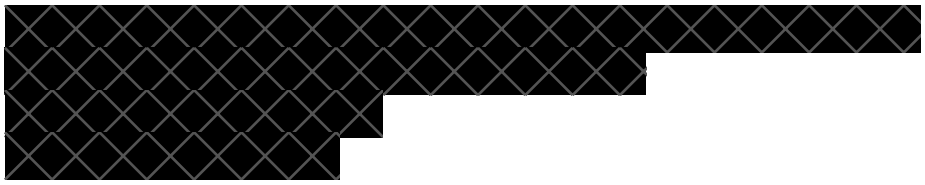
Forecast of Ebola Epidemics Project



1. Introduction

Ebola virus is a highly lethal virus that mainly affects humans and nonhuman primates. (CDC, n.d.). The 2014 West African Ebola epidemic was the largest Ebola outbreak in history. (WHO, 2021). According to the Centers for Disease Control and Prevention (n.d.), the total number of cases during this outbreak, including suspected, probable, and confirmed individuals, was 28,652, and the total number of deaths was 11,325. Among various ways of transmission, funerals have been considered as a significant way to infect susceptible individuals because of cultural practices (WHO, 2021). The major reason is that funerals often attract people from different areas, increasing the risk of virus transmission. In addition, the concentration of virus on the corpse is relatively high, and washing and touching the dead's body is a cultural tradition in many African countries, leading to a higher risk of infection. (CDC, 2016). Thus, in order to control the transmission of this highly lethal virus and predict the number of cases in terms of future outbreaks, it is extremely important to look at Ebola transmission at funerals and to develop a simple disease model to account for it.

In this paper, we will compare the situation where government takes action to control Ebola spread during funerals and the one where they do nothing. We will analyse the effect of controlling funeral spread will have on the disease transmission. Our focus is on understanding how do key parameters affect the long-term behavior of the Ebola disease model, and estimating how long will it take to eliminate the disease under different level of intervention .

Based on our result, it indicates that controlling funeral spread significantly reduce the Ebola transmission. It is expected that more people will not be infected by Ebola, and the duration of pandemic will be reduced. The extent of the reduction is depend on the level of public heath intervention that government imposes on funerals. Our analysis demonstrates that public health intervention has a huge positive effect on the pandemics, and encourage governments to prioritize efforts in this area.

2. Model

2.1 Base Model

Real-world mechanism:
In our model, susceptible people become infected, then die and move off to a funeral home, and eventually are buried after their funerals. In addition, susceptible people can become infected if they have contact with dead individuals whose funeral ceremonies are not yet completed.
We have the following assumptions:

- No one is recovering from the disease.
- There is no deliberate intervention by the government or World Health Organization.
- The population size N_t is closed.
- Assume there is no interaction between different epidemic regions.
- Birth rate is equal to death rate, measured by μ.
- Time t is measured in days.
- Buried bodies will not transmit viruses.
- Once an individual becomes infected, he eventually dies, and there will be a funeral ceremony for him.

We may find reasonable real-world values with which to parameterize the model from trustworthy institutions, for example, CDC and WHO.

Modelling choices:
In the base model, we consider using a continuous-time and single-compartment model. Continuous-time models are preferred over discrete models because they enable us to take measurements within a specific range and to observe the rate of change for each variable more accurately. The advantage of using a compartment model is the diversity of applications, and adding multiple compartments to the model may help to better interpret the observed data.

Base Model Equations:

$$\frac{dS}{dt} = -\beta SI - \beta_F SF + \mu N_a - \mu S \tag{1.1}$$

$$\frac{dI}{dt} = \beta SI + \beta_F SF - \gamma I - \mu I \tag{1.2}$$

$$\frac{dF}{dt} = \gamma I - \sigma F \tag{1.3}$$

$$\frac{dR}{dt} = \sigma F \tag{1.4}$$

Model diagram:

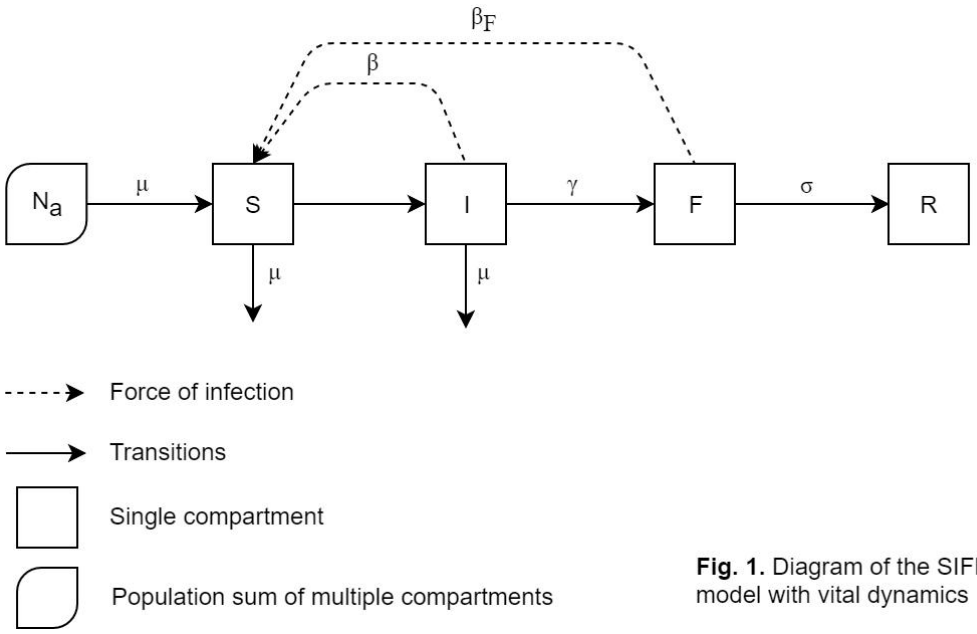


Fig. 1. Diagram of the SIFR model with vital dynamics

Variable	**Definition**	**Units**
S	Susceptible individuals	people
I	Infected individuals	people
F	Dead individuals who died from Ebola and whose funeral are not completed	people
R	Individuals who have either recovered from Ebola or died from it	people
D	Individuals who died a natural death	people
N_t	The total number of people alive and dead	people
N_a	The number of people alive	people
Parameter	**Definition**	**Units**
t	Time	day
β	Infection rate of susceptible individuals who have contact with infected individuals	1/(people * day)
β_F	Infection rate of susceptible individuals who have contact with dead individuals whose funeral ceremonies are not yet completed	1/(people * day)
γ	Rate of infected people who is dead and will have a funeral	1/day
σ	Rate of people who got buried	1/day
μ	Birth rate/Death rate	1/day

The values of parameters we are using for the simulation and analysis:

- $\gamma = 3.24$

Cause-specific death rate is calculated by the death occuring during a time period divide by size of the population among the deaths occurred multiply by 100,000. (CDC, 2012). The total population in West Africa in 2014 is 349,000,000 (United Nations, 2022), and the death occuring during 2014 West African Ebola epidemic is 11,310 (CDC, n.d.).

Thus, $\gamma = \frac{11,310}{349,000,000} \cdot 100,000 \approx 3.24$

- $\mu = 0.0392$

According to the data provided by United Nations, the crude birth rate in West Africa in 2014 is 39.2 per 1000 population. So, μ = 39.2/1000 =0.0392

- $\sigma = 2.6$ (inclusive)

There are no related data or statistics recording the proportion of West African got buried after funeral per day. We assume about 80% of the dead will have a funeral. $\sigma = 2.6 \approx 0.802\gamma$.

2.2 Analysis of Base Model

Since $N_t = S + I + F + R$ remains unchanged, we have a closed population and this four-dimensional model can be reduced to three-dimensional by dropping $\frac{dR}{dt}$.

To reduce the complexity of the model, we can nondimensionalize our model by replacing the state variables S, I and F with unitless state variables $u = \frac{S}{N_t}, v = \frac{I}{N_t}, w = \frac{F}{N_t}$.

Differentiate both sides:

$$\frac{dS}{dt} = \frac{du}{dt} \cdot N_t + u \cdot \frac{dN_t}{dt} \Rightarrow$$

$$\frac{du}{dt} = \frac{1}{N_t}\frac{dS}{dt} = \frac{1}{N_t}\left(-\beta SI - \beta_F SF + \mu(S+I) - \mu S\right)$$

$$= \frac{1}{N_t}\left(-\beta u v N_t^2 - \beta_F u w N_t^2 + \mu v N_t\right)$$

$$= -\beta N_t u v - \beta_F N_t u w + \mu v$$

Similarly, we have

$$\frac{dv}{dt} = \beta N_t u v + \beta_F N_t u w - (\gamma + \mu)v$$

$$\frac{dw}{dt} = \gamma v - \sigma w$$

Let $\tau = (\gamma + \mu)t$ represents the unitless time; and $\frac{dt}{d\tau} = \frac{1}{\gamma + \mu}$.

$$\frac{du}{d\tau} = \frac{du}{dt} \cdot \frac{dt}{d\tau} = -\frac{\beta N_t}{\gamma + \mu} u v - \frac{\beta_F N_t}{\gamma + \mu} u w + \frac{\mu}{\gamma + \mu} v$$

$$\frac{dv}{d\tau} = \frac{dv}{dt} \cdot \frac{dt}{d\tau} = \frac{\beta N_t}{\gamma + \mu} u v + \frac{\beta_F N_t}{\gamma + \mu} u w - v$$

$$\frac{dw}{d\tau} = \frac{dw}{dt} \cdot \frac{dt}{d\tau} = \frac{\gamma}{\gamma + \mu} v - \frac{\sigma}{\gamma + \mu} w$$

Let $R_0 = \frac{\beta N_t}{\gamma + \mu}, R_1 = \frac{\beta_F N_t}{\gamma + \mu}, B_1 = \frac{\mu}{\gamma + \mu}, B_2 = \frac{\gamma}{\gamma + \mu}, B_3 = \frac{\sigma}{\gamma + \mu}$. So then we have:

$$\frac{du}{d\tau} = -R_0 u v - R_1 u w + B_1 v \tag{1.5}$$

$$\frac{dv}{d\tau} = R_0 u v + R_1 u w - v \tag{1.6}$$

$$\frac{dw}{d\tau} = B_2 v - B_3 w \tag{1.7}$$

as the nondimensionalized system.

The values of the parameters we use in the analysis and the simulations:

- $R_0 = 2.0$: R_0 is around 1.51 ~ 2.53, (more information in Discussion about the value).
- $R_1 = R_0 + 0.5 = 2.5$
- $B_1 = 0.01195, B_2 = 0.9880, B_3 = 0.7904$

Next, we need to find the equilibrium points of the system,

Solve $\frac{du}{d\tau}=\frac{dv}{d\tau}=\frac{dw}{d\tau}=0$ for u,v,w: $\begin{cases}-R_0uv-R_1uw+B_1v=0\\ R_0uv+R_1uw-v=0\\ B_2v-B_3w=0\end{cases}$

since $w=\frac{B_2}{B_3}v$, we have $R_0uv+\frac{R_1B_2}{B_3}uv-v=v\left(R_0u+\frac{R_1B_2}{B_3}u-1\right)=0$

We can find one of the fixed points $(u^*,v^*,w^*)=(u,0,0)$, where u can be any non-negative number.

For the other case, we have $(u^*,v^*,w^*)=(\frac{B_3}{B_3R_0+R_1B_2},0,0)$.

Since there exists infinite numbers of disease-free equilibrium points due to the various combination of parameters, we consider the more general case $(u^*,v^*,w^*)=(u,0,0)$.

To analysis the steady state, we need to find the Jacobian matrix and the eigenvalues.

Compute the Jacobian matrix for our model.

$$J=\begin{bmatrix}\frac{\partial f_1}{\partial u} & \frac{\partial f_1}{\partial v} & \frac{\partial f_1}{\partial w}\\ \frac{\partial f_2}{\partial u} & \frac{\partial f_2}{\partial v} & \frac{\partial f_2}{\partial w}\\ \frac{\partial f_3}{\partial u} & \frac{\partial f_3}{\partial v} & \frac{\partial f_3}{\partial w}\end{bmatrix}=\begin{bmatrix}-R_0v-R_1w & -R_0u+B_1 & -R_1u\\ R_0v+R_1w & R_0u-1 & R_1u\\ 0 & B_2 & -B_3\end{bmatrix}$$

Evaluate J at DFE.

$$J_{(u,0,0)}=\begin{bmatrix}0 & -R_0u+B_1 & -R_1u\\ 0 & R_0u-1 & R_1u\\ 0 & B_2 & -B_3\end{bmatrix}$$

Compute the dominant eigenvalue λ_d of J.

$$\det(A-\lambda I)=\begin{vmatrix}-\lambda & -R_0u+B_1 & -R_1u\\ 0 & R_0u-1-\lambda & R_1u\\ 0 & B_2 & -B_3-\lambda\end{vmatrix}=(-\lambda)(R_0u-1-\lambda)(-B_3-\lambda)-(-\lambda)B_2R_1u=0$$

$\lambda_1=0,$

$$\lambda_2=-\frac{1+B_3-R_0u+\sqrt{{R_0}^2u^2+4B_2R_1u-2R_0u+2B_3R_0u+{B_3}^2-2B_3+1}}{2},$$

$$\lambda_3=-\frac{1+B_3-R_0u-\sqrt{{R_0}^2u^2+4B_2R_1u-2R_0u+2B_3R_0u+{B_3}^2-2B_3+1}}{2}$$

Since the eigenvalues are too complex to analyze, we choose to substitute the values we picked for those parameters instead, here is the calculation:

$\sqrt{{R_0}^2u^2+4B_2R_1u-2R_0u+2B_3R_0u+{B_3}^2-2B_3+1}\approx 0.6216$

Then we have $\lambda_1=0,\ \lambda_2=u-1.206,\ \lambda_3=-u-1.206$

Since $u>0$, so $\lambda_1=0$ is the dominant eigenvalue, then the stability of the equilibrium is inconclusive. Therefore, we decided to use R code to model the system and simulate the entire process using the Euler's method, and obtain corresponding plots.

Fig. 2. Nondimensionalized Ebola Transmission Model

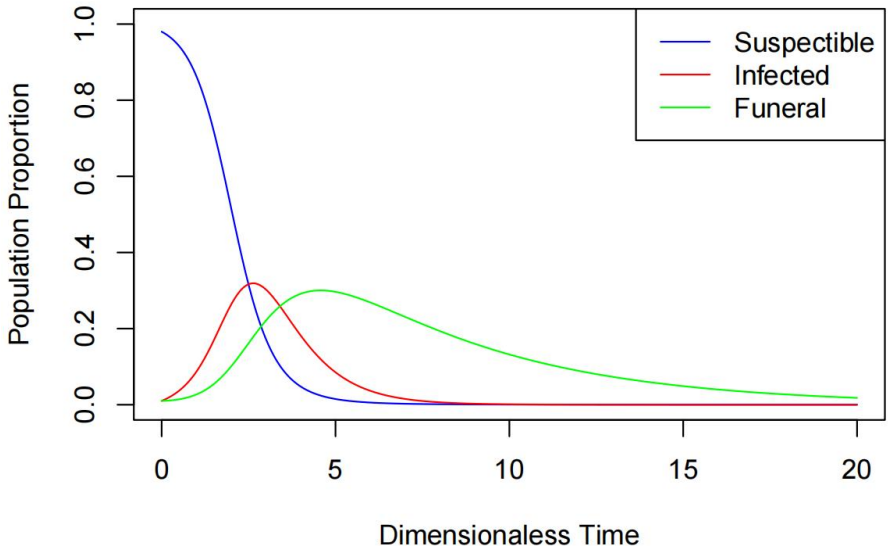
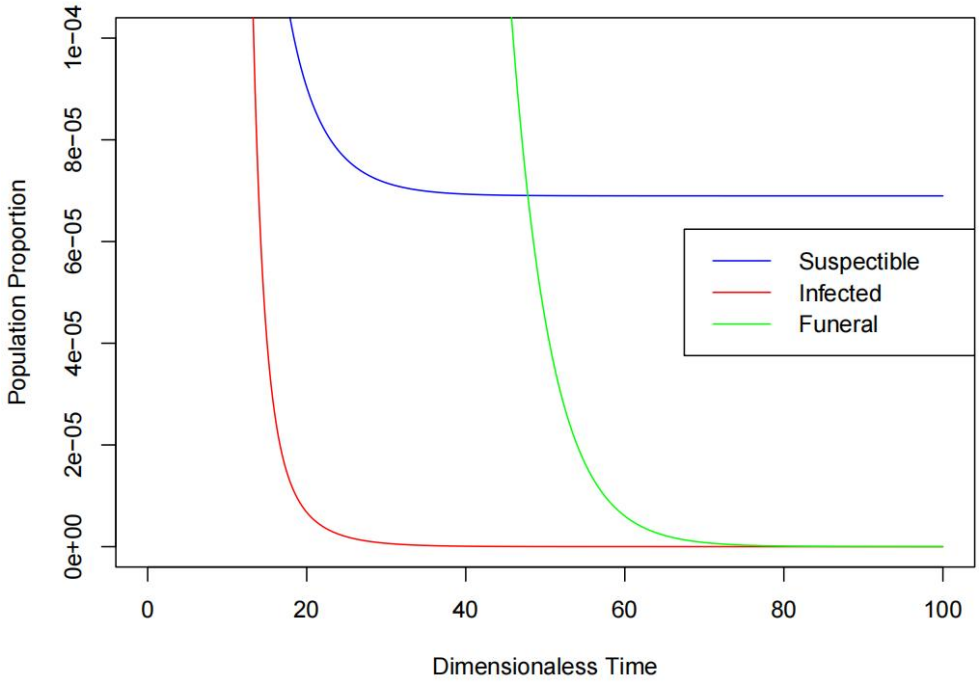


Fig. 3. Nondimensionalized Ebola Transmission Model (enlarged)



From analyzing the plots **Fig. 2** and **Fig. 3**, we can observe that the system will ultimately reach a stable state with certain values for the variables. Specifically, the curve representing the proportion of susceptible individuals to the total population (u) will converge to a value of approximately 6.9*10^-5, while the proportions of infected individuals (v) and funeral attendees (w) will converge to 0.

During the spread of the disease from its initial state to its eventual elimination, the proportion of susceptible individuals will decrease drastically from 98% to 0.0069% of the total population. At the same time, the proportion of infected individuals will rapidly increase from 1% to a peak of approximately 32%, before gradually declining to 0%. Similarly, the proportion of funeral attendees will rise from 1% to a peak of approximately 30%, before also gradually declining to 0%.

Once the disease is eradicated, the system will reach a stable equilibrium state, where there are no infected or deceased individuals in the entire system. At this point, all individuals will be in the susceptible state and the disease will no longer be transmitting. This equilibrium state is characterized by the values (u,0,0) = (6.9*10^-5,0,0), which is a stable equilibrium point.

Based on this mathematical model and analysis of simulation results, we can draw several conclusions. When disease transmission is eliminated, the system reaches an equilibrium state in which all individuals are susceptible, and there is no disease transmission occurring. This is the only equilibrium state of the system. Therefore, the key to controlling disease transmission is to take timely measures such as isolating patients and strengthening hygiene protection. Secondly, the model shows us that the rate of disease transmission depends on the contact rate and infection rate between susceptible and infected individuals, as well as between susceptible individuals and funerals. Therefore, measures such as isolating infected individuals and restricting funerals can be taken to reduce the contact rate between susceptible and infected individuals or funerals, thereby controlling the outbreak.

2.3 Model Extenstion

The proposed model extension of our group is controlling funeral spread. With the intervention of public health, the transmission at funerals could be reduced by diverting some people from I to R without going through F meaning directly burying the people who have died from Ebola without holding funerals.

We have the following assumptions:

- No one is recovering from the disease.
- There is no deliberate intervention by the government or World Health Organization.
- The population size N_t is closed.
- Assume there is no interaction between different epidemic regions.
- Birth rate is equal to death rate, measured by μ.
- Time t is measured in days.
- Buried bodies will not transmit viruses.
- Once an individual becomes infected, he/she will eventually die, and there will be a funeral ceremony for him.
- $N_a, N_t, \gamma_F, \gamma_R, \mu, \sigma, \beta, \beta_F$ are all greater than 0.

Modelling choices:

Similar to base model, we are using a continuous-time and compartmental model, since we are modeling what happens to the population of different individuals (S,I,F,R) at any moment in time.

Extended Model Equations:

$$\frac{dS}{dt} = -\beta SI - \beta_F SF + \mu N_a - \mu S \tag{2.1}$$

$$\frac{dI}{dt} = \beta SI + \beta_F SF - \gamma_N I - \gamma_R I - \mu I \tag{2.2}$$

$$\frac{dF}{dt} = \gamma_F I - \sigma F \tag{2.3}$$

$$\frac{dR}{dt} = \gamma_R I + \sigma F \tag{2.4}$$

Extended Model Diagram:

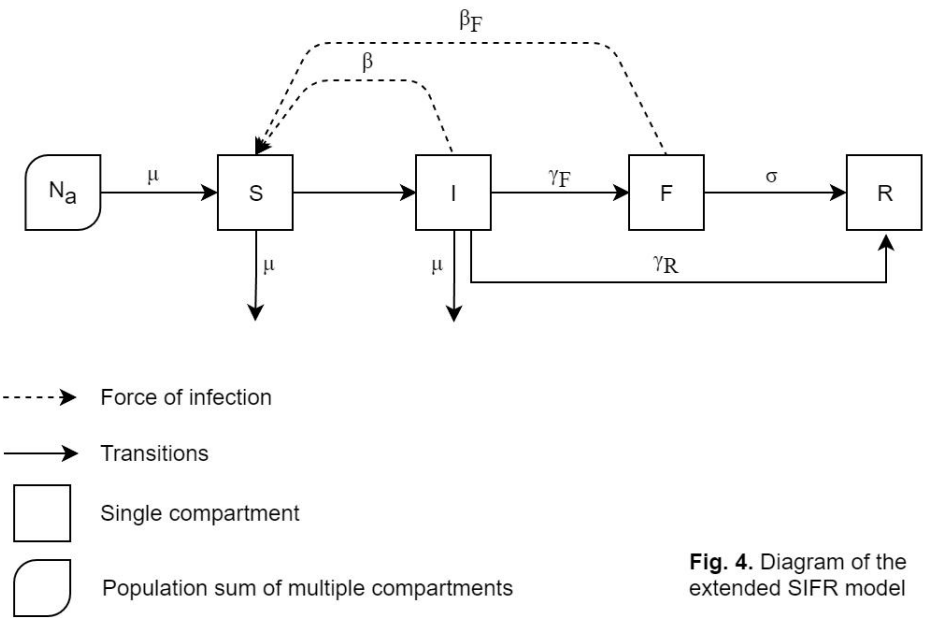


Fig. 4. Diagram of the extended SIFR model

Variable	Definition	Units
S	Susceptible individuals	people
I	Infected individuals	people
F	Dead individuals who died from Ebola and whose funeral are not completed	people
R	Individuals who have either recovered from Ebola or died from it	people
D	Individuals who died a natural death	people
N_t	The total number of people alive and dead	people
N_a	The number of people alive	people
Parameter	**Definition**	**Units**
t	Time	day
β	Infection rate of susceptible individuals who have contact with infected individuals	1/(people * day)
β_F	Infection rate of susceptible individuals who have contact with dead individuals whose funeral ceremonies are not yet completed	1/(people * day)
σ	Rate of people who got buried	1/day
μ	Birth rate/Death rate	1/day
γ_F	Rate of infected people who is dead and will have a funeral	1/day
γ_R	Rate of infected people directly get buried after death	1/day

Compared to the base model, we introduce two new parameters, γ_F and γ_R, where γ_F is the γ in the base model. The infected people still die eventually, γ remains unchanged and $\gamma = \gamma_F + \gamma_R$. By burying the people who have died from Ebola without holding funerals, it shall reduce the transmissions at funerals and eliminate the disease in the long-term.

3. Results

Since $N_t = S + I + F + R$ remains unchanged, we have a closed population and this four-dimensional model can be reduced to three-dimensional by dropping $\frac{dR}{dt}$.

Step 1: Nondimensionalize

First, we need to nondimensionalize the system:

Let

$$u = \frac{S}{N_t}, \quad v = \frac{I}{N_t}, \quad w = \frac{F}{N_t}$$

Then the new system of differiential equations is:

$$\frac{du}{dt} = -\beta N_t uv - \beta_F N_t uw + \mu v \tag{3.1}$$

$$\frac{dv}{dt} = \beta N_t uv + \beta_F N_t uw - \gamma_F v - \gamma_R v - \mu v \tag{3.2}$$

$$\frac{dw}{dt} = \gamma_F v - \sigma w \tag{3.3}$$

To further reduce the complexity, we can nondimensionalize our time varaible by replacing time variable by a new unitless time variable $\tau = (\gamma_F + \gamma_R + \mu)t$.

Like we did in base model, we define five unitless variables:

$$R_0 = \frac{\beta N_t}{\gamma_F + \gamma_R + \mu}, R_1 = \frac{\beta_F N_t}{\gamma_F + \gamma_R + \mu}, B_1 = \frac{\mu}{\gamma_F + \gamma_R + \mu}, B_2 = \frac{\gamma_F}{\gamma_F + \gamma_R + \mu}, B_3 = \frac{\sigma}{\gamma_F + \gamma_R + \mu}$$

After applying the chain rule $\frac{du}{d\tau} = \frac{du}{dt} \cdot \frac{dt}{d\tau}$, $\frac{dv}{d\tau} = \frac{dv}{dt} \cdot \frac{dt}{d\tau}$, $\frac{dw}{d\tau} = \frac{dw}{dt} \cdot \frac{dt}{d\tau}$, we have:

$$\frac{du}{d\tau} = -R_0 uv - R_1 uw + B_1 v \tag{3.4}$$

$$\frac{dv}{d\tau} = R_0 uv + R_1 uw - v \tag{3.5}$$

$$\frac{dw}{d\tau} = B_2 v - B_3 w \tag{3.6}$$

Step 2: Equilibriums

Then we want to find out the equilibriums of our model, especially the disease-free equilibrium, because we are interested in eliminating Ebola in long run.

So, we want to find the solutions to $\frac{du}{d\tau} = \frac{dv}{d\tau} = \frac{dw}{d\tau} = 0$.

By adding (3.4) and (3.5) toghether, we have $B_1 v - v = 0 \Rightarrow v(B_1 - 1) = 0$.

Since $B_1 \neq 1$, we have $v^* = 0$. By (3.2c), we can know that $w = \frac{B_2}{B_3} v$, so $w^* = 0$.

When $w^* = v^* = 0$, we have (3.4) = (3.5) = (3.6) = 0.

Thus, the equilibrium of the extended model is (u*, v*, w*) = (u*, 0, 0), where $u \in \mathbb{Z}^+ \bigcap [0, N_t]$. When there is no infective individuals or dead individuals who died from Ebola and whose funeral are not completed, Ebola cannot be transmitted, and thus, we have a diease-free equilibrium when (u*, v*, w*) = (u*, 0, 0). There is no endemic equalibrium in

our model, since we assume that everyone who gets infected eventually dies, which means that the fatality rate is 100%. Under this circumstance, we cannot reach an endemic equalibrium.

Step 3: Stability

Next, we want to know the stability of the disease-free equilibrium (u*, v*, w*) = (u*, 0, 0), since we are interested in how stable the system is near the disease-free equilibrium.
The Jacobian matrix J is as follows:

$$J=\begin{bmatrix} \frac{\partial f_1}{\partial u} & \frac{\partial f_1}{\partial v} & \frac{\partial f_1}{\partial w} \\ \frac{\partial f_2}{\partial u} & \frac{\partial f_2}{\partial v} & \frac{\partial f_2}{\partial w} \\ \frac{\partial f_3}{\partial u} & \frac{\partial f_3}{\partial v} & \frac{\partial f_3}{\partial w} \end{bmatrix}=\begin{bmatrix} -R_0v-R_1w & -R_0u+B_1 & -R_1u \\ R_0v+R_1w & R_0u-1 & R_1u \\ 0 & B_2 & -B_3 \end{bmatrix}$$

Evaluate J at DFE.

$$J_{(u,0,0)}=\begin{bmatrix} 0 & -R_0u+B_1 & -R_1u \\ 0 & R_0u-1 & R_1u \\ 0 & B_2 & -B_3 \end{bmatrix}$$

Compute the dominant eigenvalue λ_d of J.

$$\det(A-\lambda I)=\begin{vmatrix} -\lambda & -R_0u+B_1 & -R_1u \\ 0 & R_0u-1-\lambda & R_1u \\ 0 & B_2 & -B_3-\lambda \end{vmatrix}=(-\lambda)(R_0u-1-\lambda)(-B_3-\lambda)-(-\lambda)B_2R_1u=0$$

$$\lambda_1=0,$$

$$\lambda_2=-\frac{1+B_3-R_0u+\sqrt{R_0{}^2u^2+4B_2R_1u-2R_0u+2B_3R_0u+B_3{}^2-2B_3+1}}{2},$$

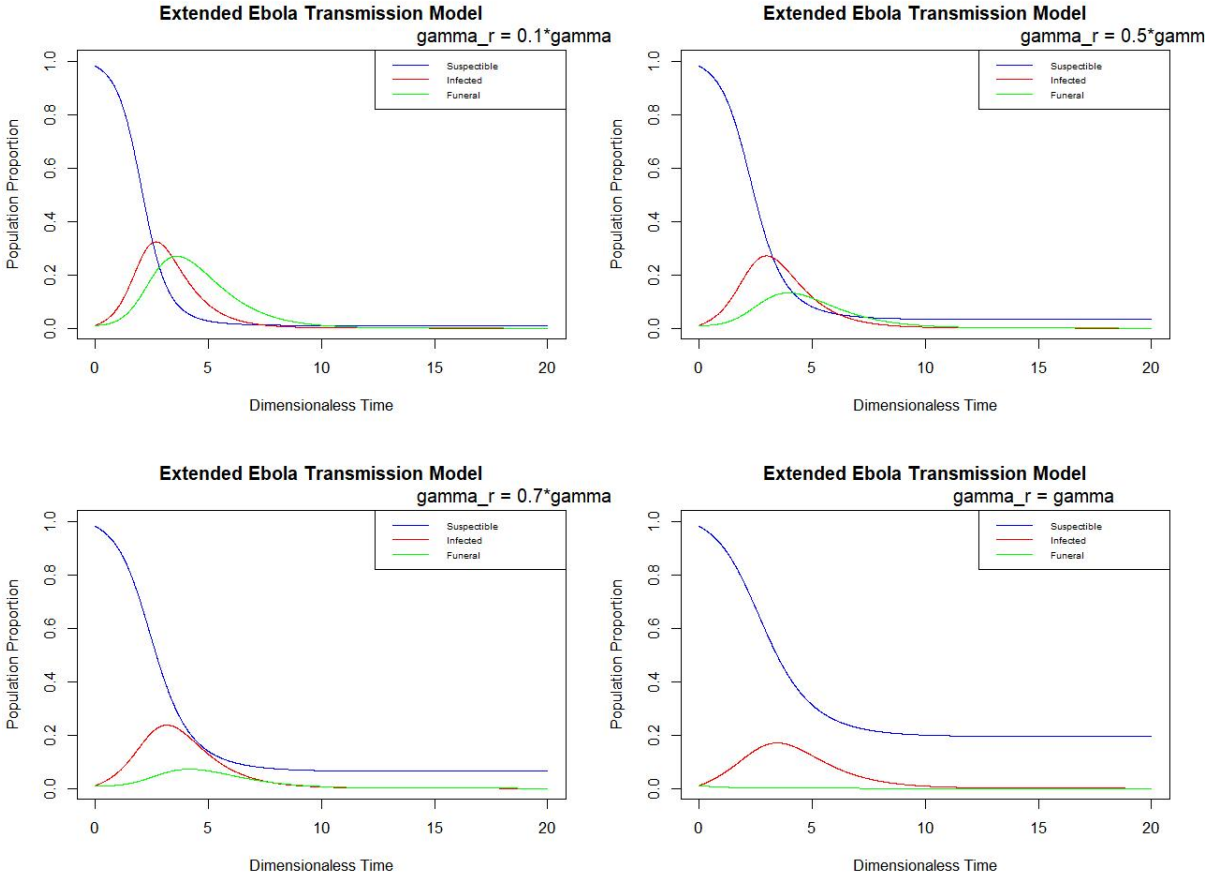
$$\lambda_3=-\frac{1+B_3-R_0u-\sqrt{R_0{}^2u^2+4B_2R_1u-2R_0u+2B_3R_0u+B_3{}^2-2B_3+1}}{2}$$

The eigenvalues are totally the same as in analysis of base model, so by mathematical analyses of stablity, we cannot conclude anything.

Step 4: Simulation

Since it is hard to determine the stability of DFE and the long term behaviour of extension model, we will analyse them through simultation.

Fig. 5. Extended Ebola Transmission Model for different values of γ_R



The figure above consists of four subfigures, each demonstrating the system under different level of public health intervention γ_R. It can be observed that both the proportion of infected individuals v and funeral compartments w converge to 0 eventually, and the proportion of suspectible individuals u converges a value that is corresponding to different values of γ_R.The following table shows different values of γ_R with the approximate proportion of suspectible individuals when reaching equilibrium:

γ_R	u
$0.1\gamma = 0.324$	0.009
$0.5\gamma = 1.620$	0.017
$0.7\gamma = 2.268$	0.065
$1.0\gamma = 3.240$	0.200

Thus, the DFE of extended model is stable under our assumptions and proposed parameters. It can be seen that as γ_R increases, v and w decrease to 0 at a higher rate, and u stablizes at a higher value. Therefore, controlling funeral spread is useful for the local government in order to stop Ebola from transmitting in long run.

4. Discussion

In the extended model analysis, we have identified a disease-free equilibrium when (u*, v*, w*) = (u*, 0, 0), and it is stable under our assumptions and proposed parameters. When $\gamma_R = 3.24$, which means that all the funerals are cancelled, Ebola dies out in approximately 18 units of time, and about 20% of the total population remains uninfected. As γ_R decreases, v and w decrease to 0 at a slower rate, and u eventually stablizes at a lower level. Compared to base model, we found that a significantly larger propotion of suspectible population are not infected by Ebola, and the system can reach disease-free equilibrium faster, therefore, reduces the duration of the pandemic. Thus, controlling funeral spread greatly helps eliminating Ebola. Our analysis highlights the importance of public health intervention in controlling the transmission of Ebola, and we encourage governments to prioritize efforts in this area.

Due to the complexity of the real world situation, we simplify our model by adding a list of assumptions and omitting some factors. In particular, our model only considers the rate of infection. However, in reality, R_0 is also based on the duration of contagiousness after infection and the contact rate. (Shabir, 2021). Therefore, the R_0 in our model will be greater than the one we have in reality. In this paper, we let R_0 be the range of values from 1.51 to 2.53. (Eisenberg, 2020). Additionally, our model assumes that no one recovers from Ebola, and every infected individual eventually dies. While Ebola is a highly lethal disease in real life, its fatality rate does not reach 100%, and with current medical treatment and healthcare, more infected individuals can recover. It is therefore important to consider the impact of medical interventions in future models.

To improve the accuracy of our model in the future, we suggest taking additional factors into consideration, such as the contact rate and the duration of contagiousness after infection. It would also be beneficial to refine different components of the total population, for example, adding medical workers to our system. Furthermore, future research could explore the impact of behavioral changes, such as social distancing and personal protective measures, on the spread of Ebola. Plus, as the Ebola virus can spread through animal-to-human and human-to-human transmission, modeling the transmission dynamics in animal populations and the spillover of the virus from animals to humans would be important to gain a comprehensive understanding of the disease.

5. References

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Appendix: R code

Base Model Simultion:

```r
miu <- 0.0392
gamma<-3.24
sigma <- gamma*0.8
R_0 <- 2
R_1 <- 2.5
B_1 <-  (miu)/(gamma+miu)
B_2 <-  (gamma)/(gamma+miu)
B_3 <-  (sigma)/(gamma+miu)



u_model <- function(R_0,R_1,u=1,v=1,w=1,B_1){
  val1 <- -R_0*u*v-R_1*u*w+B_1*v
  return(val1)
}

v_model <- function(R_0,R_1,u=1,v=1,w=1){
  val2 <- R_0*u*v+R_1*u*w-v
  return(val2)
}

w_model <- function(B_2,B_3,v=1,w=1){
  val3 <- B_2*v-B_3*w
  return(val3)
}

t_vals <- seq(0, 0, by = 0.01)
u_vals <- rep(NA, times = length(t_vals))
u_vals[1] <- 0.98

v_vals <- rep(NA, times = length(t_vals))
v_vals[1] <- 0.01

w_vals <- rep(NA, times = length(t_vals))
w_vals[1] <- 0.01
```

```r
h = t_vals[2]-t_vals[1]
for (i in 2:length(t_vals)){
  u_vals[i]=u_vals[i-1]+h*u_model(R_0,R_1,u=u_vals[i-1],v=v_vals[i-1],w=w_vals[i-1],B_1)
  v_vals[i]=v_vals[i-1]+h*v_model(R_0,R_1,u=u_vals[i-1],v=v_vals[i-1],w=w_vals[i-1])
  w_vals[i]=w_vals[i-1]+h*w_model(B_2,B_3,v=v_vals[i-1],w=w_vals[i-1])
}

plot(t_vals,u_vals, type = "l", col = "blue", xlab = "Dimensionaless Time",
     ylab = "Population Proportion",ylim=c(0,1),
     main = "Base Ebola Transmission Model")
lines(t_vals, v_vals, col = "red")
lines(t_vals, w_vals, col = "green")
legend("topright", legend = c("Suspectible","Infected","Funeral"),col=c("blue","red","green"),lwd=1)
```

Extended Model Simulation:

```r
#Origin Parameters
proportion <-c(0.1,0.5,0.7,1)
miu <- 0.0392
gamma_R <- rep(0,time=4)
gamma_F <- rep(0,time=4)
for (i in 1:4) {
  gamma_R[i] = proportion[i]*3.24
  gamma_F[i] = (1-proportion[i])*3.24
}
gamma_R
gamma_F
sigma <- 3.24*0.8

#Summative Parameters
R_0 <- 2
R_1 <- 2.5
B_1 <- rep(0,time=4)
B_2 <- rep(0,time=4)
B_3 <- rep(0,time=4)

for (i in 1:4) {
  B_1[i] <-  (miu)/(gamma_F[i]+gamma_R[i]+miu)
  B_2[i] <-  (gamma_F[i])/(gamma_F[i]+gamma_R[i]+miu)
  B_3[i] <-  (sigma)/(gamma_F[i]+gamma_R[i]+miu)
}
B_1
B_2
B_3

u_model <- function(R_0=2,R_1=2.5,u=1,v=1,w=1,B_1=1){
  val1 <- -R_0*u*v-R_1*u*w+B_1*v
  return(val1)
}

v_model <- function(R_0=2,R_1=2.5,u=1,v=1,w=1){
  val2 <- R_0*u*v+R_1*u*w-v
  return(val2)
}

w_model <- function(B_2=1,B_3=1,v=1,w=1){
  val3 <- B_2*v-B_3*w
  return(val3)
}

t_vals <- seq(0, 20, by = 0.01)
u_vals<-matrix(,nrow=4,ncol=length(t_vals))
u_vals[,1] <- 0.98

v_vals<-matrix(,nrow=4,ncol=length(t_vals))
v_vals[,1] <- 0.01

w_vals<-matrix(,nrow=4,ncol=length(t_vals))
w_vals[,1] <- 0.01

h = t_vals[2]-t_vals[1]
for(i in 1:4){
  for (j in 2:length(t_vals)){
    u_vals[i,j]=u_vals[i,j-1]+h*u_model(R_0,R_1,u=u_vals[i,j-1],v=v_vals[i,j-1],w=w_vals[i,j-1],B_1[i])
    v_vals[i,j]=v_vals[i,j-1]+h*v_model(R_0,R_1,u=u_vals[i,j-1],v=v_vals[i,j-1],w=w_vals[i,j-1])
    w_vals[i,j]=w_vals[i,j-1]+h*w_model(B_2[i],B_3[i],v=v_vals[i,j-1],w=w_vals[i,j-1])
  }
}
```

```r
par(mfrow=c(2,2))
###First Plot
plot(t_vals,u_vals[1,], type = "l", col = "blue", xlab = "Dimensionaless Time",
     ylab = "Population Proportion",ylim=c(0,1),title(main = "Extended Ebola Transmission Model"),
     sub ="gamma_r = 0.1*gamma" )
lines(t_vals, v_vals[1,], col = "red")
lines(t_vals, w_vals[1,], col = "green")
legend("topright", legend = c("Suspectible","Infected","Funeral"),col=c("blue","red","green"),lwd=1,cex=0.6)

###Second Plot
plot(t_vals,u_vals[2,], type = "l", col = "blue", xlab = "Dimensionaless Time",
     ylab = "Population Proportion",ylim=c(0,1),title(main = "Extended Ebola Transmission Model"),
     sub ="gamma_r = 0.5*gamma" )
lines(t_vals, v_vals[2,], col = "red")
lines(t_vals, w_vals[2,], col = "green")
legend("topright", legend = c("Suspectible","Infected","Funeral"),col=c("blue","red","green"),lwd=1,cex=0.6)



###Third Plot
plot(t_vals,u_vals[3,], type = "l", col = "blue", xlab = "Dimensionaless Time",
     ylab = "Population Proportion",ylim=c(0,1),title(main = "Extended Ebola Transmission Model"),
     sub ="gamma_r = 0.7*gamma" )
lines(t_vals, v_vals[3,], col = "red")
lines(t_vals, w_vals[3,], col = "green")
legend("topright", legend = c("Suspectible","Infected","Funeral"),col=c("blue","red","green"),lwd=1,cex=0.6)


###Forth Plot
plot(t_vals,u_vals[4,], type = "l", col = "blue", xlab = "Dimensionaless Time",
     ylab = "Population Proportion",ylim=c(0,1),title(main = "Extended Ebola Transmission Model"),
     sub ="gamma_r = gamma" )
lines(t_vals, v_vals[4,], col = "red")
lines(t_vals, w_vals[4,], col = "green")
legend("topright", legend = c("Suspectible","Infected","Funeral"),col=c("blue","red","green"),lwd=1,cex=0.6)

```

Appendix: Individual Contribution

	Hanweng Ling	Qinxin Liu	Yaoyang Zhang	Yifan Yang	Ruiqi Xiong
Introduction	√				
Doing Research	√	√			√
Parameters/Variables Explanation	√	√			√
Base Model Analysis			√	√	√
Base Model Simulation			√	√	√
Extended Model Analysis	√	√			
Extended Model Simulation	√	√			
Discussion	√		√		
Reference	√				
Group Meeting Contribution	√	√	√	√	√
Formatting and Intext Formulas			√	√	
Meeting Organization	√	√			
Setting Up Group Work Infrastructure	√		√		