# Het Ebola virus

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#### ToDo

- optimalisatie model
- opmaak plot
- vergelijkingen met ander uitbraken : Moeten even weten waar we de data vandaan kunnen halen.
- introductie Done
- materiaal & methode
- resultaten
- discussie & conclusie

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#### The Paper

#### Introduction

In this day and age the world is getting smaller and smaller. To get from europe to the united states it roughly takes 11 hours. This ease of travelling everywhere in the world within one day comes with one huge risk, the risk of spreading a dangerous infectious disease. On july 20, 2014 a infected passenger, with the Ebola virus disease (EVD), arrived in Nigeria. After a total of 20 cases where 8 died, Nigeria was cleared of the ebola virus on october 20, 2014 57 days. This shows what happens if 1 person is infected with ebola and begins to get in contact with others. Luckely by handeling fast not many people got infected with EVD because the authorities handeled quickly. Through our simulations we are trying to replicate the outbreak in Nigeria and see what can happen if there wasn't a quick response and we like to show if this outbreak was a abnormlity or simular to other outbreaks. Also we would like to compare the outbreak in Nigeria with other simular type of outbreaks and see if our parameters in the model are accurate for other EVD cases.

The Paper

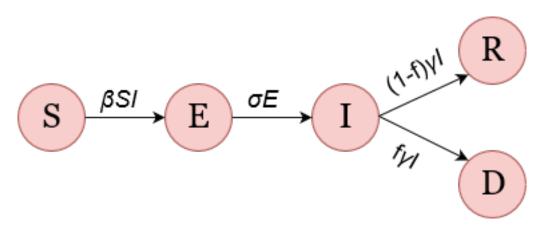


Figure 1: Model for viral infection

#### The Model

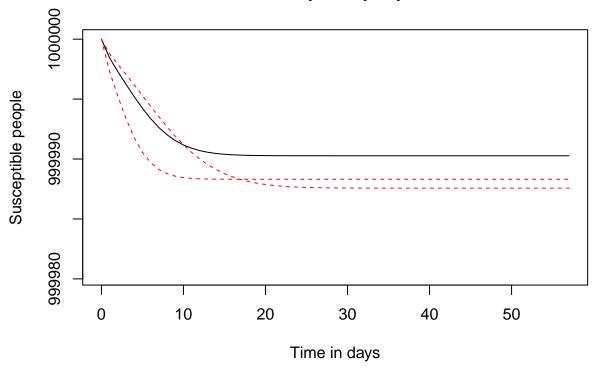
Figure 1: schemetic model for EVD infection spread. Susceptible induviduals S are infected by infectious individuals I at rate  $\beta$ . Then they go through a incubation period E at rate  $\sigma$ . After incubation induviduals become infectious I. These infectious people either recover R or die D at rate  $\gamma$ . The fatality rate so how many people die or recover is given by f.

```
dS/dT = -B(t)SI
dE/dT = B(t)SI - omegaE
dI/dT = omegaE - yI
dR/dT = (1 - f)yI
dD/dT = fyI
Rt = BtS(t)/y
Ro = BoS/y
# time 57 dagen (4924800)
time <- seq(0,57,1)
# standaard parameters
st.para <- c(k = 0.19,
             f = 0.39,
             y = 0.71,
             omega = 0.33,
             t = 3,
             Bo = 1.22*10^-6,
             e = 2.71828182459)
# standaard standaard waarden
st.state <- c(S = 10^6,
              E = 0,
              I = 1,
              R = 0,
              D = 0)
```

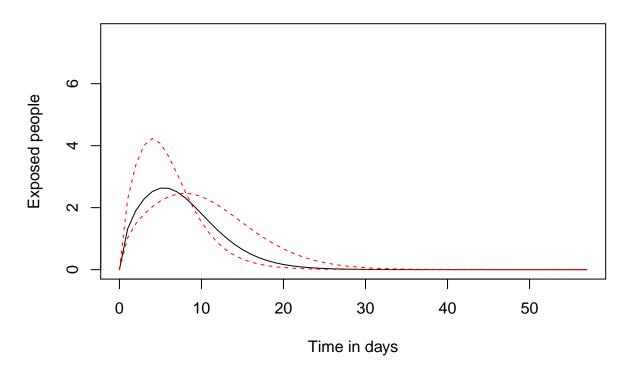
```
low.para <- st.para</pre>
low.para["k"] <- 0.1 #0.1
low.para["f"] <- 0.14
low.para["Bo"] <- 1.22*10^-6 # 0.7
high.para <- st.para
high.para["k"] <- 0.38 # 0.38
high.para["f"] <- 0.71
high.para["Bo"] <- 1.22*10^-6 # 2.1
ebola.model <- function(time, para, state){</pre>
    with(as.list(c(state, para)),{
        Bt <- Bo * e^(-k * (time - t))
        dS <- -Bt * S * I
        dE \leftarrow Bt * S * I - omega * E
        dI <- omega * E - y * I
        dR \leftarrow (1 - f) * y * I
        dD \leftarrow f * y * I
        return(list(c(dS, dE, dI, dR, dD)))
    })
}
st.out <- as.data.frame(ode(y = st.state,</pre>
                              times = time,
                              parms = st.para,
                              func = ebola.model))
high.out <- as.data.frame(ode(y = st.state,
                                times = time,
                                parms = high.para,
                                func = ebola.model))
low.out <- as.data.frame(ode(y = st.state,</pre>
                               times = time,
                               parms = low.para,
                               func = ebola.model))
colnames(st.out) <- c("Time",</pre>
                        "S",
                        "E",
                        "I",
                        "R",
                        "D")
colnames(high.out) <- c("Time",</pre>
                        "S",
```

```
"E",
                       "I",
                       "R",
                       "D")
colnames(low.out) <- c("Time",</pre>
                       "E",
                       "I",
                       "R",
                       "D")
round.out <- round(st.out)</pre>
# plots maken
# geen round meer, wel CL
# Susceptible people
plot(st.out$Time, st.out$S,
     type = "1",
     main = "amount of susceptible people over time",
     ylab = "Susceptible people",
     xlab = "Time in days",
     ylim = c(min(st.out\$S) - 10, 10^6))
lines(high.out$Time, high.out$S,
      col = "red",
      type = "1",
      lty = 2)
lines(low.out$Time, low.out$S,
     col = "red",
      type = "1",
      lty = 2)
```

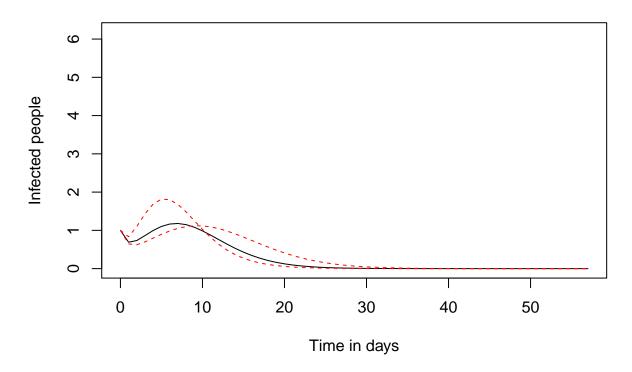
### amount of susceptible people over time



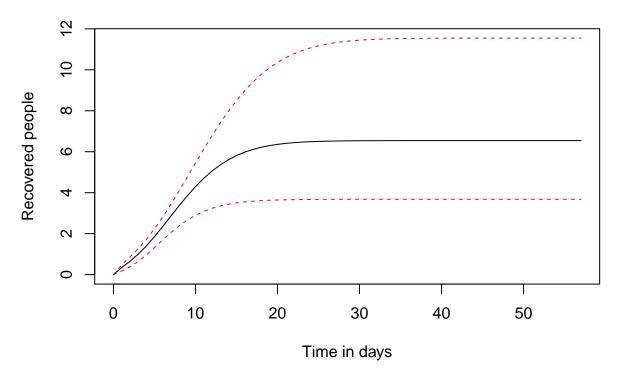
### Amount of exposed people over time



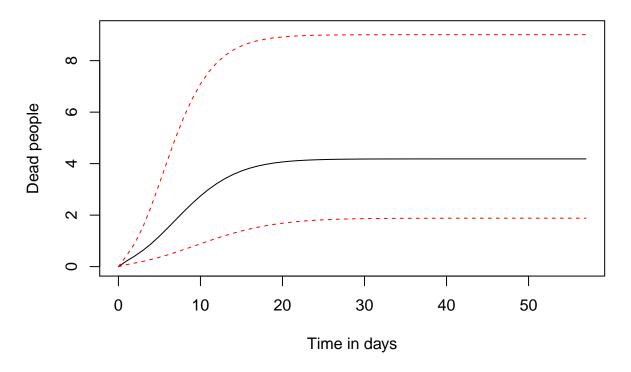
### Amount of infected people over time



### Amount of people that have recoverd over time



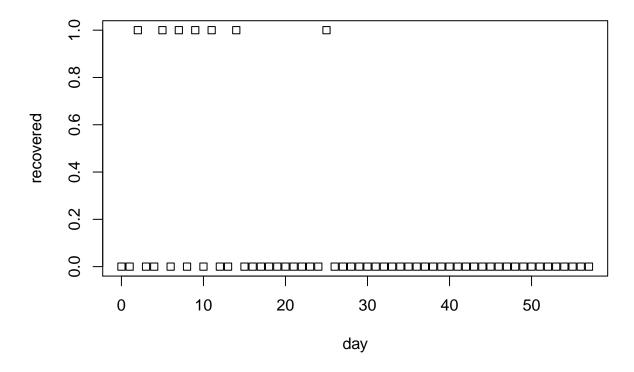
#### Amount of dead people over time



```
difference.by.day <- function(x, collumn){</pre>
  day.before <- as.numeric(subset(round.out,Time == x[1] - 1, select = collumn))</pre>
  diff <- x[collumn] - day.before</pre>
  if (is.na(diff)) {
      diff <- 0
  }
  return(diff)
}
difference.by.day.norm <- function(x, collumn){</pre>
  day.before <- as.numeric(subset(st.out,Time == x[1] - 1, select = collumn))
  diff <- x[collumn] - day.before</pre>
  if (is.na(diff)){
      diff <- 0
  }
  return(diff)
}
diffrence.infections <- function(x){
  collumns <- c("I", "R", "D")</pre>
  total.cases.before <- sum(as.numeric(subset(st.out,</pre>
                                                  Time == x[1] - 1,
                                                  select = collumns)))
  total.cases.after <- sum(as.numeric(subset(st.out,</pre>
```

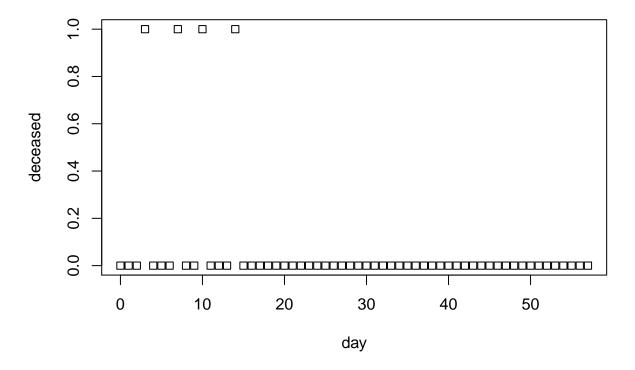
```
Time == x[1],
                                               select = collumns)))
  diffrence <- total.cases.after - total.cases.before</pre>
 return(diffrence)
}
difference.dead.norm <- apply(st.out, 1, difference.by.day.norm, "D")</pre>
difference.recovered <- apply(round.out, 1, difference.by.day, "R")</pre>
difference.dead <- apply(round.out, 1, difference.by.day, "D")</pre>
daily.new.cases <- apply(st.out, 1, diffrence.infections)</pre>
# plot(time, difference.susceptible,
      pch = 16)
# plot(time, difference.exposed,
      pch = 16)
# plot(time, difference.infected,
      pch = 16)
plot(time, difference.recovered,
     main = "amount of recovered people per day",
     ylab = "recovered",
     xlab = "day",
     pch = 0)
```

# amount of recovered people per day



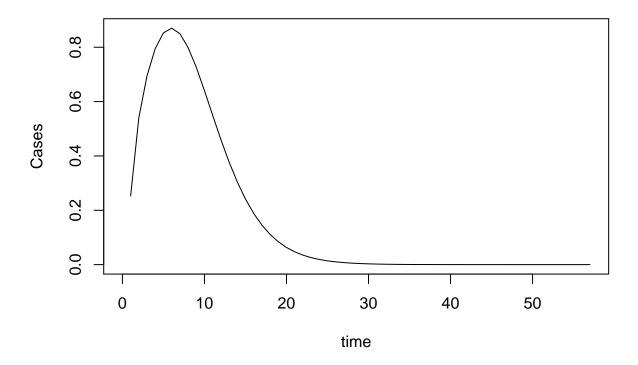
```
plot(time, difference.dead,
    main = "amount of deceased per day",
    ylab = "deceased",
    xlab = "day",
    pch = 0)
```

# amount of deceased per day



```
plot(time, daily.new.cases,
    main = "New cases per day",
    ylab = "Cases",
    xlab = "time",
    type = "l")
```

# New cases per day



#### aantekeningen verslag

• let op de bronnen, zorg ervoor dat er geen plagiaat is

introductie eerste paragraaf introductie onderwerp, intresse krijgen geeft context en probleem, welk probleem wil je oplossen wat is het doel

```
volgende paragraven
   achtergrond van het onderwerp
   context, zie de paper/onderzoek. wat is hier al gedaan
   Historie van model (evt.)
   Problemen
   -> Studie
```

#### Indeling Verslag

Methoden Waar komt data/model vandaan Model beschrijven visueel (inkscape, draw.oi, dia) & formules (niet als plaatjes) inline formule is met #\$, formule appart is met dubbel aanpak/ variatie Analyse hier moeten ook nog de programma's in de je gebruikt("we doen analyse met R")(veel programma's met versie erbij in een apparte tabel)

Resultaten

Conclusie/Discussie

Bronnen