Mathematical Modelling of Ebola Disease

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Abstract

Ebola is a virus that causes a highly virulent infectious disease that has plagued Western Africa, impacting Liberia, Sierra Leone, and Guinea heavily in 2014. Understanding the spread and con- tainment of this disease is vital to its containment and eventual elimination. In this paper, we formulate and analyze a mechanistic SIFR type outbreak model, to simulate the transmission of the disease. The model is validated with data from the World Health Organization. Optimal control theory is used to explore the effect of vaccination on the SIFR model. The goal is to explore the use of these control strategies to effectively contain the Ebola virus. Codes and graphs are written and generated in Python.

1 Background and Motivation

For many years, epidemics have plagued many countries around the world, resulting in the deaths of millions. With the advancement of technology in today's world, most infectious diseases are able to be kept under control. However, underdeveloped countries are less fortunate in controlling such diseases due to unsanitary environments and lack of resources. Before the Coronavirus, one of the largest epidemics in the world that occurred was the 2014 Ebola virus that was widespread in West Africa. This disease was transmitted directly by vectors, through human-to-human contact of bodily fluids, contaminated clothing of infected or deceased individuals, and many more. The fatality rate of Ebola is extremely high. In this study, we will focus specifically on the transmission of Ebola during funerals.

One might wonder why funerals were pertinent in the spread of Ebola. In some West African countries such as Guinea, traditional funerals and burials of the deceased involved physical contact with the bodies of the deceased, such as washing, kissing and touching the corpses. As a result of these funeral traditions, spreading bodily fluids from the deceased to attendees of the funerals became one of the main contributors to the spread of Ebola. Which is why it is important to study the impact of funerals during the Ebola epidemic. In Africa, traditional funeral practices and burials pose a substantial risk and have proven to be the main contributors to the spread of the infectious disease, Ebola. Safely burying Ebola infected individuals is acknowledged to be an important factor for controlling Ebola epidemics.[1]

The outbreak of Ebola caused panic in people around the world. Due to modern transportation, infectious people are rapidly transported from country to country. In the affected countries with hundreds of funeral attendees per deceased person, many more people were put at risk of being infected. Many people were still unaware of Ebola and did not have time to yet acknowledge the severity at that point. Doctors did not have enough time to invent effective medical methods to cure this disease. Some regions in Africa blocked their borders, hospitals stopped usual diagnoses, and people were not allowed to go to work and school as they normally would. All these problems put together motivated us to make a mathematical model to help people have a better understanding of the spread of Ebola.

2 Research Question

In this project, we mainly focus on the F (Funeral) compartment in the base model. Discussions on the effects of controlling funeral spread by changing the proportion of F are elaborated. And by comparing the SIFR model with the SIR model (without funeral spread), we will see how funerals affect the Ebola spread rate in the SIFR model. Otherwise, since

Ebola cannot be contained solely by controlling funerals, intervention strategies like vaccination will be discussed.

Researches are conducted to study the interventions for controlling Ebola spread rate at funerals. This brings us to the question that if they had followed non-traditional but safe funeral protocols, placed social distancing measures at funerals, or if intervention methods such as vaccination were applied, would the spread of Ebola have been effectively slowed down?

3 Base Model Construction

There are many transmission routes of the Ebola disease. For example, a person may be infected by being in contact with wild animals, touching bodily fluids, and contaminated objects. In this model, we will only consider transmission of the virus through direct contact with infected living and deceased individuals during funeral practices. To predict the real-world situations with regards to the spread rate, death rate and funeral spread rate, we use SIFR with vital dynamics as our base model to show the predictions.

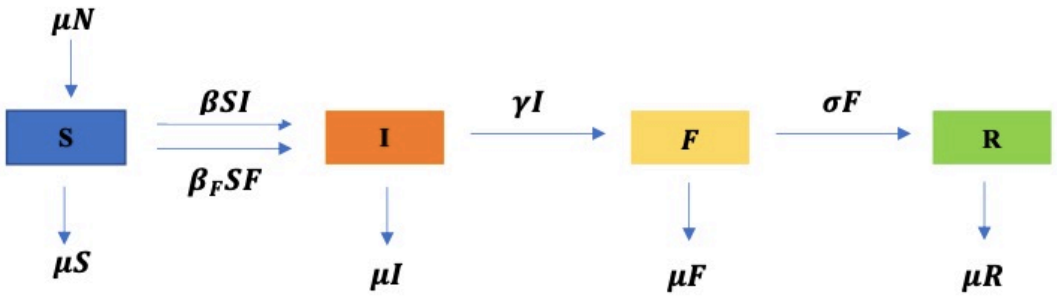
Parameter	**Unit**	**Description**
S(Susceptible)	of people	the population who is not yet infected, but at risk of being infected
F (Funeral)	F (Funeral)	people who died from Ebola waiting to be buried
I (Infectious)	of people	number of individuals who are infected with Ebola and are capable of spreading Ebola
R (Removed)	of people	number of individuals removed from the chain of transmission
β	$people^{-}1day^{-}1$	transmission or infection rate
β_F	$people^{-}1day^{-}1$	transmission or infection rate caused by contact occurring at funerals
γ	Deaths per 10 individuals	death rate
σ	Bodies buried per 10 deaths	rate of burying bodies
μ	$people^{-}1day^{-}1$	natural birth or death rate
S+I+F+R=N, where N is the total population.		

Table 1: Description of the parameters

3.1 Assumptions

A list of assumptions are made below:

- All parameters are greater than or equal to 0.
- Assume there are vital dynamics. The per capita rates of birth and death are the same (both are equal to μ).
- The birth rate and death rate of the tested regions are constant, making total population (N) to be constant.
- Average rates of all parameters are applied, because there may be uncertainties of some external elements.
- When vital dynamics are added, death can occur from causes outside Ebola.
- Assume no newborns are born infected.
- Assume all people in the surveyed region will be naturally infected by Ebola once they are in contact with the virus. In reality, there may exist a small part of people who contact the virus but don't get infected.
- Assume there's no hospitalization, since hospitalization compartment will affect transmission rate and death rate.
- All individuals with Ebola who died will go through the funeral compartment. And they are capable for transmitting the virus at funeral.
- All observed cases were assumed to be related to human-to-human transmission (by infected living humans and infected dead bodies at funerals). In fact, transmission may occur by contacting infected wild animals, like bats, mosquitoes, etc. While in this model, only the main route of transmission is discussed.
- Assume no intervention strategies are taken, as we will discuss some prevention methods, like funeral control and vaccination in the following, we can compare them with the base model.
- Infection rates are the same for each individual.



3.2 Formulation

The basic model is given by the following nonlinear ordinary differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI - \beta_F SF + \mu N - \mu S \\
\frac{dI}{dt} &= \beta SI + \beta_F SF - \gamma I - \mu I \\
\frac{dF}{dt} &= \gamma I + \mu I - \mu F \\
\frac{dR}{dt} &= \sigma F - \mu R
\end{aligned} \tag{1}$$

There are four state variables S, I, F, and R.

$\frac{dS}{dt}$ represents the change of the susceptible population (S) over time. The part of susceptible people who are infected through infectious individuals (-βSI) or through dead bodies in funeral (β_FSF) will be removed from S and then flow into the Infection compartment (I). New births (μN) and death (μS) are added into the model.

$\frac{dI}{dt}$ denotes the change in the infected population (I) over time. People who are infected by infectious individual or dead bodies at funeral (-βSI+β_FSF) are added to I. Those who are infected and died from Ebola (-γI) are removed from I, and then flow into funeral compartment (F). Natural deaths are excluded (μI).

$\frac{dF}{dt}$ represents the change in population who have died and have had funerals (F) over time. Those who died from Ebola are waiting to be buried at funeral (γI). Then those who have been buried(σF) will be removed from F, and flow into R, and they are no longer infectious. Natural deaths (μF) are excluded to keep the population constant.

$\frac{dR}{dt}$ denotes the of change of removed population (R) over time. Those who died from Ebola (σF) were buried and they are permanently removed from the population. Natural

deaths of recovered individuals are included (μR).

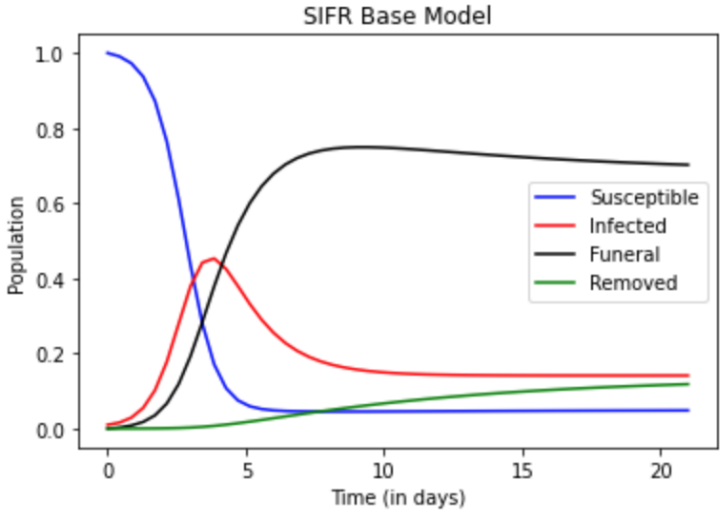
We choose to use a continuous time model here, rather than using a discrete time model (one day period, one week period, etc). Because the Ebola spread fits a continuous time scale. Continuous time models will be more practical in showing the real-world situation.

3.3 Parameter values

When simulating our base model, we set the values of parameters to: β=1.5, β_F=2.53, γ=0.58, σ=0.02, μ=0.1 [10] for which we chose reasonable values from literature: The average EVD case fatality rate is around 50%. Case fatality rates have varied from 25% to 90% in past outbreaks. The Infections is estimated to be between 44% and 90%.[1] We chose a transmission rate of 1.5 [8], and a transmission rate at funerals of 2.53 [9]. We found the death rate of infected individuals to be between 0.25 to 0.90, so we averaged and get a rate of 0.58.

4 Base Model Analysis

As our goal is to model and reduce Ebola spread, we can access the effectiveness of prevention measures, and analyze the long term effects of Ebola by finding equilibrium using the base compartmental model of Ebola transmission. By utilizing graph functions from Python packages, we will generate direction fields to find out more information about the spread rate. We look at different graphs with a focus on different variables to locate any changes.

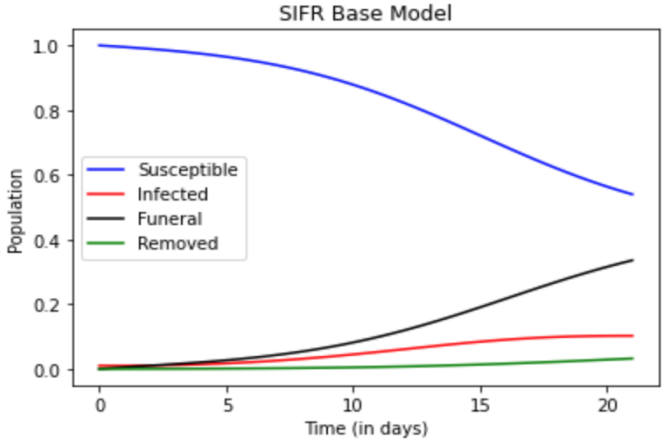


The spread rate is observed within a population of 100 individuals over 21 days. By the output of SIFR model, we notice that almost all susceptible population flow into the infected

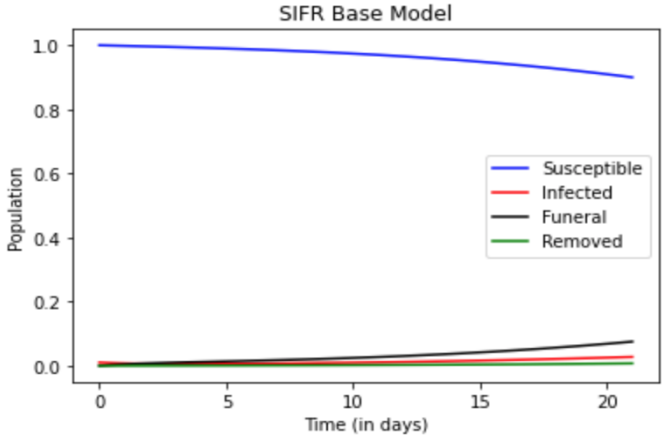
population, which denotes that the infection rate is high, and once people get susceptible, there's a high probability that they get the disease. For the I curve, the infected population will rise to the top at first and then it falls rapidly. Because as more people get infectious, they will face a high risk of death, the dead population will flow into the funeral compartment, thus there is a sharp decrease in I curve. The funeral curve (F) will gradually rise and then keep at a high level of population in the funeral as more people getting infected.

4.1 Base Model Simulation

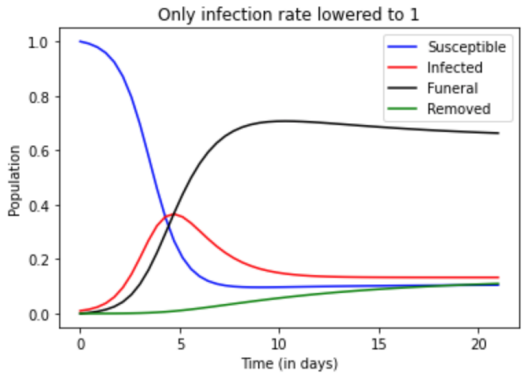
As we wanted to see a reduction on the number of infected individuals, i.e. lowering the peak of the red line, we simulated the base model with a lower transmission rate of 0.6 and a lower infection rate of 0.2 at funerals.

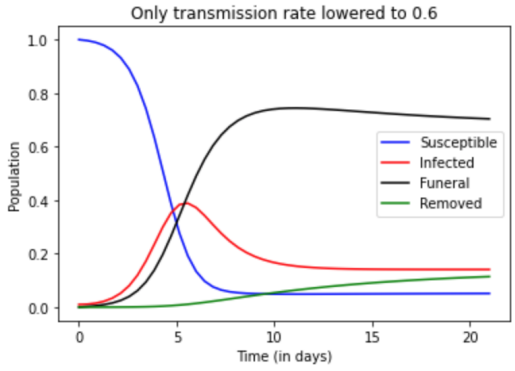


We simulated the base model below with a lower transmission rate of 0.3 and a lower infection rate of 0.2 at funerals. We were able to keep the infected and dead population (who are still capable of transmitting the virus) at a very low level after the simulations.



Both transmission(β) and infection rate(β_F) during funerals were lowered in order for the curves to change. When only one parameter is decreased, we can see merely any change





when compared to the base model. This is illustrated by the above graphs. Thus, preventative measures especially during funerals is a crucial part to reduce the spread of Ebola.

4.2 Equilibrium

For the model we consider the equilibria for the populations (S, I, F, R). At the equilibrium, the rate of change of each population is zero. Thus, these values were obtained by setting each differential equation simultaneously to zero: $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dF}{dt} = \frac{dR}{dt} = 0$. There are two types of equilibrium, disease free and endemic equilibrium. From a biological perspective, we classify these equilibria as disease free equilibrium. That is, when the values for any population at the equilibrium is zero, the virus is extinct. For instance, when $I = 0$, there are no infections in the entire population (everyone is in S) as time goes to infinity and the equilibrium is known as a disease free equilibrium (also referred to as an infection free steady state). The fixed point is $E_0 = (1,0,0,0)$. However, if the value for any population at equilibrium is not zero, the virus is persistent. For instance, when $I \neq 0$ and $I > 0$, the virus persists and the equilibrium is known as a endemic equilibrium. If the system takes on an equilibrium at any time, it will remain at the value for all remaining time; however, unless the initial conditions are exactly one of the equilibria, the system need not necessarily obtain these values. The system may approach the equilibrium, move away from the equilibrium, or cycle between specific equilibria. In order to accurately determine which type of behavior the system will yield, we must perform a stability analysis for the system.

4.3 Jacobian

The Jacobian is the matrix of the partial derivatives of each function with respect to each variable. Essentially, the Jacobian provides a linear approximation of a system at any given value. Analysis of the eigenvalues of the Jacobian matrix evaluated at the equilibrium gives

insights into the local stability properties at that equilibrium. The Jacobian for our system of differential equations is given by:

$$J = \begin{bmatrix} \frac{\partial f_1(S,I,F,R)}{\partial S} & \frac{\partial f_1(S,I,F,R)}{\partial I} & \frac{\partial f_1(S,I,F,R)}{\partial F} & \frac{\partial f_1(S,I,F,R)}{\partial R} \\ \frac{\partial f_2(S,I,F,R)}{\partial S} & \frac{\partial f_2(S,I,F,R)}{\partial I} & \frac{\partial f_2(S,I,F,R)}{\partial F} & \frac{\partial f_2(S,I,F,R)}{\partial R} \\ \frac{\partial f_3(S,I,F,R)}{\partial S} & \frac{\partial f_3(S,I,F,R)}{\partial I} & \frac{\partial f_3(S,I,F,R)}{\partial F} & \frac{\partial f_3(S,I,F,R)}{\partial R} \\ \frac{\partial f_4(S,I,F,R)}{\partial S} & \frac{\partial f_4(S,I,F,R)}{\partial I} & \frac{\partial f_4(S,I,F,R)}{\partial F} & \frac{\partial f_4(S,I,F,R)}{\partial R} \end{bmatrix}$$

where

$$\begin{aligned} f1 &= -\beta SI - \beta_F SF + \mu N - \mu S \\ f2 &= \beta SI + \beta_F SF - \gamma I - \mu I \\ f3 &= \gamma I + \mu I - \mu F \\ f4 &= \sigma F - \mu R \end{aligned} \tag{2}$$

By substituting the fixed point $E_0 = (1,0,0,0)$ and rates ($\mu = 0.1, \gamma = 0.58, \beta = 1.5, \beta_F = 2.53, \sigma = 0.02$) into the matrix, we get the following:

$$J = \begin{bmatrix} -\mu & -\beta & -\beta_F & 0 \\ 0 & \beta - \gamma - \mu & \beta_F & 0 \\ 0 & \gamma & -\sigma - \mu & 0 \\ 0 & 0 & \sigma & -\mu \end{bmatrix} = \begin{bmatrix} -0.1 & -1.5 & -2.53 & 0 \\ 0 & 0.82 & 2.53 & 0 \\ 0 & 0.58 & -1.02 & 0 \\ 0 & 0 & 0.02 & -0.1 \end{bmatrix}$$

Solving the matrix we get the eigenvalues $\lambda_1 = -0.1, \lambda_2 = -0.1, \lambda_3 = -1.62, \lambda_4 = 0.82$. All eigenvalues values are real and negative, except for one, which means the equilibrium is semistable.

The characteristic polynomial is defined by the characterstic equation, $det(A - \lambda I) = 0$ where A is a square matrix, I is the identity matrix, and λ is an eigenvalue. The roots of the characteristic polynomial of the Jacobian will tend to depend on several parameters known as threshold parameters. The values of these parameters, sometimes called the reproductive constants, influence and determine the stability of the system.

4.4 Stability Analysis

Let R_0 be the basic reproduction number, which describes how easily the disease spreads. Biologically, R_0 represents the average number of infected individuals infected by an initially infected individual over time. To better understand the spread of Ebola in the affected area, it is crucial to know the number of secondary cases generated by an infected index case in the absence and presence of control measures, i.e., R_0. The R_0 value associated with Ebola is generally accepted to range from 1 to 2.[4] This value depends upon the parameters of the individual who is infected.

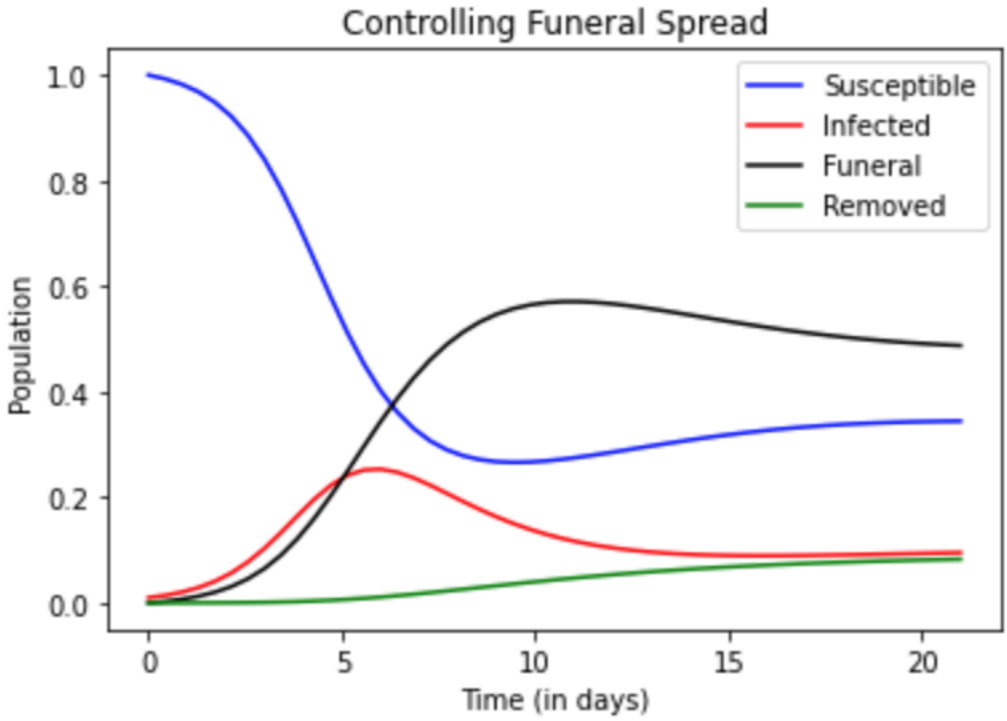
It occurs when $R_0 < 1$, the disease-free equilibrium is stable, meaning that each individual is able to infect only less than one individual on average. The equilibrium corresponds to the case when the virus dies out (no epidemic). When $R_0 > 1$(the epidemic expands), meaning that each individual is able to infect more than one individual on average. In this case, the equilibrium is unstable. The goal of controlling Ebola is to bring R_0 below one. By analyzing the stability around the equilibrium, if the traditional burial rituals such as touching corpses are allowed, the system can never achieve an endemic-free state since both γ and σ are not equal to zero, which reflects the reality in Africa. To stop the spread of Ebola, touching the dead from Ebola is prohibited and cremation of Ebola victims is required.

5 Proposed Model Extensions

5.1 Controlling Funeral Spread

Recorded by WHO that nearly 60% of all Ebola cases reported in West Africa can be linked to traditional burial practices. It is understandable that every culture wants to respect the dead through over-expenditure or hopes to cement the connection between this world and the next. However, traditional burial practices can lead to the spread of infectious disease.[6]

With this approach, only the parameter β_F (rate of transmission of infection caused by contact occurring at funerals) which deals with prevention is modified to optimize the objective function, whereas others stay the same. In this figure, it is observed that effective preventive mechanisms such as proper education and campaign will help reduce the rate of infection of Ebola in communities.

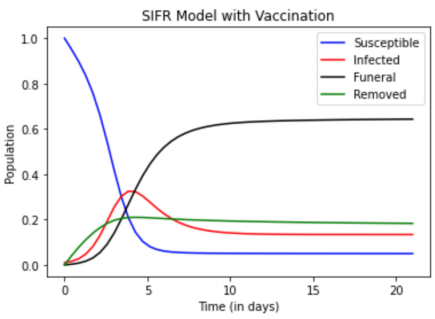


By setting the β_F parameter from rate of 2.53 to a slower rate of 0.1, we can see that there is a slight change in the infected population. Some prevention methods can be but are not limited to, avoiding funeral or burial practices that involve touching the body of individuals who died of Ebola and limiting the number of people present at funerals.

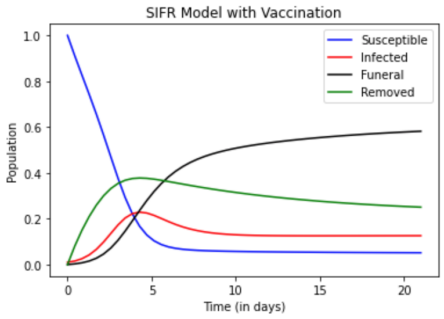
5.2 Developing Vaccine

One of the control measures adopted to limit the spread of the virus is vaccination. Therefore, we enriched the base SIFR model by implementing an additional parameter of vaccination(v), where v represents the proportion of infected people who get vaccines per day. We simulate our SIFR model with vaccination using the same parameters for different rates of vaccination. So, will the death rate be affected? Will the spread rate be reduced? The results are shown in the following figures.

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI - \beta_F SF + \mu N - \mu S - vS \\
\frac{dI}{dt} &= \beta SI + \beta_F SF - \gamma I - \mu I \\
\frac{dF}{dt} &= \gamma I + \mu I - \mu F \\
\frac{dR}{dt} &= \sigma F - \mu R + vS
\end{aligned} \tag{3}$$



[v=0.1]



[v=0.2]

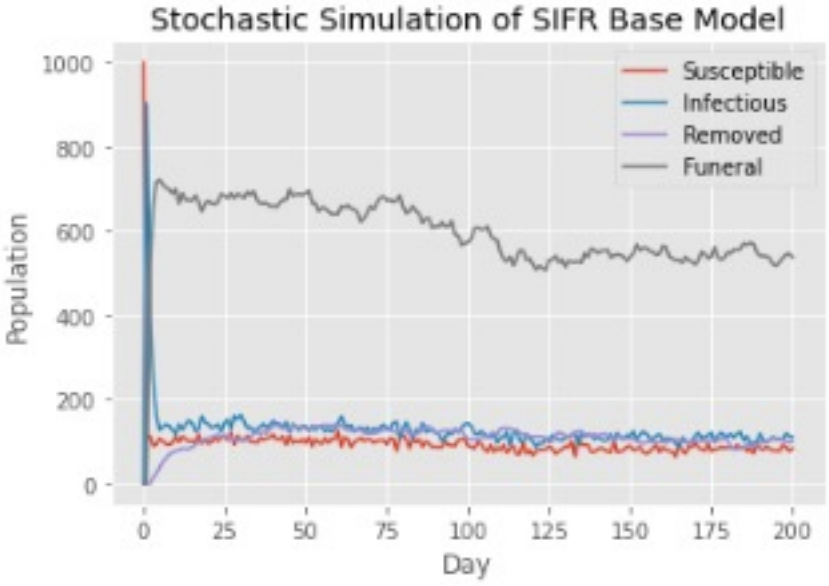
where v is the rate of vaccination rate, while other compartment and parameter values stay the same. We assume that vaccines won't provide 100% cure to this disease.

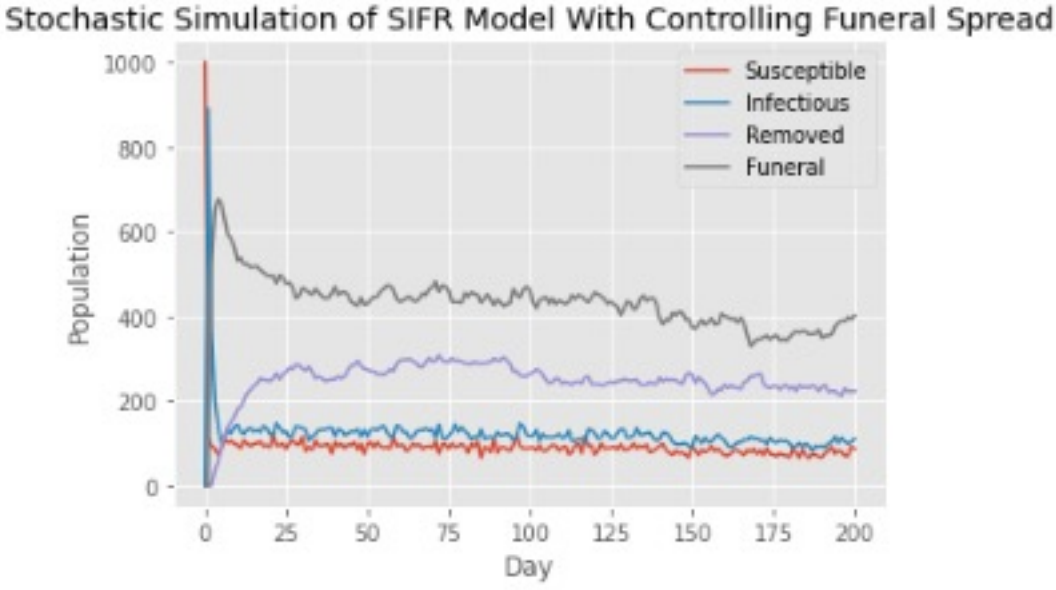
As we can see, as the vaccination rate improves, there is a slight decrease in the infected population. The infected population at the beginning will rise to lower peaks. And the funeral spread will also decrease, as there is less infected population inflows to F compartment. As a result, the growth of the susceptible population will slow down at the beginning. Therefore, the application of vaccination in this case is effective. We can see a decrease in the mortality of Ebola.

6 Proposed Stochastic Element

In the context of modeling the dynamics of Ebola, there are some stochastic elements that incorporate uncertainty in the parameter estimation process. We may get an average value of cure for all infected people and recovered people. But each infectious individual has a different probability of recovery and transmission. In a stochastic model, different simulations will have different results, distributions of different behaviors are present. Some parameters of the model are random in nature. For example, the transmission rates in urban and rural regions are relatively different because the control policies will vary among local governments. The recovery rates can also be different due to people with different medical conditions, and the proportion of susceptible individuals may vary because people at different ages have different immune systems – children and the elderly always have relatively weaker immune systems. If we use data in regions with a larger number of schools, without considering the ages of people in this region, the result will be biased. There are many uncertainties for each control parameter (β, γ and σ), thus we use the stochastic element to improve the effectiveness of our model. Since the transmission rates of the three countries are different: 0.27 for Guinea, 0.45 for Sierra Leone and 0.28 for Liberia, when the initial simulation of stochastic transmission has no interventions, we will run the simulation multiple times with different infectious values. As a result, we'd like to get a model that is close to the real-world situation. This

could lead to several important effects. For example, if an intervention is predicted to be highly effective, ie. when using a special vaccine in a therapy, it is effective but we are not sure about its exact cureness rate and some doctors may overestimate the likelihood of this type of therapy. We can use a combination of different intervention therapies to increase the likelihood of effective reduction of transmission.





From the stochastic graph we get in Python, we can see that the change of each variable is oscillating. We tested 1000 people for 200 days, and applied the data used in the base model, setting the values of parameters to: $\beta = 1.5$, F=0.73, $\gamma = 0.58$ and σ=0.02. To compare the effectiveness of controlling funeral spread. We use the change in population instead of

measuring the total population. The result is obvious, in which random fluctuations sustain nearly periodic oscillations in a system. It clearly demonstrated the actual situation in reality.

Then we make a stochastic model for the base model with controlling funeral spread. With reducing F to 0.3. In this case, the oscillation curve of the funeral decreases dramatically, which means the change of population that gets infected in the funeral decreases. The change of removed population increases, as there will be less healthy people getting infected in funerals, and the routine: susceptible, infectious and removed will not occur. Thus the change in removed population increases. By comparing the two stochastic models, the result we get is: by controlling the transmission rate in funerals, the infected population will decrease significantly.

7 Discussion and Conclusion

In this paper a deterministic mathematical model for the dynamics of Ebola Virus was formulated. We first showed that our model is mathematically and epidemiologically well posed. From the base model, the infected group rapidly increases as well as the deceased group. In order to see a change in rates, we simulated the base model with preventative measures. The most effective method is to decrease both β β_F. Further, we obtained both the disease and endemic equilibria and analyzed them for stability. We then introduced two extensions to model and control the spread of Ebola. Finally we depicted a graph of the stochastic state variable against time.

The goal of this project is to explore intervention strategies to limit the transmission of the Ebola virus using an SIFR model and to optimize control by focusing on the Funeral compartment and applying the vaccine parameter. From the experiments that scientists carried out, the death rate of Ebola can reach 50% on average. Ebola is often caused by contact of bodily fluids in funerals. Adding the funeral compartment allows a second spread period to occur, the deceased population will be infecting the susceptible. Secondly, we performed simulations that focused mainly on the effects of vaccination of the susceptible population and we studied the infection dynamics of the disease. From the simulations, it has been shown that vaccination reduces the number of those exposed and infected with the virus.

An Ebola outbreak in developing countries could be a real disaster. As demonstrated by our mathematical models, it is seen that an uncontrolled transmittable contact between the infected and the susceptible can be catastrophic, when there is no immunity policy or drugs applied. As recorded by WHO, there is evidence that shows the outbreak of Ebola in Liberia, Sierra Leone and Guinea that the death rate reached the highest, much more than the total of all deaths since the outbreak of the virus in 2014. However, by controlling the

funeral spread and applying vaccine support, the transmittable contacts will be effectively reduced. Although some interventions may be difficult in practice due to some external factors (economical, customs, social or political policies), it is still considered the best option in controlling the high fatality rate of the Ebola outbreak.

However, there are some limitations of our project. The data we gather from the parameters may be biased because it only represents the situation in a region at a certain period. To make this model reliable, we need to gather more data and run more simulations. Additionally, the effectiveness of policy control may be overestimated, as we discussed in the stochastic model, a combination of different intervention therapies should be applied to reduce this uncertainty. Last but not least, due to the lack of existing evidence, many parameter values are estimates. Using estimated values will impose some error and are not completely accurate.

According to the data we gathered and the experiments that scientists carried out, the fatality rate of Ebola can reach 90%. At least 20% of new Ebola infections occur during burials of deceased Ebola patients. Therefore, controlling funeral spread will save at least 20% lives in Africa. And with vaccination, 80% of people being vaccinated will have at least 50% chance getting recovered. So Ebola can be controlled effectively by controlling funeral spread and vaccination.

References

[1] Ebola virus disease. PAHO/WHO — Pan American Health Organization. (n.d.). Retrieved April 21, 2022, from https://www.paho.org/en/topics/ebola-virus-disease#:~:text=The%20virus%20is%20transmitted%20to,key%20to%20successfully%20controlling%20outbreaks

[2] Do, T. S., Lee, Y. S. (2016, February). Modeling the spread of ebola. Osong public health and research perspectives. Retrieved March 18, 2022, from https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4776269/

[3] O., D. M., J., A. I. (n.d.). Mathematical model of the spread and control of ebola virus disease. Applied Mathematics. Retrieved March 18, 2022, from http://article.sapub.org/10.5923.j.am.20170702.02.html

[4] Althaus, C. L. (2014, September 2). Estimating the reproduction number of ebola virus (EBOV) during the 2014 outbreak in West Africa. PLoS currents. Retrieved April 4, 2022, from https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4169395/

[5] Osemwinyen, A. C., Diakhaby, A. (2015, July 18). Mathematical modelling of the transmission dynamics of ebola virus. Applied and Computational Mathematics. Retrieved April 4, 2022, from https://article.sciencepublishinggroup.com/html/10.11648.j.acm.20150404.19.html

[6] Traditional funeral and burial rituals and ebola outbreaks ... (n.d.). Retrieved April 21, 2022, from https://journalhss.com/wp-content/uploads/jhss_51_073-090.pdf

[7] Okyere, E., De-Graft Ankamah, J., Hunkpe, A. K., Mensah, D. (2020, July 4). Deterministic epidemic models for ebola infection with time-dependent controls. Discrete Dynamics in Nature and Society. Retrieved April 4, 2022, from https://www.hindawi.com/journals/ddns/2020/2823816/

[8] Terrill, M. (2014, September 11). Ebola paper demonstrates disease transmission rate. ASU News. Retrieved April 21, 2022, from https://news.asu.edu/content/ebola-paper-demonstrates-disease-transmission-rate

[9] Centers for Disease Control and Prevention. (2017, August 25). Cluster of ebola virus disease linked to a single funeral - moyamba district, Sierra Leone, 2014. Centers for Disease Control and Prevention. Retrieved April 21, 2022, from https://www.cdc.gov/mmwr/volumes/65/wr/mm6508a2.htm#:~:text=A%20single%2C%20traditional%20funeral%20likely%20led%20to%20a,estimated%20for%20the%20outbreak%20in%20Sierra%20Leone%20%284%29.

[10] A deterministic mathematical model for ... - ijmttjournal.org. (n.d.). Retrieved April 21, 2022, from https://www.ijmttjournal.org/2016/Volume-30/number-1/IJMTT-V30P502.pdf

Individual Contributions

We came up with this report together as a group and each individual contributed equally.

- Yue Liu: Meeting organizations; Setting up Google Doc; Researched and worked on base model construction and analysis, discussions and conclusions; Coded the stochastic element
- Xiaoyan Liu: Coded the base model, model extensions and stochastic models; edited the base model and analysis part; references in APA style; converted the report into latex; worked on stochastic element; final revision

- Jia Lu: Edited the part of background and motivation and the research question
- Xiangyu Lyu: Researched and edited the proposed model analysis; final revision

Code

```
#Base Model
import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
from scipy import integrate

t=np.linspace(0,21)
def simulate(z, t, beta, betaF, gamma,sigma, mu):
    S = z[0]
    I = z[1]
    F = z[2]
    R = z[3]
    dSdt = (-1)*beta*S*I-betaF*S*F+mu*(S+I+F+R)-mu*S
    dIdt = beta*S*I + betaF*S*F - gamma*I-mu*I
    dFdt = gamma*I-sigma*F-mu*F
    dRdt = sigma*F-mu*R
    dzdt = [dSdt,dIdt,dFdt,dRdt]
    return dzdt

def plot(t,result):
    plt.plot(t,z[:,0],'b-',label='Susceptible')
    plt.plot(t,z[:,1],'r-',label='Infected')
    plt.plot(t,z[:,2],'black',label='Funeral')
    plt.plot(t,z[:,3],'g-',label='Removed')
    plt.ylabel('Population')
    plt.xlabel('Time (in days)')
    plt.legend(loc='best')
    plt.title('SIFR Base Model')
    plt.show()
```

```
z0=[1,0.01,0,0]
param=(1.5,2.53,0.58,0.02, 0.1)
z=odeint(simulate,z0,t,param)
plot(t,z)
```

```
#Base model simulation 1  0.6,0.2
z0=[1,0.01,0,0]
param=(0.6,0.2,0.58,0.02, 0.1)
z=odeint(simulate,z0,t,param)
plot(t,z)
```

```
#Only transmission rate lowered
z0=[1,0.01,0,0]
param=(0.6,2.53,0.58,0.02, 0.1)
z=odeint(simulate,z0,t,param)
plot(t,z)
```

```
#Only infection rate lowered
z0=[1,0.01,0,0]
param=(1.5,1,0.58,0.02, 0.1)
z=odeint(simulate,z0,t,param)
plot(t,z)
```

```
#base model simulation 2   0.3,0.2
z0=[1,0.01,0,0]
param=(0.3,0.2,0.58,0.02, 0.1)
z=odeint(simulate,z0,t,param)
plot(t,z)
```

```
#Controlling Funeral Spread (betaF=0.1)
z0=[1,0.01,0,0]
param=(1.5,0.1,0.58,0.02,0.1)
z=odeint(simulate,z0,t,param)
plot(t,z)
```

```
#Implementing Vaccination rate of 0.1
import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
from scipy import integrate

t=np.linspace(0,21)
def simulate(z, t, beta, betaF, gamma,sigma, mu,v):
    S = z[0]
    I = z[1]
    F = z[2]
    R = z[3]
    dSdt = (-1)*beta*S*I-betaF*S*F+mu*(S+I+F+R)-mu*S-v*S
    dIdt = beta*S*I + betaF*S*F - gamma*I-mu*I
    dFdt = gamma*I-sigma*F-mu*F
    dRdt = sigma*F-mu*R+v*S
    dzdt = [dSdt,dIdt,dFdt,dRdt]
    return dzdt

def plot(t,result):
    plt.plot(t,z[:,0],'b-',label='Susceptible')
    plt.plot(t,z[:,1],'r-',label='Infected')
    plt.plot(t,z[:,2],'black',label='Funeral')
    plt.plot(t,z[:,3],'g-',label='Removed')
    plt.ylabel('Population')
    plt.xlabel('Time (in days)')
    plt.legend(loc='best')
    plt.title('SIFR Model with Vaccination')
    plt.show()

z0=[1,0.01,0,0]
param=(1.5,2.53,0.58,0.02,0.1,0.1)
z=odeint(simulate,z0,t,param)
plot(t,z)
```

```
#Vaccination rate of 0.2
z0=[1,0.01,0,0]
param=(1.5,2.53,0.58,0.02,0.1,0.2)
z=odeint(simulate,z0,t,param)
plot(t,z)
```

```
import numpy as np
from scipy.integrate import odeint
import random
import matplotlib as mpl
import matplotlib.pyplot as plt
import pandas as pd
import seaborn as sns
```

```
# Stochastic Simulation for base SIFR model

start_population=1000
days=200
trials=1000

# Here we use the base model data

beta=1.5 #ebola transmission rate
betaF=0.73  #transmission rate during funerals
gamma=0.58  #death rate
sigma=0.02 #burying rate
mu=0.1 #natural birth/death rate

def model_N(n,mu):
    seeds=np.random.uniform(0,1,np.int_(n))
    new_population=np.zeros(4)
    for seed in seeds:
        if seed < mu:
            new_population[0] += 1
    return new_population
```

```
def model_S(s, mu, beta, betaF):
    seeds = np.random.uniform(0, 1, np.int_(s))
    new_population = np.zeros(4)
    for seed in seeds:
        if seed < mu:
            new_population[0] -= 1
        elif seed < (mu + beta + betaF):
            new_population[0] -= 1
            new_population[1] += 1
    return new_population


def model_I(i, mu, gamma) :
    seeds = np.random.uniform(0, 1, np.int_(i))
    new_population = np.zeros(4)
    for seed in seeds:
        if seed < mu:
            new_population[1] -= 1
        elif seed < (mu + gamma):
            new_population[1] -= 1
            new_population[3] += 1
    return new_population


def model_F(f, mu, sigma):
    seeds = np.random.uniform(0, 1, np.int_(f))
    new_population = np.zeros(4)
    for seed in seeds:
        if seed < mu:
            new_population[3] -= 1
        elif seed <(mu + sigma):
            new_population[3] -=1
            new_population[2] += 1
    return new_population


def model_R(r, mu):
    seeds = np.random.uniform(0, 1, np.int_(r))
    new_population = np. zeros (4)
    for seed in seeds:
        if seed < mu:
            new_population[2]-=1
    return new_population
```

	days	S	I	R	F
0	0	1000.0	0.0	0.0	0.0
1	1	105.0	903.0	0.0	0.0
2	2	113.0	397.0	0.0	516.0
3	3	90.0	245.0	15.0	662.0
4	4	93.0	164.0	24.0	716.0
...	...	...	...	...	...
196	196	77.0	107.0	108.0	526.0
197	197	92.0	104.0	105.0	536.0
198	198	87.0	119.0	100.0	544.0
199	199	77.0	113.0	98.0	546.0
200	200	84.0	111.0	99.0	538.0

201 rows × 5 columns

```
sns.lineplot(data=base,x="days",y="S",label="Susceptible")
sns.lineplot(data=base, x="days",y="I",label="Infectious")
sns.lineplot (data=base, x="days", y="R",label="Removed")
sns.lineplot(data=base, x="days", y="F", label="Funeral")
plt.title('Stochastic Simulation of SIFR Base Model')
plt.xlabel('Day')
plt.ylabel ('Population')
plt.legend (loc="upper right")
```

```
<matplotlib.legend.Legend at 0x7f542b772460>
```

```
# Stochastic Simulation for controlling funeral spread model

start_population=1000
days=200
trials=1000

# Here we reduce the funeral transmission rate : betaF to 0.3

beta=0.5 #ebola transmission rate
betaF=0.3  #transmission rate during funerals
gamma=0.58  #death rate
sigma=0.06 #burying rate
mu=0.1

def control_model (start_population, days, beta, betaF, mu, gamma, sigma):
    pop = np.zeros([4, days+1])
    pop[0,0] = start_population
    for t in range(1, days+1) :
        N= np.sum(pop, axis=0)[t-1]
        S= pop[0, t-1]
        I= pop[1, t-1]
        R= pop[2, t-1]
        F= pop[3, t-1]

        dt_N= model_N(N, mu)
        dt_S = model_S(S, mu, beta, betaF)
        dt_I = model_I(I, mu, gamma)
        dt_F = model_F(F, mu, sigma)
        dt_R = model_R(R, mu)

        pop_change= dt_N + dt_S + dt_I + dt_F + dt_R
        pop[:,t] = np.add(pop[:,t-1],pop_change)

    df = pd.DataFrame({
        'days': np.arange(days+1),
        'S': pop[0,:],
        'I': pop[1,:],
        'R': pop[2,:],
        'F': pop[3,:],
    })
    return df
```

```
funeral_control = control_model(1000, 200, beta, betaF, mu, gamma,sigma)
display(funeral_control)
```

	days	S	I	R	F
0	0	1000.0	0.0	0.0	0.0
1	1	114.0	890.0	0.0	0.0
2	2	94.0	370.0	0.0	523.0
3	3	87.0	201.0	35.0	651.0
4	4	73.0	141.0	56.0	677.0
...	...	...	...	...	...
196	196	80.0	113.0	212.0	389.0
197	197	70.0	104.0	229.0	388.0
198	198	70.0	99.0	222.0	398.0
199	199	92.0	103.0	223.0	393.0
200	200	87.0	110.0	223.0	401.0

201 rows × 5 columns

```
sns.lineplot(data=funeral_control,x="days",y="S",label="Susceptible")
sns.lineplot(data=funeral_control, x="days",y="I",label="Infectious")
sns.lineplot (data=funeral_control, x="days", y="R",label="Removed")
sns.lineplot(data=funeral_control, x="days", y="F", label="Funeral")
plt.title('Stochastic Simulation of SIFR Model With Controlling Funeral Sp
plt.xlabel('Day')
plt.ylabel ('Population')
plt.legend (loc="upper right")
```

```
<matplotlib.legend.Legend at 0x7f542b3dd100>
```