Ebola Epidemics Project

Jialin Zhang 400400788
XiaoJun Ge 400370084
Ziyao Zhang 400368829
Hengyu He 400381436
Binghe (Ruby) Li 400412789

1 Introduction

Ebolaviruses were first discovered in 1976 near the Ebola River in what is now the Democratic Republic of the Congo. Since then, periodic outbreaks have occurred, but the 2014–2016 epidemic in West Africa remains the most devastating. It resulted in more than 28,000 reported cases and over 11,000 deaths, with Guinea, Liberia, and Sierra Leone bearing the brunt of the crisis [World Health Organization, 2016, Baize et al., 2014]. The absence of effective treatment options during the outbreak placed immense pressure on public health systems and highlighted the critical role of behavioral interventions.

A growing body of evidence has identified traditional funeral rites as a key driver of Ebola virus transmission. In many affected regions, burial customs involve washing, touching, or kissing the deceased—activities that significantly increase exposure risk. One study linked a single funeral ceremony to at least 85 secondary infections, 62 of which occurred in a single week [Kucharski and Edmunds, 2018]. Another analysis estimated that over 60% of new cases in some regions could be attributed to unsafe burials [Legrand et al., 2007]. These findings underscore the urgent need to understand and mitigate funeral-associated transmission pathways.

This paper focuses on evaluating the impact of controlling funeral-related transmission on Ebola outbreak dynamics. Specifically, we incorporate cultural and behavioral variables into a compartmental transmission model. By introducing a parameter representing the proportion of the population opting for safe burials, we assess how this behavioral modification can alter the course of an epidemic.

Our simulations show that increasing safe burial coverage substantially reduces transmission rates and may drive new infections toward zero in the long term. These results align with earlier modeling studies and field interventions that demonstrated the effectiveness of modifying funeral practices during Ebola outbreaks [Camacho et al., 2014]. In conclusion, culturally tailored public health strategies targeting high-risk behaviors—such as unsafe burials—are

essential tools in containing Ebola epidemics and protecting vulnerable communities.

2 Model

2.1 Base Model

Real-world Mechanisms

This model investigates the dynamics of Ebola virus transmission among humans, specifically replicating the context of the 2014 West African Ebola epidemic. The population is divided into four key categories: susceptible individuals, infected individuals, deceased individuals whose bodies are involved in funeral activities, and those who have completed the funeral process and are no longer part of the transmission chain.

We assume that once susceptible individuals become infected, they eventually die and enter the funeral phase. Funerals are considered the principal mode of Ebola transmission in this model.

Assumptions

The following assumptions were made to construct the base model:

- No public health interventions are present to reduce transmission during funerals.
- Every individual has an equal probability of contact with others during funeral ceremonies.
- Time t is measured in days.
- Susceptible individuals can be infected through contact with both infected individuals and corpses during funeral rituals.
- There is no recovery from Ebola; all infected individuals eventually die and proceed to funerals.
- The population remains constant due to equal birth and natural death rates.
- Buried bodies are no longer capable of transmitting the virus.

Modelling Choices

This study employs a discrete-time, compartmental, dynamical model—specifically an SIFR model (Susceptible-Infected-Funeral-Removed)—for the following reasons:

- **Dynamical model:** Captures changes in compartment sizes over time to simulate the epidemic progression.
- **Compartmental model:** Segments the population into meaningful epidemiological states, allowing detailed analysis of transition dynamics.

- **Discrete model:** Uses daily time steps to represent discrete events such as funeral ceremonies, infections, and natural deaths.

System of Equations

The dynamics of the system are governed by the following set of difference equations:

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

Where:

- S_t: number of susceptible individuals at time t
- I_t: number of infected individuals
- F_t: individuals involved in funerals (dead but unburied)
- R_t: removed individuals (either buried or beyond the infectious stage)
- β: transmission rate from infected individuals
- β_F: transmission rate from unburied corpses
- γ: death rate of infected individuals (progression to funeral)
- σ: rate at which funerals are completed
- μ: natural birth and death rate
- N: total population (assumed constant)

Model Diagram

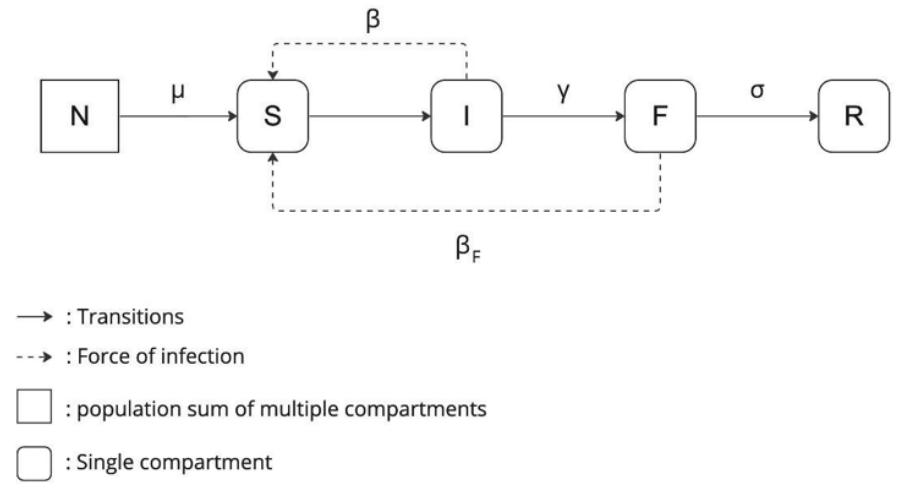

Figure 1: SIFR Base Model Diagram for Ebola Transmission

Model Parameters

Symbol	Description	Unit
S	Susceptible individuals	People
I	Infectious individuals	People
F	Deceased individuals due to Ebola involved in ongoing funeral processes	People
R	Removed individuals (those who have died and completed funeral rites)	People
N	Total population ($S + I + F + R$)	People
β	Effective contact rate between susceptible and infected individuals	$1/(\text{people} \cdot \text{day})$
β_F	Effective contact rate between susceptible individuals and unburied deceased	$1/(\text{people} \cdot \text{day})$
γ	Death rate of infected individuals who proceed to funeral stage	1/day
σ	Rate at which deceased individuals are removed (buried)	1/day
μ	Natural birth and death rate	1/day

Table 1: Description of parameters used in the base model

2.2 Extended Parameter Setup and Base Model Analysis

The following parameters were defined based on empirical data and reasonable assumptions relevant to the 2014–2016 Ebola outbreak in West Africa:

- $\beta = 0.0000384$
  This effective contact rate between susceptible and infected individuals was derived using West Africa's 2016 population estimate (367,903,544) and the number of infected individuals (14,122).

- $\beta_F = 0.0455$
  This contact rate between susceptible individuals and deceased bodies at funerals is based on the assumption that each unsafe burial involves an average of 7 contacts, and approximately 65% of those contacts resulted in infection. Thus: $0.07 \times 0.65 = 0.0455$.

- $\gamma = 0.0307$
  The rate at which infected individuals die and move to the funeral compartment is estimated using: $\frac{11{,}310}{367{,}903{,}544} \times 1000 = 0.0307$.

- $\sigma = 0.02459$
  Assuming that 80% of deceased individuals are buried per day after entering the funeral stage, we set: $\sigma = \gamma \times 0.8 = 0.02459$.

- $\mu = 0.0001$
  This represents the natural birth and death rate. We assume it to be constant and equal at 0.0001.

Analysis of the Base Model

Given the assumption that recovery from Ebola is not possible in this model, the removed compartment (R_t) includes only those who have died and completed funeral rites. This simplification eliminates any recovery term and implies that all infected individuals eventually die and progress to the funeral phase.

This assumption, while stark, enables a more focused analysis of Ebola's transmission dynamics by avoiding the complexity introduced by partial immunity or recovery. As a result, the model emphasizes the severity and potential speed of the epidemic in the absence of medical intervention.

To examine the system's equilibrium behavior, we set all compartments to steady state:

$$S_{t+1} = S_t = S^*, \quad I_{t+1} = I_t = I^*, \quad F_{t+1} = F_t = F^*$$

Substituting into the base model equations:

$$\begin{aligned} S^* &= S^* - \beta S^* I^* - \beta_F S^* F^* + \mu N - \mu S^* \\ I^* &= I^* + \beta S^* I^* + \beta_F S^* F^* - \gamma I^* - \mu I^* \\ F^* &= F^* + \gamma I^* - \sigma F^* \end{aligned}$$

Solving this system, we find the disease-free equilibrium (DFE) point:

$$(S^*, I^*, F^*) = (N, 0, 0)$$

To assess the stability of this equilibrium, we construct the Jacobian matrix of the system. The Jacobian matrix J is composed of the partial derivatives of the update equations with respect to the state variables:

$$J = \begin{bmatrix} \frac{\partial S_{t+1}}{\partial S_t} & \frac{\partial S_{t+1}}{\partial I_t} & \frac{\partial S_{t+1}}{\partial F_t} \\ \frac{\partial I_{t+1}}{\partial S_t} & \frac{\partial I_{t+1}}{\partial I_t} & \frac{\partial I_{t+1}}{\partial F_t} \\ \frac{\partial F_{t+1}}{\partial S_t} & \frac{\partial F_{t+1}}{\partial I_t} & \frac{\partial F_{t+1}}{\partial F_t} \end{bmatrix}$$

Evaluating the partial derivatives:

$$\begin{aligned} &\frac{\partial S_{t+1}}{\partial S_t} = 1 - \beta I_t - \beta_F F_t - \mu, && \frac{\partial S_{t+1}}{\partial I_t} = -\beta S_t, && \frac{\partial S_{t+1}}{\partial F_t} = -\beta_F S_t \\ &\frac{\partial I_{t+1}}{\partial S_t} = \beta I_t + \beta_F F_t, && \frac{\partial I_{t+1}}{\partial I_t} = 1 + \beta S_t - \gamma - \mu, && \frac{\partial I_{t+1}}{\partial F_t} = \beta_F S_t \\ &\frac{\partial F_{t+1}}{\partial S_t} = 0, && \frac{\partial F_{t+1}}{\partial I_t} = \gamma, && \frac{\partial F_{t+1}}{\partial F_t} = 1 - \sigma \end{aligned}$$

Substituting the disease-free equilibrium $(S^*, I^*, F^*) = (N, 0, 0)$ into the Jacobian, we obtain:

$$J(N, 0, 0) = \begin{bmatrix} 1 - \mu & -N\beta & -N\beta_F \\ 0 & 1 + N\beta - \gamma - \mu & N\beta_F \\ 0 & \gamma & 1 - \sigma \end{bmatrix}$$

This matrix can be used to assess local stability by analyzing its eigenvalues. If all eigenvalues lie within the unit circle (i.e., have a magnitude less than 1), the equilibrium point is locally asymptotically stable.

Eigenvalue Analysis and Local Stability

To evaluate the local stability of the disease-free equilibrium $(S^*, I^*, F^*) = (N, 0, 0)$, we compute the eigenvalues of the Jacobian matrix by solving the characteristic equation:

$$\det(J - \lambda I) = 0$$

Using the Jacobian matrix:

$$J(N, 0, 0) = \begin{bmatrix} 1 - \mu & -N\beta & -N\beta_F \\ 0 & 1 + N\beta - \gamma - \mu & N\beta_F \\ 0 & \gamma & 1 - \sigma \end{bmatrix}$$

We compute the determinant:

$$\det \begin{bmatrix} 1-\mu-\lambda & -N\beta & -N\beta_F \\ 0 & 1+N\beta-\gamma-\mu-\lambda & N\beta_F \\ 0 & \gamma & 1-\sigma-\lambda \end{bmatrix} = 0$$

Using cofactor expansion, we find:

$$(1-\mu-\lambda)\left[(1+N\beta-\gamma-\mu-\lambda)(1-\sigma-\lambda)-N\beta_F\gamma\right]=0$$

This gives one eigenvalue directly:

$$\lambda_1 = 1-\mu$$

The remaining eigenvalues λ_2, λ_3 are solutions of the quadratic equation:

$$(1+N\beta-\gamma-\mu-\lambda)(1-\sigma-\lambda)-N\beta_F\gamma=0$$

Expanding and simplifying, we get:

$$\lambda^2+(\gamma+\mu-N\beta+\sigma-2)\lambda+\Big[-N\beta_F\gamma+\gamma\sigma-\gamma+\mu\sigma-\mu-N\beta\sigma+N\beta-\sigma+1\Big]=0$$

Applying the quadratic formula:

$$\lambda_{2,3}=\frac{-(\gamma+\mu-N\beta+\sigma-2)\pm\sqrt{(\gamma+\mu-N\beta+\sigma-2)^2-4A}}{2}$$

Where:

$$A=-N\beta_F\gamma+\gamma\sigma-\gamma+\mu\sigma-\mu-N\beta\sigma+N\beta-\sigma+1$$

Thus, the three eigenvalues are:

$$\begin{aligned}\lambda_1 &= 1-\mu \\ \lambda_2 &= \frac{-B-\sqrt{B^2-4A}}{2} \\ \lambda_3 &= \frac{-B+\sqrt{B^2-4A}}{2}\end{aligned}$$

Where $B=\gamma+\mu-N\beta+\sigma-2$.

If all eigenvalues satisfy $|\lambda| < 1$, the disease-free equilibrium is locally asymptotically stable.

Using the parameter values from our simulation, we obtained the following approximate eigenvalues:

$$\lambda_1 \approx 0.9999$$
$$\lambda_2 \approx -0.3995$$
$$\lambda_3 \approx 0.3480$$

Since the dominant eigenvalue is less than 1 in magnitude, the disease-free equilibrium is locally asymptotically stable. This implies that the compartments S, I, and F will diminish over time without oscillations, eventually approaching zero. The entire population will ultimately transition to the removed compartment R, consisting of individuals who have died and undergone funeral rites.

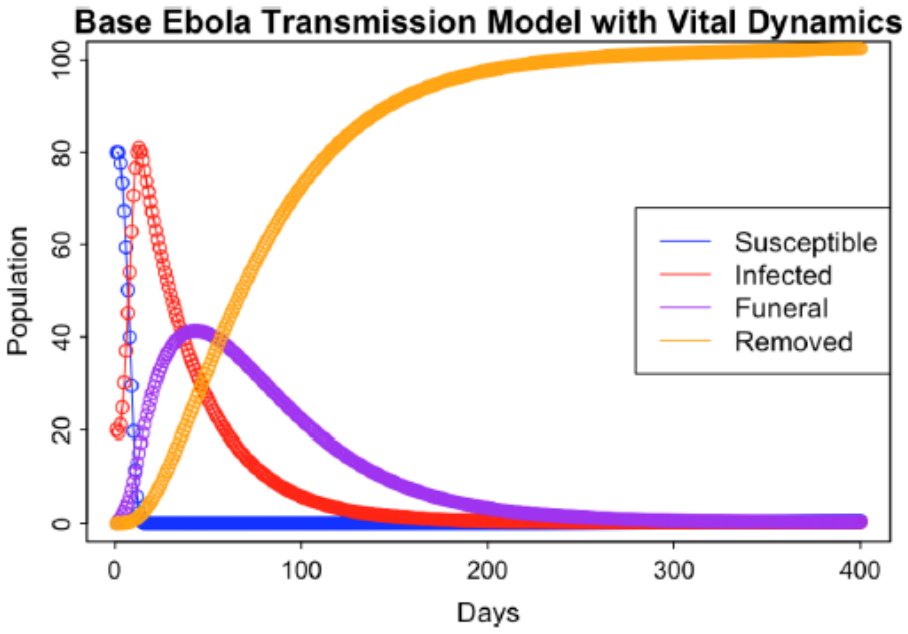

Figure 2: Time series simulation of S, I, F, and R compartments in the base model

The simulation plot above, generated using R, confirms the mathematical analysis. Over time, only the removed population persists, while the susceptible, infected, and funeral groups converge to extinction.

2.3 Model Extension

To incorporate the effects of public health interventions aimed at limiting transmission during funeral practices, we propose an extension of the base model. This version assumes that

a portion of the infected individuals bypass the funeral stage and transition directly into the removed class. This reflects the implementation of safe burial protocols or alternative handling of the deceased.

Extended Model Assumptions

- Individuals at funerals mix homogeneously.
- Time t is measured in days.
- Susceptible individuals can be infected through contact with both infected individuals and deceased bodies during funerals.
- Ebola has no recovery pathway; every infected individual eventually dies, either with or without undergoing a funeral.
- The natural birth and death rates are equal and constant, maintaining a stable total population.
- Buried individuals do not contribute to disease transmission.

Model Structure and Assumptions

To investigate the impact of public health interventions aimed at reducing Ebola transmission during funerals, we extend the base model by introducing a new pathway. In this extension, some infected individuals bypass the funeral stage and are removed directly—representing safe burial practices or alternate body handling protocols.

We continue using a dynamical, compartmental, and discrete-time model for consistency and comparability with the base model.

Extension Model Diagram

System of Equations

The modified compartmental equations are:

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

Here: - γ_F is the rate at which infected individuals die and enter the funeral stage. - γ_R is the rate at which infected individuals die and are removed without a funeral. - The total death rate remains: $\gamma = \gamma_F + \gamma_R$.

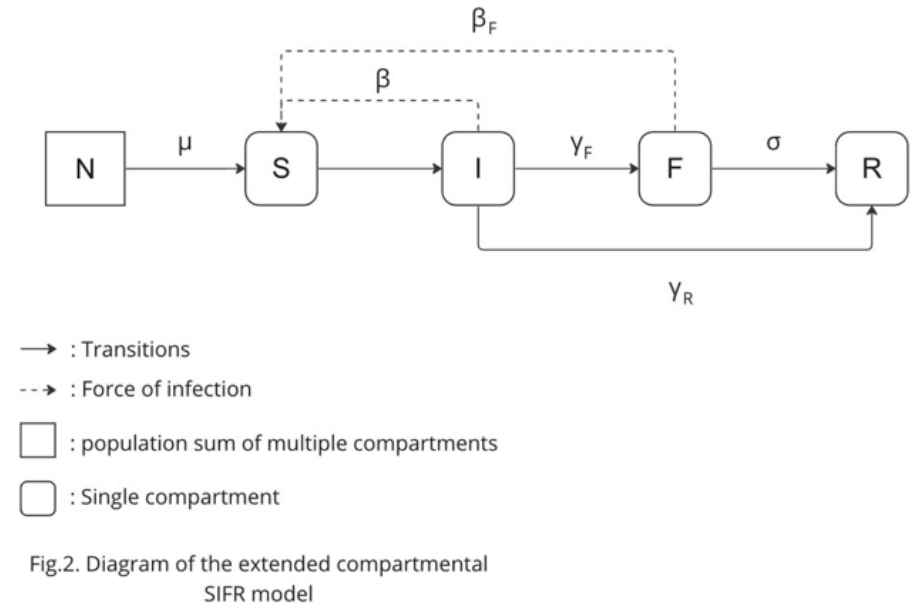

Figure 3: Diagram of the Extended SIFR Model with Funeral Intervention

Symbol	Description	Unit
S	Susceptible individuals	People
I	Infectious individuals	People
F	Deceased individuals involved in uncompleted funerals	People
R	Removed individuals (buried or safely disposed)	People
N	Total population ($N = S + I + F + R$)	People
β	Transmission rate between S and I	$1/(\text{people} \cdot \text{day})$
β_F	Transmission rate between S and F	$1/(\text{people} \cdot \text{day})$
γ_F	Death rate into the funeral compartment	1/day
γ_R	Death rate with no funeral (safe removal)	1/day
σ	Funeral completion (removal) rate	1/day
μ	Natural birth/death rate	1/day

Table 2: Parameter definitions for the extended SIFR model

Parameter Definitions

In the extension model, we've split the original rate (γ) into two parts: γ_F for those who die and have funerals, and γ_R for those who die without funerals. Maintaining the total rate ($\gamma = \gamma_F + \gamma_R$), the modification aims to reduce funeral-related transmissions and help eradicate Ebola in the long term.

3 Results

In the extension model, we've split the original rate (γ) into two parts: γ_F for those who die and have funerals, and γ_R for those who die without funerals. Maintaining the total rate ($\gamma = \gamma_F + \gamma_R$), the modification aims to reduce funeral-related transmissions and help eradicate Ebola in the long term.

As in the base model, we assume the recovery rate is zero, the model simplifies the dynamics of disease transmission by excluding any recovery terms from the equation for R_{t+1}.

Since the total population size follows the equation $N = S + I + F + R$, our model will remain constant. This means that we can partially simplify the analysis by getting rid of the equation for R since as long as we know S, I, and F we could always calculate R using $R = N - S - I - F$ (since N is constant, this wouldn't work if N was changing).

Equilibrium

To find the equilibrium points, set $S_{t+1} = S_t = S^*$, $I_{t+1} = I_t = I^*$, $F_{t+1} = F_t = F^*$ and in our extension model equations so that neither state variable is changing.

Then,

$$S^* = S^* - \beta S^* I^* - \beta_F S^* F^* + \mu N - \mu S^*,$$

$$I^* = I^* + \beta S^* I^* + \beta_F S^* F^* - \gamma_F I^* - \mu I^* - \gamma_R I^*,$$

$$F^* = F^* + \gamma_F I^* - \sigma F^*.$$

This gives:

$$-\beta S^* I^* - \beta_F S^* F^* + \mu N - \mu S^* = 0,$$

$$\beta S^* I^* + \beta_F S^* F^* - \gamma_F I^* - I^* - \mu I^* - \gamma_R I^* = 0,$$

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

By substituting $I^* = \frac{\sigma}{\gamma_F} F^*$ into the above formula, we found the equilibrium point (S^*, I^*, R^*) at

$$(N, 0, 0).$$

Stability Analysis of the Extension Model

To examine the local stability of the disease-free equilibrium, we compute the partial derivatives of the extension model equations with respect to S_t, I_t, and F_t.

Partial Derivatives

$$\frac{\partial S_{t+1}}{\partial S_t} = 1 - \beta I_t - \beta_F F_t - \mu$$
$$\frac{\partial S_{t+1}}{\partial I_t} = -\beta S_t$$
$$\frac{\partial S_{t+1}}{\partial F_t} = -\beta_F S_t$$

$$\frac{\partial I_{t+1}}{\partial S_t} = \beta I_t + \beta_F F_t$$
$$\frac{\partial I_{t+1}}{\partial I_t} = 1 + \beta S_t - \gamma_F - \mu - \gamma_R$$
$$\frac{\partial I_{t+1}}{\partial F_t} = \beta_F S_t$$

$$\frac{\partial F_{t+1}}{\partial S_t} = 0$$
$$\frac{\partial F_{t+1}}{\partial I_t} = \gamma_F$$
$$\frac{\partial F_{t+1}}{\partial F_t} = 1 - \sigma$$

Jacobian Matrix

From the partial derivatives above, we construct the Jacobian matrix J:

$$J = \begin{bmatrix} 1 - \beta I_t - \beta_F F_t - \mu & -\beta S_t & -\beta_F S_t \\ \beta I_t + \beta_F F_t & 1 + \beta S_t - \gamma_F - \mu - \gamma_R & \beta_F S_t \\ 0 & \gamma_F & 1 - \sigma \end{bmatrix}$$

At the disease-free equilibrium $(S^*, I^*, F^*) = (N, 0, 0)$, the Jacobian becomes:

$$J(N, 0, 0) = \begin{bmatrix} 1 - \mu & -\beta N & -\beta_F N \\ 0 & 1 + \beta N - \gamma_F - \mu - \gamma_R & \beta_F N \\ 0 & \gamma_F & 1 - \sigma \end{bmatrix}$$

Characteristic Equation

To assess local stability, we calculate the characteristic polynomial by solving:

$$\det(J(N,0,0) - \lambda I) = 0$$

$$\det \begin{bmatrix} 1-\mu-\lambda & -\beta N & -\beta_F N \\ 0 & 1+\beta N-\gamma_F-\mu-\gamma_R-\lambda & \beta_F N \\ 0 & \gamma_F & 1-\sigma-\lambda \end{bmatrix} = 0$$

Expanding the determinant:

$$(1-\mu-\lambda)\left[(1+\beta N-\gamma_F-\mu-\gamma_R-\lambda)(1-\sigma-\lambda)-\gamma_F\beta_F N\right] = 0$$

This implies the eigenvalues are the roots of:

- $\lambda_1 = 1-\mu$
- The two remaining eigenvalues are the solutions to the quadratic equation:

$$(1+\beta N-\gamma_F-\mu-\gamma_R-\lambda)(1-\sigma-\lambda)-\gamma_F\beta_F N = 0$$

Characteristic Equation and Eigenvalue Analysis

It follows from the previous section that the characteristic equation becomes:

$$(1-\mu-\lambda)\left[(1+\beta N-\gamma_F-\mu-\gamma_R-\lambda)(1-\sigma-\lambda)-\gamma_F\beta_F N\right] = 0$$

This implies either:

$$\lambda = 1-\mu$$

or the remaining eigenvalues satisfy the quadratic equation:

$$\begin{aligned} & (1+\beta N-\gamma_F-\mu-\gamma_R-\lambda)(1-\sigma-\lambda)-\gamma_F\beta_F N = 0 \\ \Rightarrow\quad & \lambda^2 + (\gamma_F+\mu+\gamma_R-\beta N+\sigma-2)\lambda \\ & \quad -\beta_F\gamma_F N+\gamma_F\sigma-\gamma_F+\mu\sigma-\mu-\beta N\sigma+\beta N+\sigma\gamma_R-\sigma+1 = 0 \end{aligned}$$

Using the quadratic formula, the two nontrivial eigenvalues are:

$$\lambda_{2,3} = \frac{-\gamma_F-\mu-\gamma_R+\beta N-\sigma+2 \pm \sqrt{\Delta}}{2}$$

Where Δ is the discriminant:

$$\Delta = (\gamma_F + \mu + \gamma_R - \beta N + \sigma - 2)^2 - 4(-\beta_F \gamma_F N + \gamma_F \sigma - \gamma_F + \mu\sigma - \mu - \beta N \sigma + \beta N + \sigma\gamma_R - \sigma + 1)$$

Thus, the full set of eigenvalues is:

$$\lambda_1 = 1 - \mu$$
$$\lambda_2 = \frac{-\gamma_F - \mu - \gamma_R + \beta N - \sigma + 2 - \sqrt{\Delta}}{2}$$
$$\lambda_3 = \frac{-\gamma_F - \mu - \gamma_R + \beta N - \sigma + 2 + \sqrt{\Delta}}{2}$$

Simulation Result

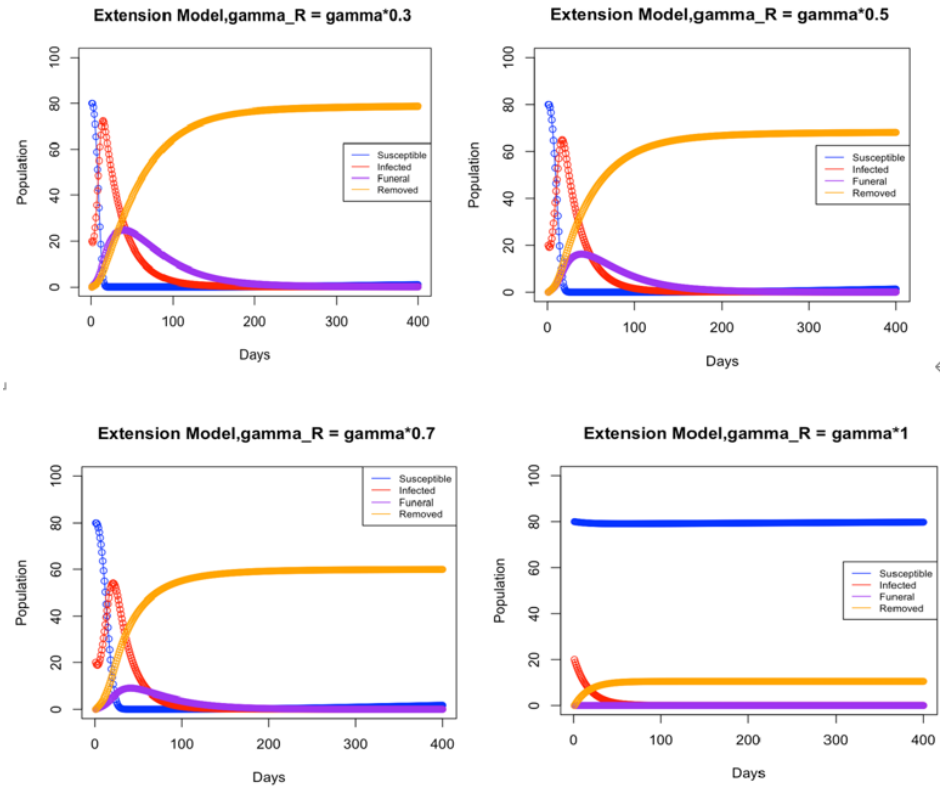

Figure 4: Corresponding simulation plot generated using R for the extended model

This extension model demonstrates that, under the assumption that all funerals are canceled, the Ebola outbreak can be eradicated within approximately 50 days, with nearly 80% of the total population remaining susceptible. Compared to the base model, the proportion of

individuals who remain uninfected increases significantly. As the proportion of individuals who die without undergoing funeral rites rises, the model predicts a corresponding increase in the uninfected population.

This comparison suggests that eliminating or strictly controlling funeral-related activities is an effective strategy for mitigating the spread of Ebola. As a result, implementing tighter regulations on funerals-or even prohibiting traditional funerals involving direct contact with the deceased-could be considered as a public health intervention. Furthermore, incorporating additional protective measures such as mask-wearing will be explored in future work. Reducing the number of funerals not only decreases transmission but also contributes to broader efforts in strengthening global health security.

4 Discussion

Model Results and Interpretation

The simulation results from the extension model indicate that if funerals are canceled for half to the entire population, Ebola transmission can be effectively suppressed, with extinction occurring in approximately 50 days. In this scenario, around 80% of the total population remains susceptible by the end of the outbreak. This represents a significant improvement in the proportion of uninfected individuals compared to the base model.

As the proportion of individuals who die without undergoing funeral ceremonies increases, the number of uninfected individuals rises accordingly. These findings reinforce the importance of controlling funeral-related transmission pathways. Stricter funeral management not only helps reduce immediate viral spread but also strengthens long-term population-level protection.

In light of these results, we recommend the implementation of stronger regulations on funeral practices, including limiting physical contact with deceased individuals. As part of future intervention strategies, additional measures such as mandatory mask usage and rapid diagnostic testing at funeral sites may further enhance disease control. Moreover, technology-assisted virtual funerals could offer a culturally sensitive solution that balances tradition with public health priorities.

Model Limitations

As with all mathematical models, simplification of real-world dynamics is necessary to achieve analytical tractability and clarity. Our model includes several idealized assumptions that limit its realism:

- **No recovery:** The model assumes all infected individuals eventually die, omitting the possibility of recovery. In reality, the Ebola case fatality rate averages approximately 50% [Johns Hopkins Medicine,], meaning a significant proportion of infected individuals survive. Including a recovery pathway would improve model accuracy.

- **Constant population:** We assume that the birth and death rates are equal, resulting in a fixed population size. This assumption may not hold during outbreaks with high mortality or migration.
- **Homogeneous mixing:** The model assumes equal contact probability among all individuals, neglecting age, social structure, and behavioral differences. In future models, stratified contact rates could better represent population heterogeneity.

Directions for Future Research

To address the limitations noted above, future extensions of this model should incorporate:

- **Medical interventions:** Introducing vaccination dynamics would offer more realistic projections. For instance, a WHO-led trial showed that among 5,837 vaccinated individuals, no Ebola cases were reported, while 23 cases occurred in the unvaccinated control group [Public Health Agency of Canada, 2023]. Individuals who are successfully vaccinated could be modeled as transitioning directly out of the susceptible pool.
- **Public health implementation:** Future work should also examine real-world constraints, such as public acceptance of interventions, resource availability, and integration into existing healthcare systems. Ethical considerations, especially those involving cultural and religious funeral practices, must be addressed thoughtfully.
- **Targeted strategies:** Tailoring interventions to high-risk subgroups using age-structured or behaviorally distinct compartments could enhance the precision of public health recommendations.

Addressing these factors will enhance the utility of the model and support global efforts to contain and eliminate Ebola outbreaks more effectively.

References

[Baize et al., 2014] Baize, S., Pannetier, D., Oestereich, L., and et al. (2014). Emergence of zaire ebola virus disease in guinea — preliminary report. *The New England Journal of Medicine*, 371:1418–1425.

[Camacho et al., 2014] Camacho, A., Funk, S., Gillet, P., and et al. (2014). Potential for large outbreaks of ebola virus disease. *Epidemics*, 9:70–78.

[Johns Hopkins Medicine,] Johns Hopkins Medicine. Ebola. `https://www.hopkinsmedicine.org/health/conditions-and-diseases/ebola`. Accessed: 2025-03-23.

[Kucharski and Edmunds, 2018] Kucharski, A. J. and Edmunds, W. J. (2018). Case fatality rate for ebola virus disease in west africa. *The Lancet Infectious Diseases*, 18(5):524–526.

[Legrand et al., 2007] Legrand, J., Grais, R. F., Boelle, P.-Y., Valleron, A.-J., and Flahault, A. (2007). Understanding the dynamics of ebola epidemics. *Epidemiology and Infection*, 135(4):610–621.

[Public Health Agency of Canada, 2023] Public Health Agency of Canada (2023). Ebola disease: Symptoms and treatment. https://www.canada.ca/en/public-health/services/diseases/ebola.html. Accessed: 2025-03-23.

[World Health Organization, 2016] World Health Organization (2016). Ebola situation report - final. Accessed: 2025-03-23.

A Appendix

A.1 Code for Base Model

```
# Base model simulation in R
beta <- 0.0000384
beta_F <- 0.0455
gamma <- 0.0307
sigma <- gamma * 0.8
mu <- 0.0001
N <- 1000

S <- rep(0, 100)
I <- rep(0, 100)
F <- rep(0, 100)
R <- rep(0, 100)

S[1] <- N - 1
I[1] <- 1
F[1] <- 0
R[1] <- 0

for (t in 1:99) {
  S[t + 1] <- S[t] - beta * S[t] * I[t] - beta_F * S[t] * F[t] + mu * N
  - mu * S[t]
  I[t + 1] <- I[t] + beta * S[t] * I[t] + beta_F * S[t] * F[t]
  - gamma * I[t] - mu * I[t]
  F[t + 1] <- F[t] + gamma * I[t] - sigma * F[t]
  R[t + 1] <- R[t] + sigma * F[t]
}

plot(S, type = "l", col = "blue", ylim = c(0, N), ylab = "Population", xlab = "Time")
lines(I, col = "red")
lines(F, col = "green")
lines(R, col = "black")
legend("right", legend = c("S", "I", "F", "R"),
col = c("blue", "red", "green", "black"), lty = 1)
```

A.2 Code for Extension Model

```
# Extension model simulation in R
beta <- 0.0000384
beta_F <- 0.0455
gamma_F <- 0.015
gamma_R <- 0.015
sigma <- 0.02459
mu <- 0.0001
N <- 1000

S <- rep(0, 100)
I <- rep(0, 100)
F <- rep(0, 100)
R <- rep(0, 100)

S[1] <- N - 1
I[1] <- 1
F[1] <- 0
R[1] <- 0

for (t in 1:99) {
  S[t + 1] <- S[t] - beta * S[t] * I[t] - beta_F * S[t] * F[t] + mu * N - mu * S[t]
  I[t + 1] <- I[t] + beta * S[t] * I[t] + beta_F * S[t] * F[t]
  - gamma_F * I[t] - gamma_R * I[t] - mu * I[t]
  F[t + 1] <- F[t] + gamma_F * I[t] - sigma * F[t]
  R[t + 1] <- R[t] + sigma * F[t] + gamma_R * I[t]
}

plot(S, type = "l", col = "blue", ylim = c(0, N), ylab = "Population", xlab = "Time")
lines(I, col = "red")
lines(F, col = "green")
lines(R, col = "black")
legend("right", legend = c("S", "I", "F", "R"),
col = c("blue", "red", "green", "black"), lty = 1)


#For gamma_R=gamma*0.5
gamma_R <- gamma*0.5
gamma_F <-gamma*0.5
# simulation loop
for (day in 2:days) {
        # Calculate new values
        S_new <- S - beta *S * I - beta_F *S *F + miu * N - miu * S
        I_new <- I + beta *S *I + beta_F *S *F - gamma * I - miu * I -
```

```
            gamma_R * I
        F_new <- F + gamma_F * I - sigma * F
        R_new <- R + sigma * F + gamma_R * I
        # Update state
        S <- S_new
        I <- I_new
        F<- F_new
        R <- R_new
    # Store results
    S_vec[day] <- S
    I_vec[day] <- I
    F_vec[day] <- F
    R_vec[day] <- R
Plotting the results
olot(s_vec, type = "o", col = "blue", ylim =c(0, N), xlab = "Days",
    ylab = "Population", main = "Extension Mode1,gamma_R = gamma*0.5 ")
points(I_vec,type = "o", col = "red")
ooints(F_vec,type = "o", col = "purple')
points(R_vec,type = "o", col = "orange")
legend("right", legend = c("Susceptib7e", "Infected", "Funeral", "Removed"),


#For gamma_R=gamma*0.7
gamma_R <- gamma*0.7
gamma_F <-gamma*0.3
# Simulation loop
for (day in 2:days) {
    # Calculate new values
    S_new <- S - beta # S # I - beta_F = S # F + miu =N - miu = S
    I_new <- I + beta *S * I + beta_F *S *F - gamma * I - miu * I -
        gamma_R * I
    F_new <- F + gamma_F # I - sigma # F
    R_new <- R + sigma * F + gamma_R * I
    # Update state
    S <- S_new
    I<- I_new
    F<- F_new
    R<- R_new
    # Store results
    S_vec[day] <- S
    I_vec[day] <- I
    F_vec[day] <- F
    R_vec[day] <- R
}
```

Individual Contribution

<table>
<tr><td>Introduction</td><td colspan="3">Model</td><td>Result</td><td>Discussion</td><td>Reference</td></tr>
<tr><td rowspan="2">Binghe Li, Xiaojun Ge</td><td>Base Model</td><td>Extended Parameter Setup and Base Model Analysis</td><td>Model Extension</td><td rowspan="2">Ziyao Zhang Hengyu He Jialin Zhang</td><td rowspan="2">Jialin Zhang, Xiaojun Ge</td><td rowspan="2">Binghe Li</td></tr>
<tr><td>Ziyao Zhang, Jialin Zhang</td><td>Xiaojun Ge, Binghe Li</td><td>Ziyao Zhang, Hengyu He</td></tr>
</table>