Obermayer_Sheth_Assignment6

Alyssa Obermayer

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```
# Load required packages
library(Ryacas)
library(deSolve)
```

Question 3:

We chose to model the Ebola Virus because of its high mortality rate and high prevalence in West Africa, causing it to evolve into a major problem for public health. There is typically a rapid decline in health one week after the onset of symptoms which can lead to death after an average of 10 days in 50%-90% of infections.

An important factor of why the Ebola Virus is important to model is the constant reemergence of the virus in various areas around West Africa, large in part due to the animal and environmental reservoirs which the virus can reside in and be transmitted, through bodily fluids or nonhuman animals. Several bat species are possible reservoirs for the Ebola Virus with transmission to humans via feces, saliva, or food. This, in concurrence with the natural movement of bat colonies from Central to West Africa could account for multiple reemergence events of Ebola Virus in various populations over relatively recent timeline.

The use of compartmental host-pathogen modeling can play an important role in simulating these Ebola Virus reemergence events as well as allow us to understand different aspects of the spread of the virus within a population over time. Furthermore, the paper from Rachan and Torres (2015), presents an additional perspective of adding the effect of vaccination on the infected individuals and help model the possible effect that may have on an outbreak over time. Overall, these models and the parameters used within them can help the researchers and public health officials determine if an infectious disease has the possibility of becoming an epidemic or spreading further and the possible actions that are necessary to take to contain the pathogen.

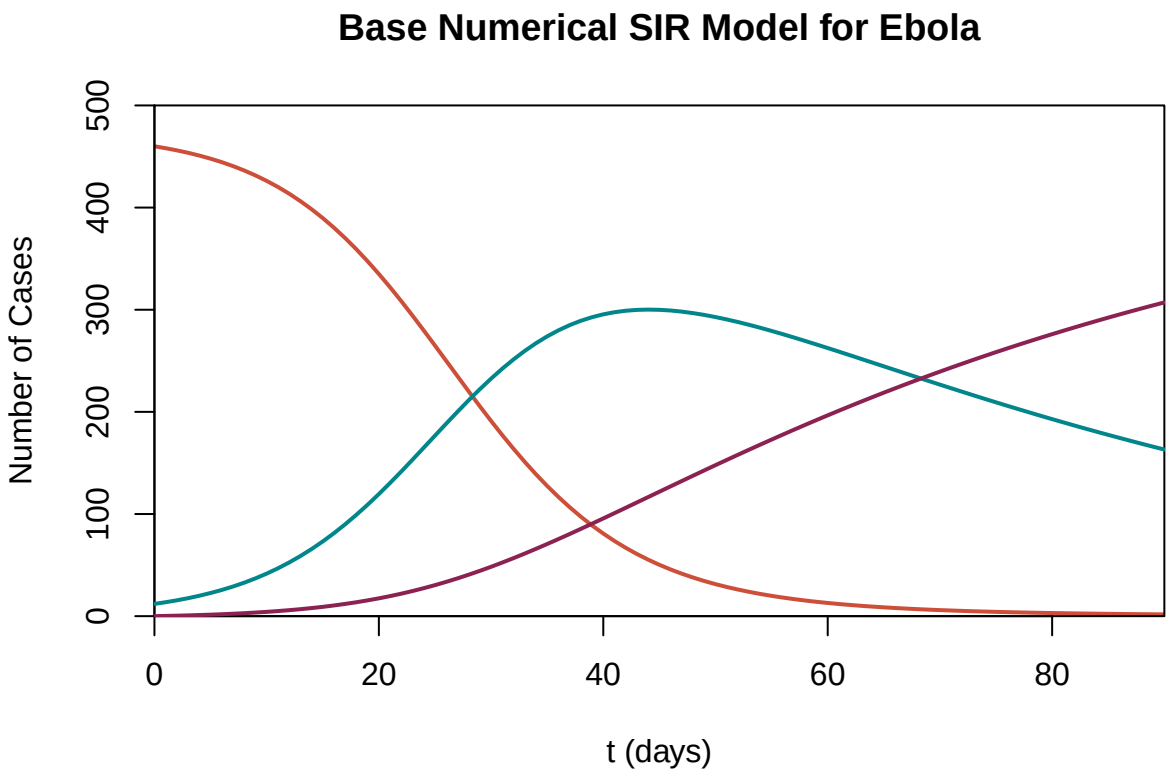
The following figure shows the SIR compartmental model based on numerical data obtained from the World Health Organization (WHO) of the 2014 Ebola Virus outbreak in Liberia. This model takes the starting data from the outbreak with a total population of 472, with 12 infected individuals, and 0 recovered individuals, along with a 0.000318 rate of infection (b) and a 0.0175 recovery rate (g). It then models the virus over a 90 day period showing that the number of infected individuals increases as the number of susceptible individuals decreases, likely because they are becoming infected. Additionally, as this occurs the number of recovered individuals increases at a slower rate but eventually surpasses the number of infected individuals, showing that the majority of the population has likely developed immunity to the virus. I will note that the research paper used also plotted actual infection data obtained from the WHO but they did not put the exact numbers that were plotted in the material. I tried to obtain this data from the WHO pages that they referenced but was unable to find the concrete numbers I needed.

```
#SIR compartmental model function
SIR <- function (t, n, parms){
  with(as.list(parms), {
```

```
    S <- -b*n[1]*n[2]
    I <- b*n[1]*n[2] - g*n[2]
    R <- g*n[2]
    list(c(S, I, R))
  })
}

N <- 472      #Initial Population
b <- 0.000318 #Rate of infection
g <- 0.0175   #Recovery Rate
s0 <- 460     #Initial susceptible
i0 <- 12      #Initial Infected
r0 <- 0       #Initial recovered
initialN <- c(s0,i0,r0) #Initial population vector

#SIR ode function showing number of cases over 90 days
SIR.out <- ode(y = initialN, times = seq(0,90,by=1), func = SIR,
               parms=c(N=N,b=b,g=g),method="ode45")
#Plotting SIR Model
SIRplot <- plot(SIR.out[,2]~SIR.out[,1], #Plotting susceptible
                type="l", lwd=2, col="tomato3",
                xlab="t (days)",ylab="Number of Cases",
                xaxs="i", yaxs="i",
                xlim=c(0,90), ylim=c(0,500),
                main="Base Numerical SIR Model for Ebola")
lines(SIR.out[,3]~SIR.out[,1], lwd=2, col="turquoise4") #Plotting infected
lines(SIR.out[,4]~SIR.out[,1], lwd=2, col="violetred4") #Plotting recovered
```



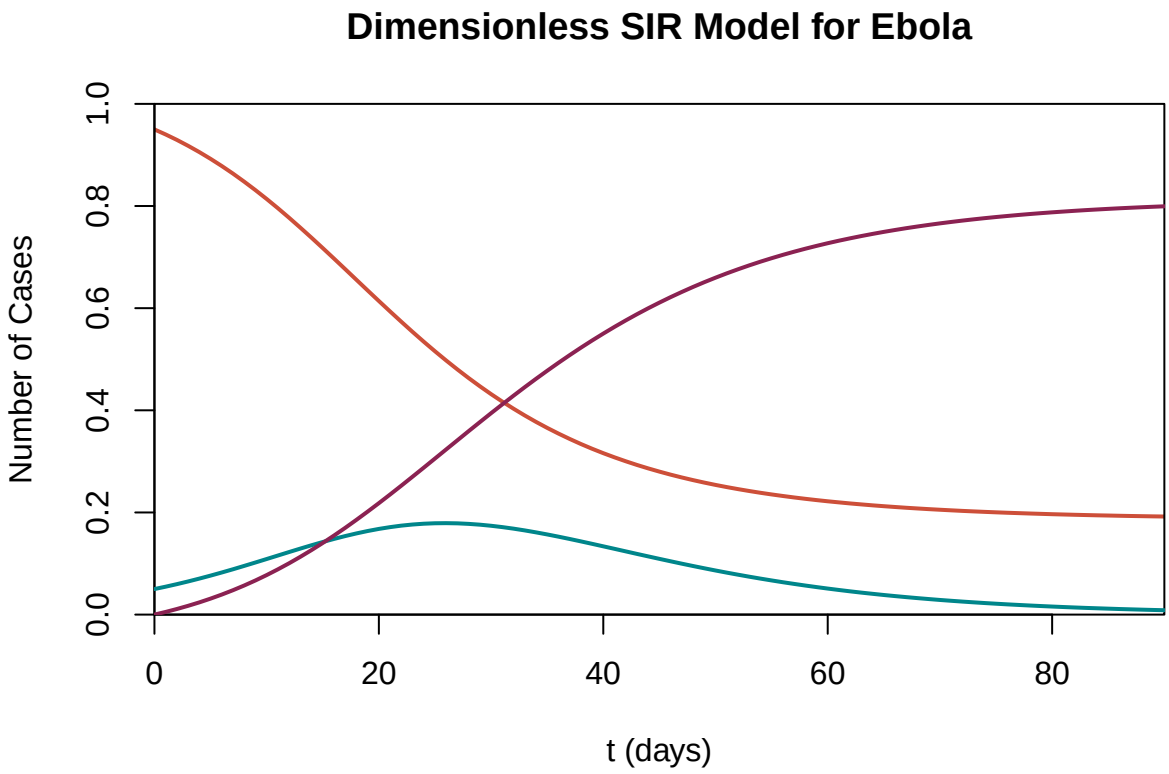
The figure below shows a dimensionless SIR compartmental model of a virus starting with 95% of the population being susceptible, 5% of the population being infected, and 0% being recovered, along with a 0.2 rate of infection (b) and 0.1 recovery rate (g). This shows a similar pattern to the numerical data model though the number of cases at a given time are given in percentages of a population.

```
# SIR dimensionless compartmental model function
SIRd <- function(t, n, parms) {
    with(as.list(parms), {
        S <- -b * n[1] * n[2]
        I <- b * n[1] * n[2] - g * n[2]
        R <- g * n[2]
        list(c(S, I, R))
    })
}

N <- 1
b <- 0.2
g <- 0.1
s0 <- 0.95
i0 <- 0.05
r0 <- 0
# Initial parameters changed because model is now based off
# of percentages of the population
initialN <- c(s0, i0, r0)

SIR.outd <- ode(y = initialN, times = seq(0, 90, 1), func = SIRd,
```

```
    parms = c(N = N, b = b, g = g), method = "ode45")
SIRdplot <- plot(SIR.outd[, 2] ~ SIR.outd[, 1], type = "l", lwd = 2,
    col = "tomato3", xlab = "t (days)", ylab = "Number of Cases",
    xaxs = "i", yaxs = "i", xlim = c(0, 90), ylim = c(0, 1),
    main = "Dimensionless SIR Model for Ebola")
lines(SIR.outd[, 3] ~ SIR.outd[, 1], lwd = 2, col = "turquoise4")
lines(SIR.outd[, 4] ~ SIR.outd[, 1], lwd = 2, col = "violetred4")
```



Lastly, the figure below represents a dimensionless SIR compartmental model of a virus with the introduction of varying vaccination rates ranging from 0 to 0.06. The addition of this parameter to the model decreases the number of days to peak infected individuals because as the rate of vaccination increases, those susceptible individuals that were vaccinated are able to transition straight to the recovered individuals group.

In the model shown, susceptible individuals are represented with reddish hues, infected individuals are represented with blue hues, and recovered individuals are represented with yellow/brown hues, additionally, the vaccination rate increases as these hues become darker in their respective categories. It can be seen that individuals that were susceptible to Ebola reduce gradually with increased vaccination and beginning of the plateau occurs in a shorter number of days. The cases for infected individuals is highest around 27 days but as vaccination rate increases the day to peak infections decrease. Moreover, the number of recovered individuals after 90 days increases from around 80% with no vaccine to 88% with a 6% vaccination rate of the population.

```
# SIR dimensionless compartmental model function with vaccine
# introduced
SIRv <- function(t, n, parms) {
    with(as.list(parms), {
```

```
        S <- -b * n[1] * n[2] - v * n[2]  #subtracting vaccinated individuals
        I <- b * n[1] * n[2] - g * n[2]
        R <- g * n[2] + v * n[2]  #adding vaccinated individuals
        list(c(S, I, R))
    })
}

N <- 1
b <- 0.2
g <- 0.1
v <- c(0, 0.005, 0.01, 0.02, 0.03, 0.04, 0.06)  #rate of vaccination, beginning at 0
s0 <- 0.95
i0 <- 0.05
r0 <- 0
initialN <- c(s0, i0, r0)

SIR.outv0 <- ode(y = initialN, times = seq(0, 90, 1), func = SIRv,
    parms = c(N = N, b = b, g = g, v = 0), method = "ode45")
SIR.outv0.005 <- ode(y = initialN, times = seq(0, 90, 1), func = SIRv,
    parms = c(N = N, b = b, g = g, v = 0.005), method = "ode45")
SIR.outv0.01 <- ode(y = initialN, times = seq(0, 90, 1), func = SIRv,
    parms = c(N = N, b = b, g = g, v = 0.01), method = "ode45")
SIR.outv0.02 <- ode(y = initialN, times = seq(0, 90, 1), func = SIRv,
    parms = c(N = N, b = b, g = g, v = 0.02), method = "ode45")
SIR.outv0.03 <- ode(y = initialN, times = seq(0, 90, 1), func = SIRv,
    parms = c(N = N, b = b, g = g, v = 0.03), method = "ode45")
SIR.outv0.04 <- ode(y = initialN, times = seq(0, 90, 1), func = SIRv,
    parms = c(N = N, b = b, g = g, v = 0.04), method = "ode45")
SIR.outv0.06 <- ode(y = initialN, times = seq(0, 90, 1), func = SIRv,
    parms = c(N = N, b = b, g = g, v = 0.06), method = "ode45")


plot(NA, type = "l", lwd = 2, xlab = "t (days)", ylab = "Number of Cases",
    xaxs = "i", yaxs = "i", xlim = c(0, 90), ylim = c(0, 1),
    main = "Dimensionless SIR Model with Vaccine")
lines(SIR.outv0[, 2] ~ SIR.outv0[, 1], lwd = 2, col = "lightpink3")
lines(SIR.outv0[, 3] ~ SIR.outv0[, 1], lwd = 2, col = "skyblue2")
lines(SIR.outv0[, 4] ~ SIR.outv0[, 1], lwd = 2, col = "lightgoldenrod")
lines(SIR.outv0.005[, 2] ~ SIR.outv0.005[, 1], lwd = 2, col = "hotpink")
lines(SIR.outv0.005[, 3] ~ SIR.outv0.005[, 1], lwd = 2, col = "steelblue1")
lines(SIR.outv0.005[, 4] ~ SIR.outv0.005[, 1], lwd = 2, col = "gold")
lines(SIR.outv0.01[, 2] ~ SIR.outv0.01[, 1], lwd = 2, col = "hotpink4")
lines(SIR.outv0.01[, 3] ~ SIR.outv0.01[, 1], lwd = 2, col = "turquoise2")
lines(SIR.outv0.01[, 4] ~ SIR.outv0.01[, 1], lwd = 2, col = "goldenrod3")
lines(SIR.outv0.02[, 2] ~ SIR.outv0.02[, 1], lwd = 2, col = "firebrick")
lines(SIR.outv0.02[, 3] ~ SIR.outv0.02[, 1], lwd = 2, col = "turquoise4")
lines(SIR.outv0.02[, 4] ~ SIR.outv0.02[, 1], lwd = 2, col = "darkorange1")
lines(SIR.outv0.03[, 2] ~ SIR.outv0.02[, 1], lwd = 2, col = "firebrick4")
lines(SIR.outv0.03[, 3] ~ SIR.outv0.03[, 1], lwd = 2, col = "royalblue3")
lines(SIR.outv0.03[, 4] ~ SIR.outv0.03[, 1], lwd = 2, col = "chocolate")
lines(SIR.outv0.04[, 2] ~ SIR.outv0.04[, 1], lwd = 2, col = "maroon")
lines(SIR.outv0.04[, 3] ~ SIR.outv0.04[, 1], lwd = 2, col = "mediumblue")
lines(SIR.outv0.04[, 4] ~ SIR.outv0.04[, 1], lwd = 2, col = "orange4")
```

```
lines(SIR.outv0.06[, 2] ~ SIR.outv0.02[, 1], lwd = 2, col = "darkorchid4")
lines(SIR.outv0.06[, 3] ~ SIR.outv0.06[, 1], lwd = 2, col = "navyblue")
lines(SIR.outv0.06[, 4] ~ SIR.outv0.06[, 1], lwd = 2, col = "saddlebrown")
```