PART 2: SEIR EBOLA DISEASE MODEL

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May 10, 2019

Abstract:
In Part 1, this study aims to provide an understanding of mathematical modelling applied to the population dynamics of infectious diseases. It will begin with an introduction to the problems and terminology in mathematical modelling in gerneral. Later, it will deal with an SIR (**S**usceptible, **I**nfected, **R**ecovered) model of a generic disease which will be thoroughly analyzed through the use of phase plane analysis, looking at the eigenvalues of the Jacobian matrix, and converting the mathematical conclusions back into biological conclusions about the system.

In Part 2, we will look into creating a disease model for Ebola. Ebola is a rare and deadly disease caused by infection with one of the Ebola virus strains. Understanding the spread of this disease is vital to its containment and eventual elimination. An SEIR epidemic model is used to study the behavior of Ebola spreading through Liberia and is then compared against the World Health Organisation data from Liberia. The SEIR model is further explored by the addition of treatment and vaccine interventions. The introduction of these interventions causes the disease free equilibrium to become stable, which will be studied through the use of the Next Generation Matrix.

In this paper, I will explore how to create a mathematical model of Ebola spreading through Liberia. We will look at a SEIR(**S**usceptible, **E**xposed, **I**nfectious, **R**ecovered) model, and then advance the model to make it more accurate.

Section 1. Ebola

Ebola Virus Disease is a rare and deadly disease which can affect humans and nonhuman primates. There are six strains of the Ebola virus, but only four can cause disease in humans. Ebola was first discovered in 1976 in the Democratic Republic of Congo, and since then, the virus has been infecting humans leading to several outbreaks in several African countries. Scientists do not know where the Ebola virus comes from, but they believe the virus is animal-borne with bats being the most likely source. Ebola is not an airborne disease - it is transferred through bodily fluids like blood. What Ebola does to a human's body is it destroys the immune system by destroying blood clotting cells which causes internal bleeding, leading to other symptoms. Other symptoms can be a fever, severe headaches, muscle pains, weakness, fatigue, diarrhea, vomitting, stomach pain, and unexplained hemorrhage (internal bleeding and bruising). This is why understanding the spread of this disease is critical, so a mathematical model will be made to help explain the spread to lead to the eventual elimination of the disease. [1]

Section 2. SEIR Model

Using the tools discussed in the first report, we will construct our SEIR model.

Describe the model

We will split the population into four groups: individuals who are susceptible to Ebola; individuals who have Ebola, but aren't yet infectious; individuals who are infectious with Ebola; and individuals who have recovered from Ebola; You can move from the susceptible group to the exposed group after contact with an infected individual; You move from the exposed class to the infected class after some average time; When in the infectious class, you either die from Ebola, or move to the recovered class; There will be a per capita death rate which affects all populations; Susceptibles can be infected at some mass action incidence rate.

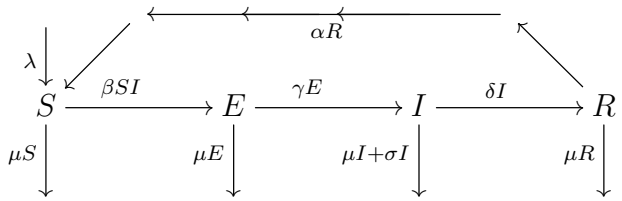
Other assumptions that are to be made:

- Birth rate is a constant $\lambda > 0$
- Per capita death rate $\mu > 0$
- Exposed individuals move to the infectious class at a rate of $\gamma > 0$
- The per capita death rate due to disease is $\sigma > 0$
- New infections occur at rate $\beta SI > 0$ with mass action incidence

- Infected individuals that recover do so after an average infection period of $\frac{1}{\delta}$ days. This means that the per capita recovery rate is $\delta I(t)$, with $\delta > 0$
- Assume that you are not immune to the disease once you reach the recovered class, so at some rate $\alpha > 0$, you return to the suscepitble class from the recovered class.

Turn into math

The transfer diagram is as follows



The corresponding differential equations are:

$$\begin{aligned} \frac{dS}{dt} &= \lambda + \alpha R - \mu S - \beta SI \\ \frac{dE}{dt} &= \beta SI - \mu E - \gamma E \\ \frac{dI}{dt} &= \gamma E - \mu I - \delta I - \sigma I \\ \frac{dR}{dt} &= \delta I - \mu R - \alpha R \end{aligned} \tag{2.1}$$

Unlike before when we had a three-dimensional system that had the recovered class decouple, we have a four-dimensional system that does not decouple. Other methods will be used to calculate the equilibria and stability.

Finding the Disease Free Equilibrium(DFE)

Set all equations equal to 0, and set I=0. (I=0 because at the DFE, there is no disease)

$$\begin{aligned} 0 &= \lambda + \alpha R - \mu S - \beta SI \\ 0 &= \beta SI - \mu E - \gamma E \\ 0 &= \gamma E - \mu I - \delta I - \sigma I \\ 0 &= \delta I - \mu R - \alpha R \end{aligned} \tag{2.2}$$

Set I = 0.

$$\begin{aligned} 0 &= \lambda + \alpha R - \mu S - 0 \\ 0 &= 0 - \mu E - \gamma E \\ 0 &= \gamma E - 0 - 0 - 0 \\ 0 &= 0 - \mu R - \alpha R \end{aligned} \tag{2.3}$$

We see that the only way the fourth equation is satisfied is if R = 0, and the second and third equation are only satisfied if E = 0, leaving us with equation one:

$$0 = \lambda - \mu S \tag{2.4}$$

Which gives us $S = \frac{\lambda}{\mu}$. So we have a DFE at (S,E,I,R) = $\left(\frac{\lambda}{\mu}, 0, 0, 0\right)$.

Find $\mathcal{R}_0$

Finding $\mathcal{R}_0$ will tell us the stability at the DFE. If $\mathcal{R}_0 > 1$, it is unstable. If $\mathcal{R}_0 < 1$, then it is stable.

A method called the Next Generation Matrix will tell us this $\mathcal{R}_0$, so let's walk through it.

Section 3. Next Generation Matrix

Using the notation

$$\mathbf{x} = \begin{bmatrix} x_1 \\ x_2 \\ \vdots \\ x_n \end{bmatrix} \qquad \mathbf{f} = \begin{bmatrix} f_1 \\ f_2 \\ \vdots \\ f_n \end{bmatrix}$$

Where $x_1, ..., x_n$ are infected groups (in our case, E and I). We can re-write the differential equations as $x' = \mathscr{F} - \mathscr{V}$ where $\mathscr{F}$ consists of all terms that represent new infections, and all other terms go in $\mathscr{V}$ but with the signs flipped.

Now we can write $\mathscr{V} = \mathscr{V}^- - \mathscr{V}^+$. The vector functions $\mathscr{F}, \mathscr{V}^+, \mathscr{V}^-$ must satisfy the following assumptions:

(1) If $x \in R^n_{\geq 0}$, then $\mathscr{F}, \mathscr{V}^+, \mathscr{V}^- \in (R^n)_{\geq 0}$
(2) If $x_i = 0$, then $\mathscr{V}^- = 0$
(3) If there is no disease in the population, then the infected groups should remain constant, so their derivatives are 0
(4) If $\mathscr{F}$ is replaced with the zero vector, then the DFE is LAS.

Now define:

$$\mathbf{F} = \begin{bmatrix} \frac{\partial \mathscr{F}_1}{\partial x_1} & \cdots & \frac{\partial \mathscr{F}_1}{\partial x_n} \\ \frac{\partial \mathscr{F}_2}{\partial x_2} & \cdots & \frac{\partial \mathscr{F}_2}{\partial x_n} \\ & \vdots & \\ \frac{\partial \mathscr{F}_n}{\partial x_n} & \cdots & \frac{\partial \mathscr{F}_n}{\partial x_n} \end{bmatrix} (DFE)$$

and:

$$\mathbf{V} = \begin{bmatrix} \frac{\partial \mathscr{V}_1}{\partial x_1} & \cdots & \frac{\partial \mathscr{V}_1}{\partial x_n} \\ \frac{\partial \mathscr{V}_2}{\partial x_2} & \cdots & \frac{\partial \mathscr{V}_2}{\partial x_n} \\ & \vdots & \\ \frac{\partial \mathscr{V}_n}{\partial x_n} & \cdots & \frac{\partial \mathscr{V}_n}{\partial x_n} \end{bmatrix} (DFE)$$

The matrix (FV^{-1}) is called the next generation matrix, and $\mathcal{R}_0$ is given by the largest eigenvalue. Using our SEIR model, we can follow along to build our next generation matrix: Insert all terms that involve new infections into the matrix $\mathscr{F}$. Insert all other terms into

the matrix $\mathscr{V}$ with the signs flipped. We only need to account for the infected groups as stated above.

$$\mathscr{F}_{\mathbf{E},\mathbf{I}} = \begin{bmatrix} \beta SI \\ 0 \end{bmatrix}$$

$$\mathscr{V}_{\mathbf{E},\mathbf{I}} = \begin{bmatrix} E(\mu+\gamma) \\ -\gamma E + I(\sigma+\mu+\delta) \end{bmatrix}$$

Differentiate $\mathscr{F}$ and $\mathscr{V}$ w.r.t E and I (Like doing a Jacobian Matrix) and evaluate at the DFE point (S,E,I,R) = $\left(\frac{\lambda}{\mu}, 0, 0, 0\right)$

$$\mathbf{F} = \begin{bmatrix} 0 & \beta\frac{\lambda}{\mu} \\ 0 & 0 \end{bmatrix}$$

$$\mathbf{V} = \begin{bmatrix} \mu+\gamma & 0 \\ -\gamma & \sigma+\mu+\delta \end{bmatrix}$$

$$\mathbf{V}^{-1} = \begin{bmatrix} \frac{1}{\mu+\gamma} & 0 \\ \frac{\gamma(\sigma+\mu+\delta)}{\mu+\gamma} & \sigma+\mu+\delta \end{bmatrix}$$

$$\mathbf{FV}^{-1} = \begin{bmatrix} \beta\lambda\gamma\left(\frac{\sigma+\mu+\delta}{\mu(\mu+\gamma)}\right) & \left(\beta\lambda\frac{\sigma+\mu+\delta}{\mu}\right) \\ 0 & 0 \end{bmatrix}$$

Here, we get our max eigenvalue of $\beta\lambda\gamma\left(\frac{\sigma+\mu+\delta}{\mu(\mu+\gamma)}\right) = \mathcal{R}_0$. We can substitute the parameters from the World Health Organization (WHO) into this eigenvalue to see what the value is. Using
$\lambda = 76, \mu = 0.000152, \beta = 0.00001, \gamma = 1, \delta = 0.5, \alpha = \frac{1}{20}, S(0) = 500,000, E(0) = 10, I(0) = 2, R(0) = 0$, we get a $\mathcal{R}_0$ value of $3.33 > 1$
This means the DFE is unstable, and the system will tend towards an Endemic Equilibrium Point (EEP). Using Euler's Numerical Approximation, the following graphs were made.

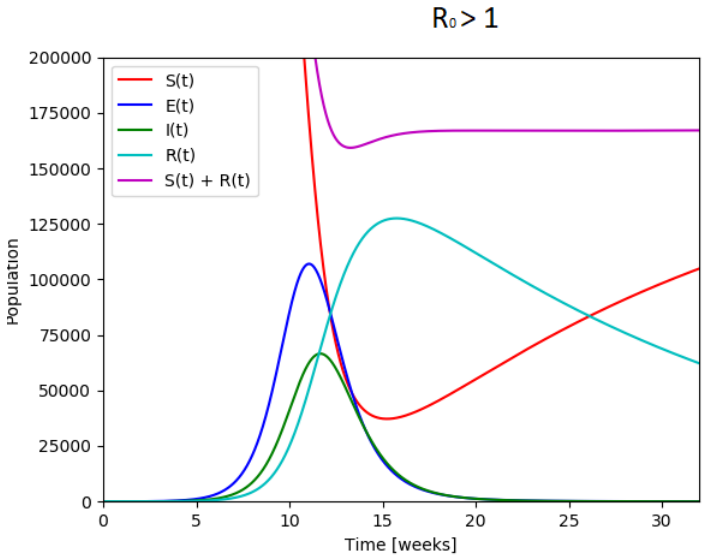


FIGURE 1. SEIR

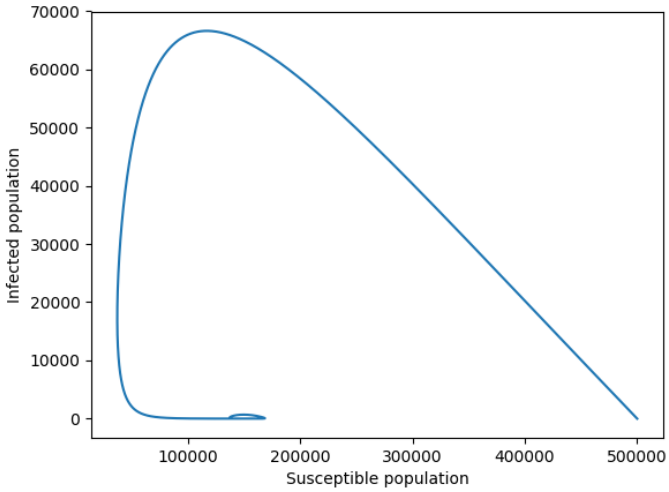
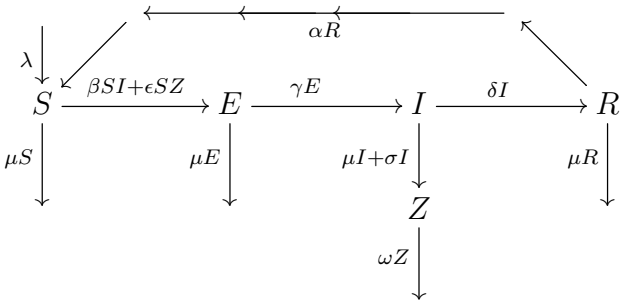


FIGURE 2. S vs I

We can see from Figure 2 that the infected population stays above zero, meaning we are approaching the EEP. However, looking at the bigger picture in Figure 1, we see that our total population is about 175,000 (S+ R) + 5,000 (E + I), meaning our total population went from 500,000 to a little under 200,000, meaning about 300,000 people died. According to the WHO, only 4,809 people died, concluding our model is not very accurate. Changing our assumptions may make our model more accurate.

New assumptions

When you die from Ebola, your body is still infectious for some time after death. This should be taken into account into our model as this is a major concern of health workers dealing with the bodies. With reference to our model, this is a susceptible individual coming in contact with an infected dead body. We will draw our new transfer diagram:



Where ωZ is the average time a body is infectious and ϵSZ is the rate at which susceptible people come in contact with infectious dead people. The new differential equations are as follows:

$$\begin{aligned}
\frac{dS}{dt} &= \lambda + \alpha R - \mu S - \beta SI - \underline{\epsilon SZ} \\
\frac{dE}{dt} &= \beta SI - \mu E - \gamma E + \underline{\epsilon SZ} \\
\frac{dI}{dt} &= \gamma E - \mu I - \delta I - \sigma I \\
\frac{dZ}{dt} &= \mu I + \sigma I - \underline{\omega Z} \\
\frac{dR}{dt} &= \delta I - \mu R - \alpha R
\end{aligned} \tag{3.1}$$

Following the same process to find the DFE as before, we will find the E=I=Z=R=0, and we have the same DFE as before at (S,E,I,Z,R) = $(\frac{\lambda}{\mu}, 0, 0, 0, 0)$. Again, we find $\mathcal{R}_0$ to see if the DFE is stable or not. We do this by using the Next Generation Matrix Method again. The matrices are as follow:

$$\mathscr{F}_{\mathbf{E,I,Z}} = \begin{bmatrix} \beta SI + \epsilon SZ \\ 0 \\ 0 \end{bmatrix}$$

$$\mathscr{V}_{\mathbf{E,I,Z}} = \begin{bmatrix} E(\mu + \gamma) \\ -\gamma E + I(\sigma + \mu + \delta) \\ -I(\sigma + \mu) + \omega Z \end{bmatrix}$$

Differentiate $\mathscr{F}$ and $\mathscr{V}$ w.r.t E, I, and Z and evaluate at the DFE point (S,E,I,Z,R) = $(\frac{\lambda}{\mu}, 0, 0, 0, 0)$

$$\mathbf{F} = \begin{bmatrix} 0 & \beta\frac{\lambda}{\mu} & \epsilon\frac{\lambda}{\mu} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \mathbf{V} = \begin{bmatrix} \mu+\gamma & 0 & 0 \\ -\gamma & \sigma+\mu+\delta & 0 \\ 0 & -\sigma-\mu & \omega \end{bmatrix}$$

$$\mathbf{V}^{-1} = \begin{bmatrix} \frac{1}{\mu+\gamma} & 0 & 0 \\ \frac{\gamma}{(\mu+\gamma)(\sigma+\mu+\delta)} & \frac{1}{\sigma+\mu+\delta} & 0 \\ \frac{\gamma(\sigma+\mu)}{\omega(\mu+\gamma)(\mu+\sigma+\delta)} & \frac{\mu+\sigma}{\omega(\mu+\sigma+\delta)} & \frac{1}{\omega} \end{bmatrix} \mathbf{FV}^{-1} = \begin{bmatrix} \frac{\beta\lambda\gamma\omega+\epsilon\lambda\gamma(\sigma+\mu)}{\mu\omega(\mu+\gamma)(\delta+\mu+\sigma)} & MESS & MESS \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

MESS is denoted to values in the matrix that will not affect the eigenvalue. We see that the eigenvalue comes out to be $\frac{\beta\lambda\gamma\omega+\epsilon\lambda\gamma(\sigma+\mu)}{\mu\omega(\mu+\gamma)(\delta+\mu+\sigma)}$ and substituting our parameters in with the same values as before, and $\omega = 2, \epsilon = 0.000001$, we get a value of $\mathcal{R}_0 > 1$. $\therefore$ the DFE is unstable and the system will tend towards the EEP. The following graph was generated with Euler's numerical approximation:

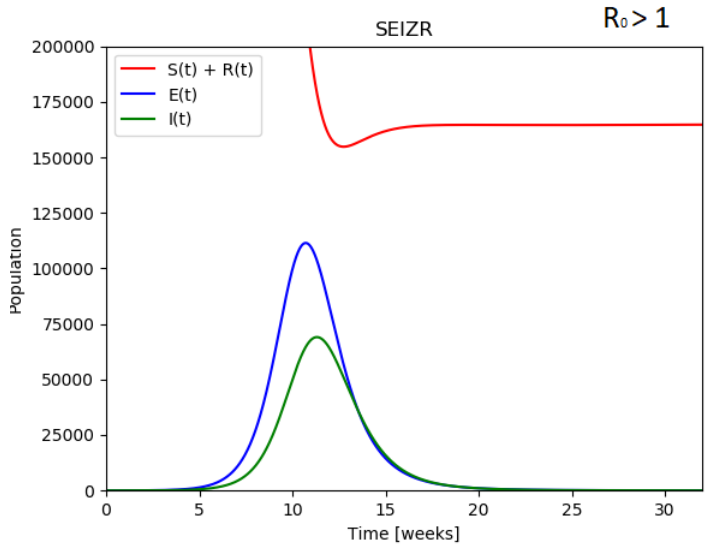
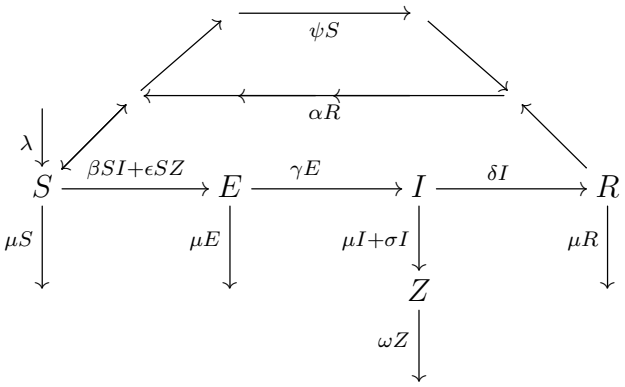


FIGURE 3. SEIZR

But again, we have a death toll of about 300,000, which is not accurate in accordance to the WHO. So again, we must make more assumptions to be able to become more accurate. Vaccination is a very influential intervention that has not been taken into account. So let us assume that susceptible individuals may be vaccinated at some average rate ψ. Our new transfer diagram is as follows:



Our new differential equations are:

$$\begin{aligned}
\frac{dS}{dt} &= \lambda + \alpha R - \mu S - \beta SI - \epsilon SZ - \underline{\psi S} \\
\frac{dE}{dt} &= \beta SI + \epsilon SZ - \mu E - \gamma E \\
\frac{dI}{dt} &= \gamma E - \mu I - \delta I - \sigma I \\
\frac{dZ}{dt} &= \mu I + \sigma I - \omega Z \\
\frac{dR}{dt} &= \delta I - \mu R - \alpha R + \underline{\psi S}
\end{aligned} \tag{3.2}$$

Finding the DFE is slightly trickier this time around, we we will follow the same procedure. Set all derivatives and I = 0.

$$\begin{aligned} 0 &= \lambda + \alpha R - \mu S - \epsilon S Z - \psi S \\ 0 &= -\mu E - \gamma E \\ 0 &= \gamma E \\ 0 &= \omega Z \\ 0 &= -\mu R - \alpha R + \psi S \end{aligned} \tag{3.3}$$

Clearly, for equation 2,3,4 to hold, E=Z=0, which eliminates some other terms for us, and we just need to look at the two remaining equations.

$$\begin{aligned} (1) 0 &= \lambda + \alpha R - \mu S - \psi S \\ (2) 0 &= -\mu R - \alpha R + \psi S \end{aligned} \tag{3.4}$$

Solving for S in equation 1 from (3.4) gives us:

$$\begin{aligned} 0 &= \lambda + \alpha R - S(\mu + \psi) \\ S(\mu + \psi) &= \lambda + \alpha R \\ S &= \frac{\lambda + \alpha R}{(\mu + \psi)} \end{aligned} \tag{3.5}$$

Substituting into equation 2 from (3.4) yields:

$$\begin{aligned} 0 &= -\mu R - \alpha R + \psi S \\ 0 &= -\mu R - \alpha R + \psi(\frac{\lambda + \alpha R}{(\mu + \psi)}) \\ 0 &= -R(\mu + \alpha) + \psi(\frac{\lambda}{\mu + \psi}) + (\frac{\psi \alpha R}{\mu + \psi}) \\ 0 &= -R(\mu + \alpha + \frac{\psi \alpha}{\mu + \psi}) + \psi(\frac{\lambda}{\mu + \psi}) \\ R &= \frac{\psi(\frac{\lambda}{\mu+\psi})}{(\mu + \alpha + \frac{\psi\alpha}{\mu+\psi})} \\ R &= \frac{\psi \lambda}{(\mu + \psi)(\mu + \alpha + \frac{\psi\alpha}{\mu+\psi})} \end{aligned} \tag{3.6}$$

Back substitution gives $S = \frac{\lambda + \alpha(\frac{\psi\lambda}{(\mu+\psi)(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})})}{\mu+\psi} = \frac{\lambda}{\mu+\psi} + \frac{\alpha\psi\lambda}{(\mu+\psi)^2(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})}$ So we have a DFE at (S,E,I,Z,R) = $(\frac{\lambda}{\mu+\psi} + \frac{\alpha\psi\lambda}{(\mu+\psi)^2(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})}, 0, 0, 0, \frac{\psi\lambda}{(\mu+\psi)(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})})$

Now we must check if this stable or not. Again, we use the Next Generation matrix and

obtain:

$$\mathscr{F}_{\mathbf{E},\mathbf{I},\mathbf{Z}} = \begin{bmatrix} \beta SI + \epsilon SZ \\ 0 \\ 0 \end{bmatrix}$$

$$\mathscr{V}_{\mathbf{E},\mathbf{I},\mathbf{Z}} = \begin{bmatrix} E(\mu+\gamma) \\ -\gamma E + I(\sigma+\mu+\delta) \\ -I(\mu+\sigma) + \omega Z \end{bmatrix}$$

Differentiate $\mathscr{F}$ and $\mathscr{V}$ w.r.t E, I, and Z and evaluate at the DFE point (S,E,I,Z,R) = $((\frac{\lambda}{\mu+\psi} + \frac{\alpha\psi\lambda}{(\mu+\psi)^2(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})}, 0, 0, 0, \frac{\psi\lambda}{(\mu+\psi)(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})})$

$$\mathbf{F} = \begin{bmatrix} 0 & \beta(\frac{\lambda}{\mu+\psi} + \frac{\alpha\psi\lambda}{(\mu+\psi)^2(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})}) & \epsilon(\frac{\lambda}{\mu+\psi} + \frac{\alpha\psi\lambda}{(\mu+\psi)^2(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})}) \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \mathbf{V} = \begin{bmatrix} \mu+\gamma & 0 & 0 \\ -\gamma & \sigma+\mu+\delta & 0 \\ 0 & -\sigma-\mu & \omega \end{bmatrix}$$

$$\mathbf{V}^{-1} = \begin{bmatrix} \frac{1}{\mu+\gamma} & 0 & 0 \\ \frac{\gamma}{(\mu+\gamma)(\sigma+\mu+\delta)} & \frac{1}{\sigma+\mu+\delta} & 0 \\ \frac{\gamma\sigma}{\omega(\mu+\gamma)(\mu\sigma\delta)} & \frac{\sigma+\mu}{\omega(\mu+\sigma+\delta)} & \frac{1}{\omega} \end{bmatrix}$$

The Matrix FV^{-1} will be a similar matrix as to the first FV^{-1} matrix we found, so we only care about the top left entry. This value is:

$\beta\lambda(\frac{1}{\mu+\psi)(\mu+\gamma)} + \frac{\alpha\psi}{(\mu(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})+\psi(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi}))^2(\mu+\gamma)}) +$

$\epsilon\lambda\gamma(\frac{1}{\mu+\psi)(\mu+\gamma)(\sigma+\mu+\delta)} + \frac{\alpha\psi}{(\mu(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})+\psi(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi}))^2(\mu+\gamma)(\sigma+\mu+\delta)})$

Substituting in our values with $\psi = 0.11$ and all the other parameters the same as before, we will see that $\mathcal{R}_0 < 1$. Now let's look at the graphs with all the same parameter values.

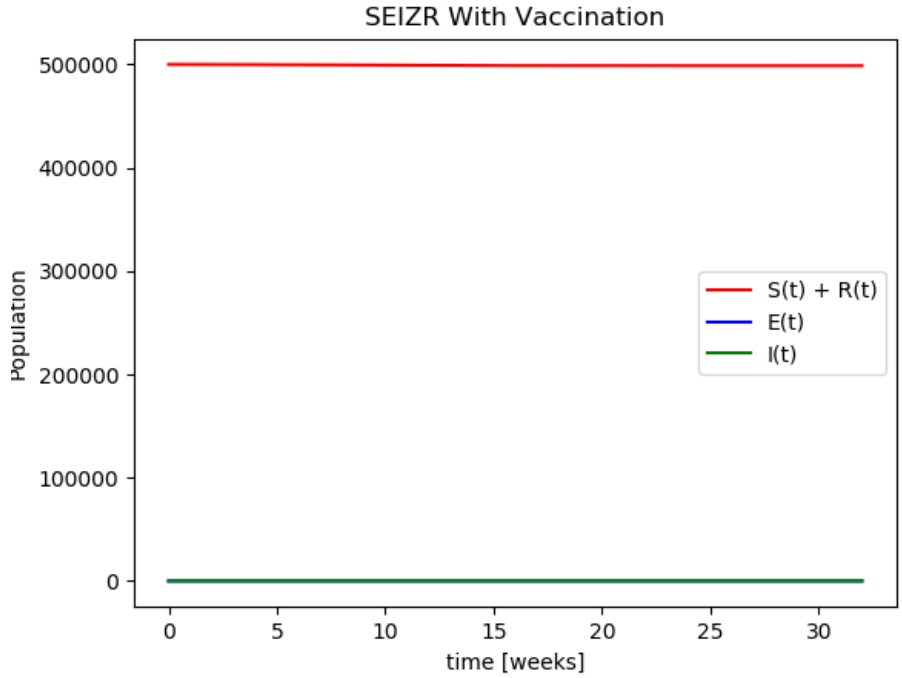


FIGURE 4. SEIZR

We can see that the total population stays more-or-less constant from this view of the graph. So we will zoom in to see what happens.

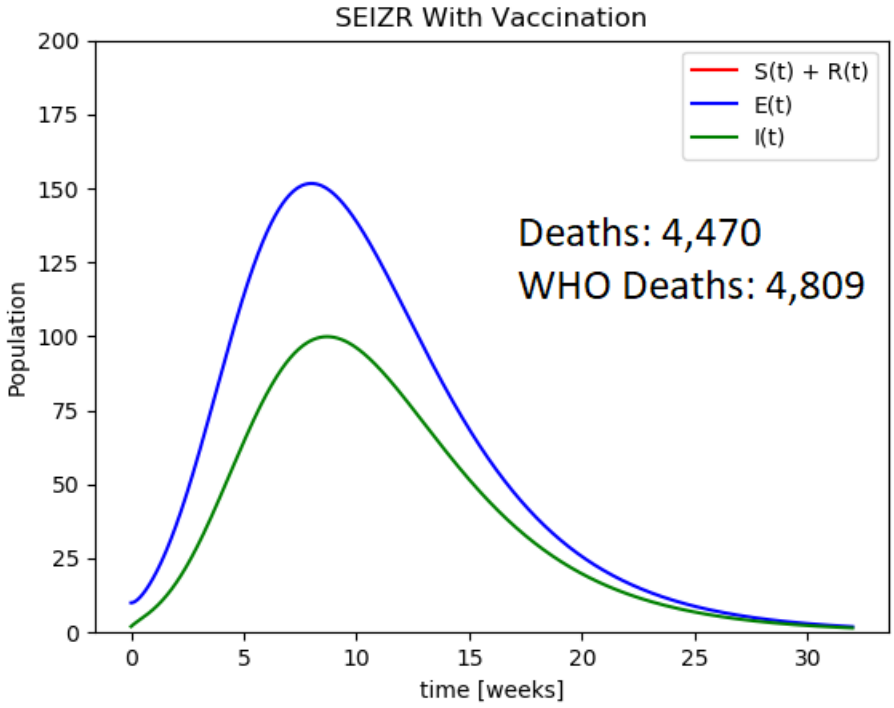
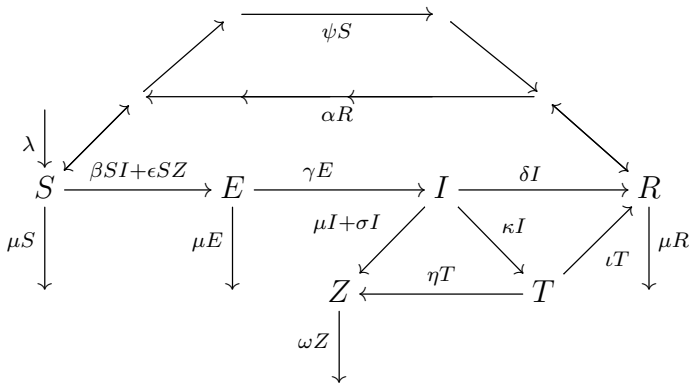


FIGURE 5. SEIZR

Looking at Figure 6, we can see we get quite close to the given number of deaths from the WHO, but the model can still be made more accurate. We have not accounted for treatment of individuals in hospitals that are infectious with the disease which was a very prominant feature during this time. This will be added in as a new population T(treatment). So we will have a new transfer diagram as follows:



Infected individuals may transfer into the Treatment population after an average time κI. When in the treatment population, if an infected individual dies, it will enter the Z population after some average time ηT. Or, the treated patient survives, and it enters the recovered population after some average time ιT. The corresponding equations are:

$$\begin{aligned}
\frac{dS}{dt} &= \lambda + \alpha R - \mu S - \beta SI - \epsilon SZ - \psi S \\
\frac{dE}{dt} &= \beta SI + \epsilon SZ - \mu E - \gamma E \\
\frac{dI}{dt} &= \gamma E - \mu I - \delta I - \sigma I - \underline{\kappa I} \\
\frac{dZ}{dt} &= \mu I + \sigma I - \omega Z + \underline{\eta T} \\
\frac{dT}{dt} &= \underline{\kappa I - \eta T - \iota T} \\
\frac{dR}{dt} &= \delta I - \mu R - \alpha R + \psi S + \underline{\iota T}
\end{aligned} \tag{3.7}$$

Again, we look for the DFE to see if it is stable. Set all equations = 0 and I=0.

$$\begin{aligned}
&(1) 0 = \lambda + \alpha R - \mu S - \epsilon SZ - \psi S \\
&(2) 0 = \epsilon SZ - \mu E - \gamma E \\
&(3) 0 = \gamma E \\
&(4) 0 = -\omega Z + \eta T \\
&(5) 0 = -\eta T - \iota T \\
&(6) 0 = -\mu R - \alpha R + \psi S + \iota T
\end{aligned} \tag{3.8}$$

Now we see from the third equation that E = 0. and from the fourth and fifth equation, Z,T = 0, which yields:

$$\begin{aligned} 0 &= \lambda + \alpha R - \mu S - \psi S \\ 0 &= -\mu R - \alpha R + \psi S \end{aligned} \tag{3.9}$$

(3.9) is the same system of equations as (3.4), so we will get the same DFE at (S,E,I,Z,T,R) = $((\frac{\lambda}{\mu+\psi} + \frac{\alpha\psi\lambda}{(\mu+\psi)^2(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})}, 0, 0, 0, 0, \frac{\psi\lambda}{(\mu+\psi)(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})})$

Now we will computer the Next Generation Matrix to see if the DFE is stable. Now we will have a 4x4 matrix as T is a population of infected individuals.

$$\mathscr{F}_{\mathbf{E,I,Z,T}} = \begin{bmatrix} \beta SI + \epsilon SZ \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

$$\mathscr{V}_{\mathbf{E,I,Z,T}} = \begin{bmatrix} E(\mu+\gamma) \\ -\gamma E + I(\sigma+\mu+\delta+\kappa) \\ -\mu I - \sigma I - \eta T + \omega Z \\ -\kappa I + \eta T + \iota T \end{bmatrix}$$

Differentiate $\mathscr{F}$ and $\mathscr{V}$ w.r.t E, I, Z, and T and evaluate at the DFE point.

$$\mathbf{F} = \begin{bmatrix} 0 & \beta(\frac{\lambda}{\mu+\psi} + \frac{\alpha\psi\lambda}{(\mu+\psi)^2(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})}) & \epsilon(\frac{\lambda}{\mu+\psi} + \frac{\alpha\psi\lambda}{(\mu+\psi)^2(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi})}) & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad \mathbf{V} = \begin{bmatrix} \mu+\gamma & 0 & 0 & 0 \\ -\gamma & \sigma+\mu+\delta+\kappa & 0 & 0 \\ 0 & -\sigma-\mu & \omega & -\eta \\ 0 & -\kappa & 0 & \eta+\iota \end{bmatrix}$$

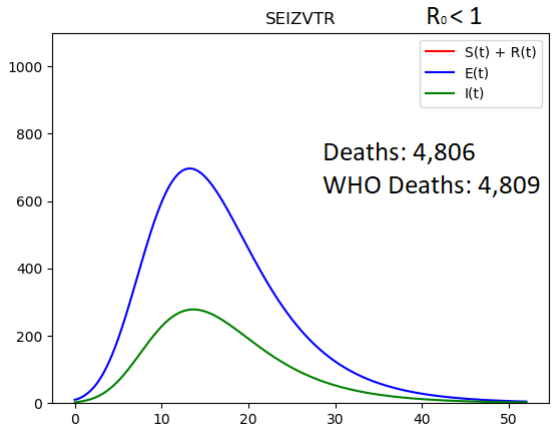
$$\mathbf{V}^{-1} = \begin{bmatrix} \frac{1}{\mu+\gamma} & 0 & 0 & 0 \\ \frac{\gamma}{(\mu+\gamma)(\sigma+\mu+\gamma+\kappa)} & \frac{1}{\sigma+\mu+\gamma+\kappa} & 0 & 0 \\ \frac{\gamma(\eta\kappa+\mu\eta+\sigma\eta+\mu\iota+\sigma\iota)}{(\mu+\gamma)(\sigma+\mu+\gamma+\kappa)\omega(\eta+\iota)} & \frac{\eta\kappa+\mu\eta+\sigma\eta+\mu\iota+\sigma\iota}{(\sigma+\mu+\gamma+\kappa)(\eta+\iota)\omega} & \frac{1}{\omega} & \frac{\eta}{(\eta+\iota)\omega} \\ \frac{\kappa\gamma}{(\sigma+\mu+\gamma+\kappa)(\mu+\gamma)(\eta+\iota)} & \frac{\kappa}{(\sigma+\mu+\gamma+\kappa)(\eta+\iota)} & 0 & \frac{1}{\eta+\iota} \end{bmatrix}$$

1

[1]Matrices were generated from Maple

$$FV^{-1} = \begin{bmatrix} \frac{\beta\lambda}{\mu+\psi} + \frac{B\alpha\psi\lambda}{\left(\mu\left(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi}\right)+\psi\left(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi}\right)\right)^2} & \left(\frac{e\lambda}{\mu+\psi} + \frac{\epsilon\alpha\psi\lambda}{\left(\mu\left(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi}\right)+\psi\left(\mu+\alpha+\frac{\psi\alpha}{\mu+\psi}\right)\right)^2}\right)\gamma \\ \mu+\gamma & (\mu+\gamma)(\sigma+\mu+\gamma+\kappa) \\ 0 & \text{MESS} \quad 0 \; 0 \\ 0 & 0 \quad 0 \; 0 \\ 0 & 0 \quad 0 \; 0 \end{bmatrix}$$

[2] When the parameter values are substituted in, you will find that $\mathcal{R}_0 < 1$, meaning our DFE is stable, and the system will tend to this equilibrium. Let's analyze the graphs with $\kappa = 1, \iota = 1, \psi = 0.1108, \eta = 2$



We see that we get very close to the amount of deaths as listed by the WHO after taking into account both vaccination and treatment into our model. Since the parameter values used are all within a range (i.e the incubation period for an individial is between 2-21 days, but a value of 7 was used in the graphs), changing all parameter values may yield slightly different results. Tampering with the parameters within reason allows us to get an exact number of deaths.

Section 4. Conclusion

With a complicated disease such as Ebola, it is no wonder why interventions such as vaccination and treatment must be taken into account to produce a somewhat accurate model. What measures can be taken to increase the accuracy of the model? Some measures could be to split the susceptible population into different groups on the basis that not every susceptible individual will have the same chance of coming in contact with an infectious body.

[2]Matrices were generated from Maple

Health workers will have a much higher ϵ and β value than an average person. On another note, it has never been proven that you may get Ebola twice, but vaccination is proven to be temporary. So another population should possibly be added for vaccinated individuals, as opposed to assuming that you do not have immunity to Ebola after receiving it. These measures may be studied in a future paper.

CITATIONS:

(1) https://www.cdc.gov/vhf/ebola/about.html
(2) https://www.who.int/csr/disease/ebola/ebola-6-months/liberia/en/

Communication with Dr. C. McCluskey at Wilfrid Laurier University aided in the completion of this paper.