: Output data analysis," *ISYE 6644*, 2023, [Accessed: (Nov. 20, 2023)].

LIST OF FIGURES

ACKNOWLEDGMENTS

We'd like to thank Professor Dave Goldsman, Ph.D. for putting together a great class. The TAs have been very kind and helpful as well.