MATH 3MB3

Group 17 Final Project

Topic 4: Ebola

Submitted to

Dr. Richard Zhao

Department of Mathematics and Statistics

McMaster University

Hamiltion, Ontario, Canada L8S 4K1

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Reported by

Ivy Xie (400376889)

Yincheng Zhu (400371892)

Xun Cheng (400431392)

Yuchen Jin (400371815)

Yijie Zhu (400468593)

1 Introduction

In 2014, the West Africa Ebola epidemic outbreak caused massive infection and death, and became one of the most severe public health crises of the decade. The outbreak resulted in more than 28,000 cases and claimed more than 11000 lives, reminding people of the significance of epidemiological forecast and control (Bosa et al., 2024). Data from the Centers for Disease Control (CDC) showed that, in some cases, more than 60% of infected individuals were linked to traditional burial ceremonies, transmission occurring through burial approaches. These include touching the corpse and direct contact with pharmacists during the ceremony (Curran et al., 2014). This finding highlighted the critical intersection between burial practice and disease transmission patterns, emphasizing the need to understand how burial practices impact Ebola transmission for more effective and culturally sensitive disease control strategies.

Mathematical modeling is an effective way for understanding and predicting the spread of epidemics. While the traditional fundamental model used to describe virus transmission dynamics is the Susceptible-Infected-Recovered (SIR) model, it fails to capture the Ebola transmission pathway associated with funerals. By incorporating F, which represents the funeral transmission component, to create a Susceptible-Infected-Funeral-Recovered (SIFR) model, we developed a more accurate representation of how Ebola virus spreads through funerals during outbreaks.

Our research investigates how interventions in funeral practice could influence the trajectory of the Ebola epidemic outbreak. We estimate this in model extension by editing the parameter funeral transmission rate. The plan for doing this research is, firstly, to determine parameters to build mathematical models using R, from which we get the simulation and prediction of epidemic populations with no intervention on funeral transmission. Then, we are adding intervention parameters to reduce funeral transmission to see how these interventions affect population dynamics. We will also analyze both models about their equilibrium and then the stabilization. The main finding is that reducing transmission rate could effectively lower the infected population, but it would also slightly increase the persistence time of epidemic.

2 Model

2.1 Base Model

$$
\begin{aligned}
S_{t+1} &= S_t + \mu - \mu S_t - \beta_S S_t I_t - \beta_F S_t F_t \\
I_{t+1} &= I_t - \mu I_t + \beta_S S_t I_t + \beta_F S_t F_t - \gamma I_t \\
F_{t+1} &= F_t + \gamma I_t - \sigma F_t \\
R_{t+1} &= R_t + \sigma F_t
\end{aligned}
$$

Parameter	**Description**	**Value**	**Source of Assumption**
β_S	Transmission rate between susceptible and infected	0.27 Day^{-1}	Estimating the Reproduction Number of Ebola Virus (EBOV)
β_F	Transmission rate between susceptible and funerals	0.79 Day^{-1}	Ebola Transmission Linked to a Funeral Ceremony
γ	Recovery rate	0.1782 Day^{-1}	Estimating the Reproduction Number of EBOV
σ	Funeral clearance rate	0.5 Day^{-1}	Forecast Ebola Synthetic Epidemics
μ	Natural birth and death rate	0.0111/365 Day^{-1}	United Nations Data Portal
N	Total population	1 (normalized)	Simplified for modeling

Table 1: Description of Parameters

Variable	Description	Units
S	Susceptible population	Proportion of total population ($0 \leq S \leq 1$)
I	Infected population	Proportion of total population ($0 \leq I \leq 1$)
F	Funeral population	Proportion of total population ($0 \leq F \leq 1$)
R	Recovered population	Proportion of total population ($0 \leq R \leq 1$)

Table 2: Description of Variables

We divided the total population of Guinea into four state variables: the susceptible population, the infected population, the recovered population, and the funeral population. We assume that on the first day, the number of infected individuals is 1, with the remainder of the population being susceptible. These state variables are measured in units of individuals. We omit the exposed population and the hospitalized population, focusing instead on modeling the data for general infection rates and funeral-related infections.

Our SIFR model simulates the dynamics of a population categorized into Susceptible (S), Infected (I), Funeral (F), and Recovered (R) states.

According to our Model, susceptible population decreases as individuals contract the infection (through interaction with infected individuals or funerals) and keeping stable with no infected individuals remains.

The infected population grows due to transmission from susceptible individuals but decreases as infected individuals either recover or die.

The funeral population grows from the individual who dies in the epidemic and decreases due to Funeral clearance.

The recovered population growth as infected individuals recover. Approach steady since no reinfection happened.

2.2 Analysis of Base Model

2.2.1 Equilibrium Analysis

The equilibrium equations for the system are as follows:

$$
\begin{aligned}
S^* &= S^* + \mu - \mu S^* - \beta_S S^* I^* - \beta_F S^* F^*, \\
I^* &= I^* - \mu I^* + \beta_S S^* I^* + \beta_F S^* F^* - \gamma I^*, \\
F^* &= F^* + \gamma I^* - \sigma F^*, \\
R^* &= R^* + \sigma F^*.
\end{aligned}
$$

At equilibrium, $S_{t+1} = S_t = S^*$, $I_{t+1} = I_t = I^*$, $F_{t+1} = F_t = F^*$, and $R_{t+1} = R_t = R^*$. Substituting these conditions, we simplify the equations:

$$
0 = \mu - \mu S^* - \beta_S S^* I^* - \beta_F S^* F^* \quad \Rightarrow \quad S^* = \frac{\mu}{\mu + \beta_S I^* + \beta_F F^*}.
$$

$$
0 = -\mu I^* + \beta_S S^* I^* + \beta_F S^* F^* - \gamma I^* \quad \Rightarrow \quad I^*(\mu + \gamma) = \beta_S S^* I^* + \beta_F S^* F^*.
$$

$$
0 = \gamma I^* - \sigma F^* \quad \Rightarrow \quad F^* = \frac{\gamma I^*}{\sigma}.
$$

Disease-Free Equilibrium: If $I^* = 0$, then:

$$
S^* = 1, \quad I^* = 0, \quad F^* = 0, \quad R^* = 0.
$$

Endemic Equilibrium: If $I^* > 0$,

$$
S^* = \frac{\mu}{\mu + \beta_S I^* + \beta_F F^*}, \quad I^*(\mu + \gamma) \quad = \beta_S S^* I^* + \beta_F S^* F^*, \quad F^* = \frac{\gamma I^*}{\sigma}, \quad R^* \quad = 1 - S^* - F^* - I^*.
$$

The solution to the system of equations reveals an equilibrium point where F*=I*=R*=0 ,and S*=1(All populations are susceptible). At this disease free equilibrium, the number of infected individuals, individuals at funerals, and recovered individuals all reach zero. This represents a baseline where no disease is circulating in the population, and everyone remains at risk if the disease is introduced. It reflects a healthy population with no infection dynamics. At the endemic equilibrium, the disease persists in the population at a steady state. This means that while people continue to get infected, the rates of new infections, recoveries, and environmental decay balance out over time. The disease becomes a constant, manageable presence in the population.

2.2.2 Stability Analysis

For the state vector $[S, I, F, R]$, the Jacobian matrix J is the matrix of partial derivatives:

$$J = \begin{bmatrix} \frac{\partial S'}{\partial S} & \frac{\partial S'}{\partial I} & \frac{\partial S'}{\partial F} & \frac{\partial S'}{\partial R} \\ \frac{\partial I'}{\partial S} & \frac{\partial I'}{\partial I} & \frac{\partial I'}{\partial F} & \frac{\partial I'}{\partial R} \\ \frac{\partial F'}{\partial S} & \frac{\partial F'}{\partial I} & \frac{\partial F'}{\partial F} & \frac{\partial F'}{\partial R} \\ \frac{\partial R'}{\partial S} & \frac{\partial R'}{\partial I} & \frac{\partial R'}{\partial F} & \frac{\partial R'}{\partial R} \end{bmatrix}$$

At disease-free equilibrium point, substituting the equations:

$$\frac{\partial S'}{\partial S} = 1 - \mu - \beta_S I - \beta_F F, \quad \frac{\partial S'}{\partial I} = -\beta_S S, \quad \frac{\partial S'}{\partial F} = -\beta_F S, \quad \frac{\partial S'}{\partial R} = 0$$

$$\frac{\partial I'}{\partial S} = \beta_S I + \beta_F F, \quad \frac{\partial I'}{\partial I} = 1 - \mu + \beta_S S - \gamma, \quad \frac{\partial I'}{\partial F} = \beta_F S, \quad \frac{\partial I'}{\partial R} = 0$$

$$\frac{\partial F'}{\partial S} = 0, \quad \frac{\partial F'}{\partial I} = \gamma, \quad \frac{\partial F'}{\partial F} = 1 - \sigma, \quad \frac{\partial F'}{\partial R} = 0$$

$$\frac{\partial R'}{\partial S} = 0, \quad \frac{\partial R'}{\partial I} = 0, \quad \frac{\partial R'}{\partial F} = \sigma, \quad \frac{\partial R'}{\partial R} = 1$$

$$J = \begin{bmatrix} -F\beta_F - I\beta_S - \mu + 1 & -S\beta_S & -S\beta_F & 0 \\ F\beta_F + I\beta_S & S\beta_S - \gamma - \mu + 1 & S\beta_F & 0 \\ 0 & \gamma & 1 - \sigma & 0 \\ 0 & 0 & \sigma & 1 \end{bmatrix}$$

$$J = \begin{bmatrix} 0.999969589041096 & -0.27 & -0.79 & 0 \\ 0 & 1.0917695890411 & 0.79 & 0 \\ 0 & 0.1782 & 0.5 & 0 \\ 0 & 0 & 0.5 & 1 \end{bmatrix}$$

The determinant of the Jacobian matrix calculated at the equilibrium point is approximately det(J), and the eigenvalues of the Jacobian matrix are [0.99996959, 1.0, 0.31805029, 1.2737193]. The dominant eigenvalue is 1.2737193, which is greater than 1. This result means that the equilibrium point is unstable. In this context, even minor deviations from equilibrium, such as a small increase in infection numbers, will result in the system moving further away from the disease-free equilibrium rather than returning to it. So, the infection can spread rapidly and leading to a significant outbreak of Ebola. This emphasizes the importance of effective intervention strategies to control the spread of the virus and restore stability to the system.

2.2.3 Simulation

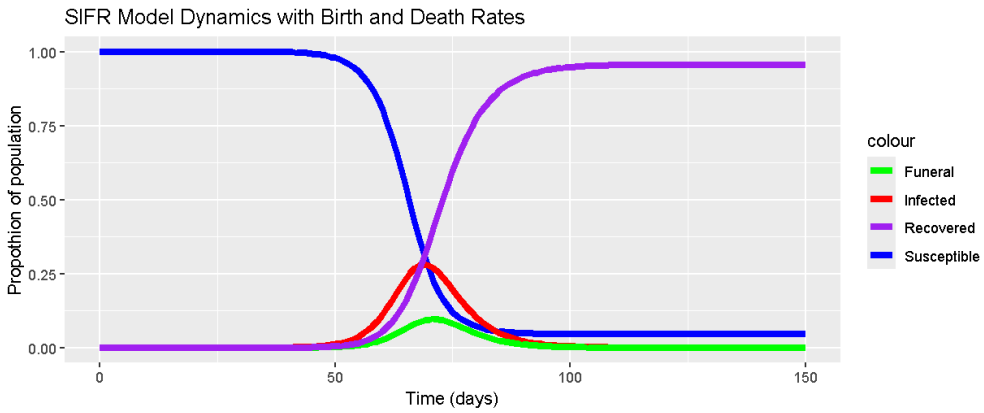

Figure 1: SIFR Model Dynamics with Birth and Death Rates

Simulations show that the susceptible population decreases as individuals become infected, the infected population grows and later decreases as individuals recover or die, and the funeral and recovered populations behave accordingly.

2.3 Model Extension

2.3.1 Extended Model Introduction

$$S_{t+1} = S_t + \mu - \mu S_t - \beta_S S_t I_t - \beta_F \cdot \frac{1}{1 + c \cdot F_t} S_t F_t$$

$$I_{t+1} = I_t - \mu I_t + \beta_S S_t I_t + \beta_F \cdot \frac{1}{1 + c \cdot F_t} S_t F_t - \gamma I_t$$

$$F_{t+1} = F_t + \gamma I_t - \sigma F_t$$

$$R_{t+1} = R_t + \sigma F_t$$

Term	Description
k	**Feedback Strength**: A dynamic term defined as $k = c \cdot F = c \cdot F$, representing the restriction strength proportional to funeral-associated individuals.
c	**Policy Multiplier**: Represents the intensity of government restrictions on funeral gatherings. Higher c values indicate stricter policies, reducing funeral transmission more significantly as funeral-associated individuals (F) increase.
F	**Number of funeral-associated individuals at time** t: Representing the population currently driving funeral-related transmissions.
$k = c \cdot F$	**Feedback relationship**: The restriction strength increases linearly with F.
$\frac{1}{1+k}$	**Feedback Mechanism**: The adjustment factor applied to β_F where $k = c \cdot F$. This term dynamically reduces the funeral transmission rate as F increases, based on the policy multiplier c.

Table 3: Description of Terms Used in the Model

The purpose of our extended model is to expand the impact of government interventions in controlling funeral-related transmissions of the Ebola virus. We will dynamically adjust the funeral transmission rate β_F based on the number of funeral-associated individuals (F). Our goal is to simulate how limiting funeral gatherings could mitigate the epidemic. This extension adds a feedback mechanism that reflects real-world responses to rising fatalities during outbreaks.

2.3.2 Extended Model Equilibrium Analysis

The extended model equations are as follows:

$$
\begin{aligned}
S^* &= S^* + \mu - \mu S^* - \beta_S S^* I^* - \beta_F \frac{1}{1 + c \cdot F^*} S^* F^*, \\
I^* &= I^* - \mu I^* + \beta_S S^* I^* + \beta_F \frac{1}{1 + c \cdot F^*} S^* F^* - \gamma I^*, \\
F^* &= F^* + \gamma I^* - \sigma F^*, \\
R^* &= R^* + \sigma F^*.
\end{aligned}
$$

At equilibrium, $S_{t+1} = S_t = S^*$, $I_{t+1} = I_t = I^*$, $F_{t+1} = F_t = F^*$, and $R_{t+1} = R_t = R^*$. Substituting these conditions, we simplify the equations:

$$
0 = \mu - \mu S^* - \beta_S S^* I^* - \beta_F \frac{1}{1 + c \cdot F^*} S^* F^*.
$$

Rearranging:

$$
S^* = \frac{\mu}{\mu + \beta_S I^* + \beta_F \frac{F^*}{1 + c \cdot F^*}}.
$$

$$
0 = -\mu I^* + \beta_S S^* I^* + \beta_F \frac{1}{1 + c \cdot F^*} S^* F^* - \gamma I^*.
$$

Simplify:

$$
I^*(\mu + \gamma) = \beta_S S^* I^* + \beta_F \frac{1}{1 + c \cdot F^*} S^* F^*.
$$

$$
0 = \gamma I^* - \sigma F^*.
$$

Rearranging:

$$
F^* = \frac{\gamma I^*}{\sigma}.
$$

$$
R^* = 1 - S^* - I^* - F^*.
$$

Disease-Free Equilibrium If $I^* = 0$, then:

$$
S^* = 1, \quad F^* = 0, \quad R^* = 0.
$$

Endemic Equilibrium If $I^* > 0$, substitute $F^* = \frac{\gamma I^*}{\sigma}$ into the equations for S^* and I^*:

$$S^* = \frac{\mu}{\mu + \beta_S I^* + \beta_F \frac{\frac{\gamma I^*}{\sigma}}{1 + c \cdot \frac{\gamma I^*}{\sigma}}}.$$

$$I^*(\mu + \gamma) = \beta_S S^* I^* + \beta_F \frac{1}{1 + c \cdot \frac{\gamma I^*}{\sigma}} S^* \frac{\gamma I^*}{\sigma}.$$

Finally:

$$R^* = 1 - S^* - I^* - \frac{\gamma I^*}{\sigma}.$$

The solution to the system of equations reveals an equilibrium point where I*=F*=R*=0, and S*=1(the entire population is susceptible). At this disease-free equilibrium, there are no infected individuals, no environmental contamination, and no recoveries because the disease is absent. This represents a state where the population is completely healthy, with no infection circulating. However, everyone remains vulnerable if the disease is introduced, highlighting the importance of preventative measures to maintain this equilibrium. At the endemic equilibrium, the disease becomes a persistent part of the population. Here, S*, I*, F*, and R* may stabilize at some non-zero values. This indicates that while some people continue to get infected, others recover, and the environment maintains a level of contamination, all processes balance over time. As the government intervention the disease does not disappear but remains a steady, manageable presence, requiring ongoing efforts to control its spread and reduce its impact on public health.

2.3.3 Extended Model Stability Analysis

At the equilibrium point when the system is free from disease, only susceptible populations exist. To find the stability, we calculated for the Jacobian matrix for the four-variable model substituted with parameters and variable values at equilibrium. $\mu = 0.0111/365 < 10^{-4}$ is approximate to 0 for simplification, as this subtle modification would not impact the range of eigenvalues. Then, eigenvalues of the Jacobian matrix are calculated to be 0.99996959, 1.0, 0.31805029, and 1.2737193. Since the largest absolute value among all eigenvalues is 1.2737 and is larger than 1, it is indicated that this disease free equilibrium point is also unstable.

$$\begin{bmatrix} \frac{-F_{star}\beta_F+(F_{star}c+1)(-I_{star}\beta_S-\mu+1)}{F_{star}c+1} & -S_{star}\beta_S & -\frac{S_{star}\beta_F}{(F_{star}c+1)^2} & 0 \\ \frac{F_{star}\beta_F+I_{star}\beta_S(F_{star}c+1)}{F_{star}c+1} & S_{star}\beta_S-\gamma-\mu+1 & \frac{S_{star}\beta_F}{(F_{star}c+1)^2} & 0 \\ 0 & \gamma & 1-\sigma & 0 \\ 0 & 0 & \sigma & 1 \end{bmatrix}$$

```
[0.999969589041096,          -0.27, -0.79, 0]
[                 0, 1.0917695890411,  0.79, 0]
[                 0,          0.1782,   0.5, 0]
[                 0,               0,   0.5, 1]
```

We get our eigenvalues of the Jacobian matrix which are equal to [0.99996959, 1.0, 0.31805029, 1.2737193]. $|\lambda|_{\max} = 1.27371929686259 > 1 \implies$ The disease free equilibrium is unstable

3 Results

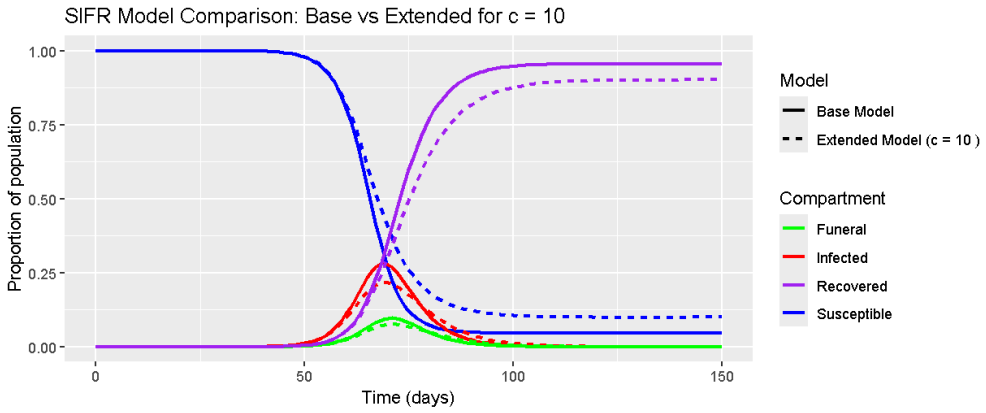

Figure 2: Base vs Extended for c = 10

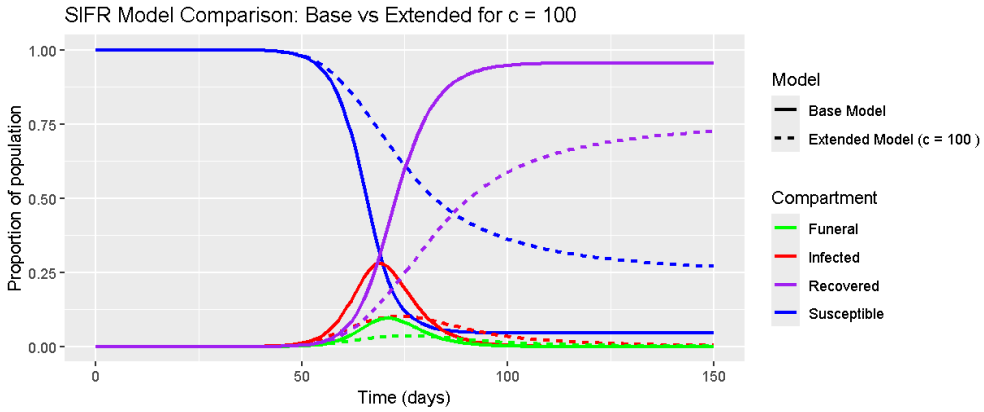

Figure 3: Base vs Extended for c = 100

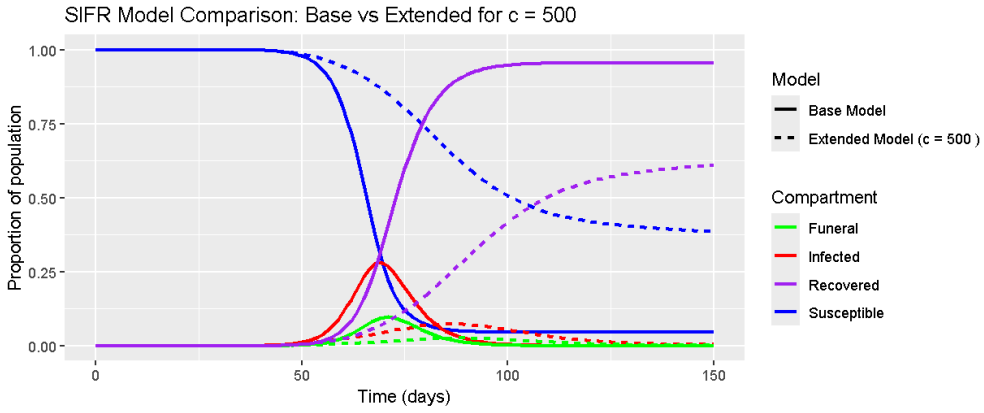

Figure 4: Base vs Extended for c = 500

Those three graphs above (Figure 2, 3, 4) represent an extended model with varying levels of government intervention, denoted by the variable c. As the variable c increases from 10 to 100 to 500, the most notable change in the graphs is the significant decline in the red curve, which represents the number of infections decreasing from around 25% to 12%. Additionally, the peak of the red curve is shifted almost 10 days later. However, despite the significant decline in the peak, the duration of infection at lower levels stretched from 40 days to 70 days.

This is understandable because when an infectious disease spreads on a large scale, the government is more likely to implement strong measures. This will lead to rapid and effective containment. However, if the outbreak is relatively small, it may not attract significant attention from the government, which leads to slower and more gradual control of the disease.

In real-world scenarios, we can draw the following conclusion: stronger government measures can prevent a sharp, short-term outbreak in infections, but it may lead to a prolonged period of gradual reduction in the number of cases.

The extended model introduces a dynamic funeral transmission rate β_F that adjusts based on a feedback mechanism, $1/(1+cFt)$, which reflects government restrictions on funeral gatherings. By varying c, the model can simulate different levels of intervention, ranging from weak to strong restrictions, allowing for a nuanced analysis of policy impacts. Despite this modification, the model preserves the simplicity of the base SIFR structure, avoiding additional state variables and ensuring that equilibrium and stability analyses remain straightforward. This extended framework provides a flexible and realistic tool to evaluate how funeral-related interventions could influence the progression of the Ebola epidemic.

The extended model introduces a dynamic feedback mechanism to adjust the funeral transmission rate β_F based on the number of funeral-associated individuals (F). This reflects the effect of government interventions.

4 Discussion

Our study demonstrates that funeral-related interventions can significantly influence the spread of the Ebola virus. Using the extended SIFR model, we tested how different levels of government restrictions on funerals affect the epidemic. We found that stronger interventions (higher c) reduce the peak number of infections and delay the peak time. However, these restrictions may also extend the overall duration of the epidemic. This finding suggests a trade-off between managing the peak infection load and shortening the epidemic's duration.

Our stability analysis revealed that the disease-free equilibrium is unstable, meaning even small increases in infections can cause a rapid outbreak. This highlights the need for early and decisive interventions to control transmission. These results align with the established understanding that timely and effective actions can mitigate the spread of infectious diseases.

There are several limitations in this study. First, the model assumes a homogeneous population, which may not reflect real-world differences between regions or demographic groups. Second, it excludes factors such as asymptomatic carriers and individuals in the exposed phase of infection,

potentially underestimating the true spread of the virus. Lastly, the model does not consider external influences like limited healthcare resources or whether the public complies with funeral restrictions, which may alter the epidemic's progression. Our future studies could improve the model by incorporating additional compartments, such as exposed or hospitalized populations, to make the simulations more realistic. Other dynamic feedback mechanisms, such as policy changes based on infection rates or public compliance levels, should also be explored. Additionally, more in-depth analysis of how different combinations of intervention policies interact could provide better insights into controlling outbreaks.

This research highlights the critical role of managing funeral gatherings in controlling Ebola outbreaks. The extended SIFR model offers a flexible tool to analyze the effects of different interventions. It supports the development of informed public health strategies for future epidemics.

5 Reference

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6 Appendix: R Code

base_vs_extend

YIJIE ZHU

2024-12-07

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.4.2
```

```
# Define parameters
beta_S <- 0.27      # Transmission rate between susceptible and infected
beta_F <- 0.79      # Transmission rate between susceptible and funerals
gamma <- 0.1782     # Recovery rate
sigma <- 0.5        # Funeral clearance rate
mu <- 0.0111 / 365  # Birth and natural death rate (per day)
c                   # Exponential decay factor for funeral transmission (extended model)
```

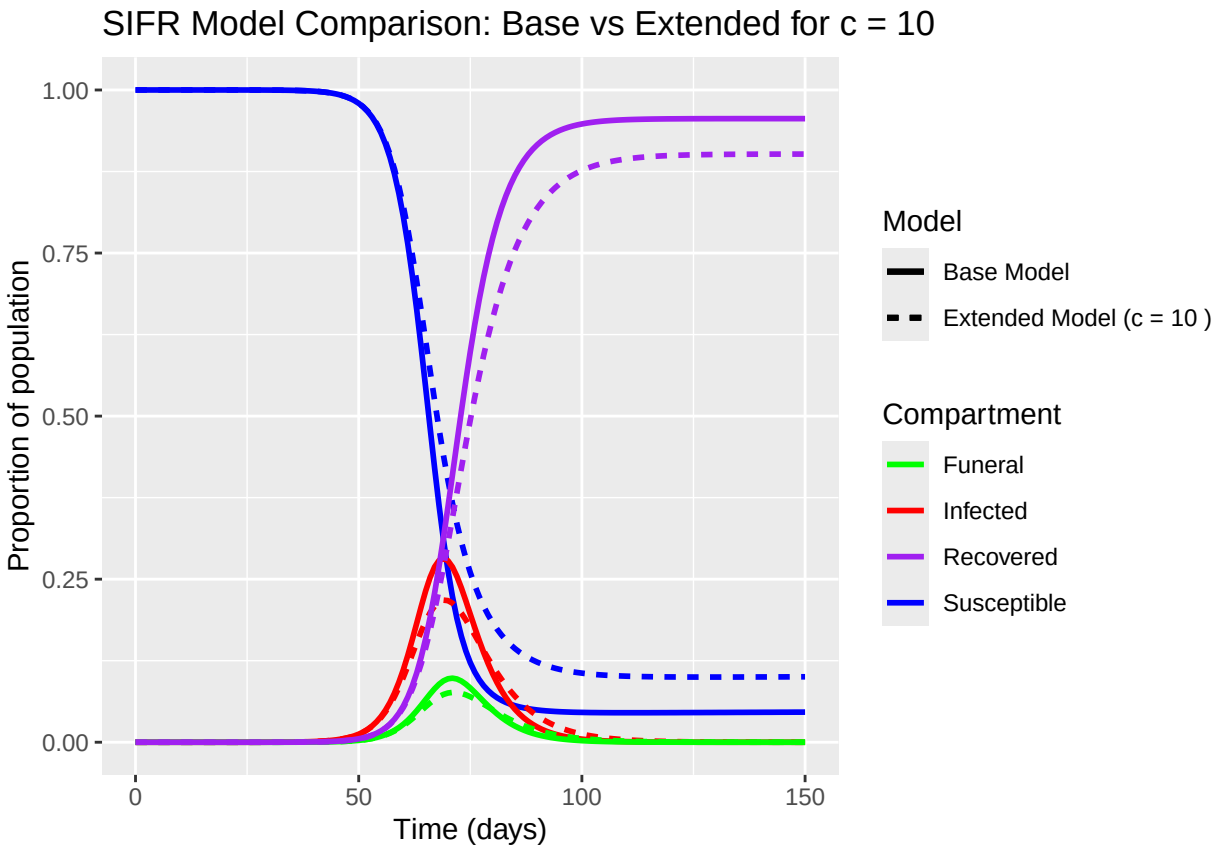
```
## function (...)  .Primitive("c")
```

```
# Initial conditions
N <- 1                 # Total population
initial_state <- list(
  S = 1 - 1 / 11472914, # Initial susceptible population
  I = 1 / 11472914,     # Initial infected individuals
  F = 0,                # Initial funeral population
  R = 0                 # Initial recovered individuals
)

# Time frame for simulation
time_steps <- 150      # Simulate for 150 days

# Function to run the base model
run_base_model <- function() {
  # Initialize vectors to store results
  S <- numeric(time_steps + 1)
  I <- numeric(time_steps + 1)
  F <- numeric(time_steps + 1)
  R <- numeric(time_steps + 1)

  # Set initial values
  S[1] <- initial_state$S
  I[1] <- initial_state$I
  F[1] <- initial_state$F
  R[1] <- initial_state$R
```

```
  # Simulation loop for base model
  for (t in 1:time_steps) {
    S[t + 1] <- S[t] + mu - mu * S[t] - beta_S * S[t] * I[t] - beta_F * S[t] * F[t]
    I[t + 1] <- I[t] - mu * I[t] + beta_S * S[t] * I[t] + beta_F * S[t] * F[t] - gamma * I[t]
    F[t + 1] <- F[t] + gamma * I[t] - sigma * F[t]
    R[t + 1] <- R[t] + sigma * F[t]
  }

  data.frame(time = 0:time_steps, Susceptible = S, Infected = I, Funeral = F, Recovered = R)
}

# Function to run the extended model
run_extended_model <- function(c) {
  # Initialize vectors to store results
  S <- numeric(time_steps + 1)
  I <- numeric(time_steps + 1)
  F <- numeric(time_steps + 1)
  R <- numeric(time_steps + 1)

  # Set initial values
  S[1] <- initial_state$S
  I[1] <- initial_state$I
  F[1] <- initial_state$F
  R[1] <- initial_state$R

  # Simulation loop for extended model
  for (t in 1:time_steps) {
    S[t + 1] <- S[t]+mu-mu*S[t]-beta_S*S[t]*I[t]-beta_F*S[t]*F[t]*exp(-c * F[t])
    I[t + 1] <- I[t]-mu*I[t]+beta_S*S[t]*I[t]+beta_F*S[t]*F[t]*exp(-c*F[t])-gamma*I[t]
    F[t + 1] <- F[t]+gamma*I[t]-sigma*F[t]
    R[t + 1] <- R[t]+sigma*F[t]
  }

  data.frame(time = 0:time_steps, Susceptible = S, Infected = I, Funeral = F, Recovered = R)
}

# Run the base model
base_model_results <- run_base_model()

# Run the extended model for c = 10, 100, 500
extended_model_results_c10 <- run_extended_model(c = 10)
extended_model_results_c100 <- run_extended_model(c = 100)
extended_model_results_c500 <- run_extended_model(c = 500)

# Define custom colors
colours <- c(
  "Susceptible" = "blue",
  "Infected" = "red",
  "Funeral" = "green",
  "Recovered" = "purple"
)

# Function to plot comparison
```

```r
plot_comparison <- function(base_results, extended_results, c_value) {
  base_results$model <- "Base Model"
  extended_results$model <- paste("Extended Model (c =", c_value, ")")
  combined_results <- rbind(base_results, extended_results)

  ggplot(combined_results, aes(x = time)) +
    geom_line(aes(y = Susceptible, colour = "Susceptible", linetype = model), lwd = 1) +
    geom_line(aes(y = Infected, colour = "Infected", linetype = model), lwd = 1) +
    geom_line(aes(y = Funeral, colour = "Funeral", linetype = model), lwd = 1) +
    geom_line(aes(y = Recovered, colour = "Recovered", linetype = model), lwd = 1) +
    labs(
      x = "Time (days)",
      y = "Proportion of population",
      title = paste("SIFR Model Comparison: Base vs Extended for c =", c_value),
      colour = "Compartment",
      linetype = "Model"
    ) +
    scale_colour_manual(values = colours)
}

# Generate plots for c = 10, 100, 500
plot_c10 <- plot_comparison(base_model_results, extended_model_results_c10, 10)
plot_c100 <- plot_comparison(base_model_results, extended_model_results_c100, 100)
plot_c500 <- plot_comparison(base_model_results, extended_model_results_c500, 500)
```

```r
print(plot_c10)
```


SIFR Model Comparison: Base vs Extended for c = 10
Proportion of population
1.00
0.75
0.50
0.25
0.00
0
50
100
150
Time (days)
Model
Base Model
Extended Model (c = 10)
Compartment
Funeral
Infected
Recovered
Susceptible

BASE_MODEL

YIJIE ZHU

2024-12-05

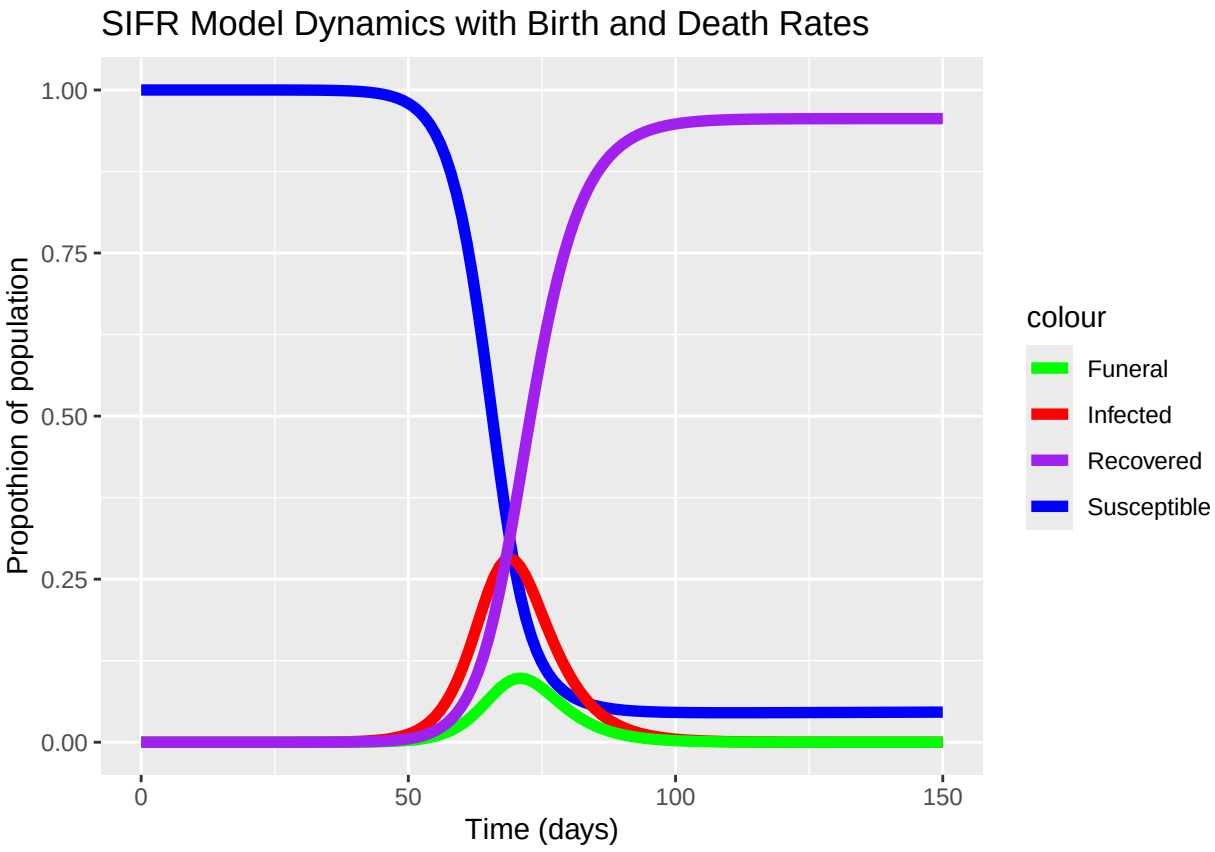
```r
# Plot using ggplot2
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.4.2
```

```r
# Define parameters

beta_S = 0.27      # Transmission rate between susceptible and infected
beta_F = 0.79      # Transmission rate between susceptible and funerals
gamma = 0.1782     # Recovery rate
sigma = 0.5       # Funeral clearance rate
mu = 0.0111 / 365   # Birth and natural death rate (per day)


# Initial conditions
N = 1                 # Total population
initial_state <- list(
  S = 1 - 1 / 11472914, # Initial susceptible population
  I = 1 / 11472914,     # Initial infected individuals
  F = 0,                # Initial funeral population
  R = 0                 # Initial recovered individuals
)

# Time frame for simulation
time_steps <- 150      # Simulate for 1 year (365 days)

# Initialize vectors to store results
S <- numeric(time_steps + 1)
I <- numeric(time_steps + 1)
F <- numeric(time_steps + 1)
R <- numeric(time_steps + 1)

# Set initial values
S[1] <- initial_state$S
I[1] <- initial_state$I
F[1] <- initial_state$F
R[1] <- initial_state$R

# Simulation loop
for (t in 1:time_steps) {
  # Update each compartment using the discrete equations with birth and death
```

```
  S[t + 1] <- S[t] + mu - mu * S[t] - beta_S * S[t] * I[t] - beta_F * S[t] * F[t]
  I[t + 1] <- I[t] - mu * I[t] + beta_S * S[t] * I[t] + beta_F * S[t] * F[t] - gamma * I[t]
  F[t + 1] <- F[t] + gamma * I[t] - sigma * F[t]
  R[t + 1] <- R[t] + sigma * F[t]
}
# Time vector
time <- 0:time_steps

# Combine results into a data frame
soln <- data.frame(
  time = time,
  Susceptible = S,
  Infected = I,
  Funeral = F,
  Recovered = R
)
```

```
# Define custom colors
colours <- c(
  "Susceptible" = "blue",
  "Infected" = "red",
  "Funeral" = "green",
  "Recovered" = "purple"
)

# Plot using ggplot2
library(ggplot2)
ggplot(soln) +
  geom_line(mapping = aes(x = time, y = Susceptible, colour = "Susceptible"), lwd = 2) +
  geom_line(mapping = aes(x = time, y = Infected, colour = "Infected"), lwd = 2) +
  geom_line(mapping = aes(x = time, y = Funeral, colour = "Funeral"), lwd = 2) +
  geom_line(mapping = aes(x = time, y = Recovered, colour = "Recovered"), lwd = 2) +
  labs(
    x = "Time (days)",
    y = "Propothion of population",
    title = "SIFR Model Dynamics with Birth and Death Rates",
  ) +
  scale_colour_manual(values = colours)
```


SIFR Model Dynamics with Birth and Death Rates
Propothion of population
1.00
0.75
0.50
0.25
0.00
0
50
100
150
Time (days)
colour
Funeral
Infected
Recovered
Susceptible

7 Appendix: Individual Contributions

Ivy Xie: Stability Analysis for Base Model, Extended Model Introduction, Discussion, R Code

Xun Cheng: Base model Reality explanation, extended model Reality explanation, R Code

Yijie Zhu: Base Model, R Simulation for Base and Extended Model, R Code

Yuchen Jin: Introduction, Extended Model Stability at Equilibrium

Yincheng Zhu: Base Model and Extended Model Equilibrium Analysis