

# Het Ebola virus

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*June 1, 2018*



Figure 1: Image of Ebola

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## Abstract

Since traveling is a lot easier than 50 years ago, we travel a lot more. Globalisation is not a bad thing but it comes with a huge risk, the risk of easily spreading infection diseases. Ebola virus disease (EVD) is one of these infection diseases. On 20 July, 2014 an infected passenger landed in Nigeria and started an outbreak. This outbreak was a pretty small one of only 20 cases, this was because of the quick response of only 3 days. Showing how important it is to react quickly to an infection. In this paper we tried to match an EVD model to the outbreaks of Nigeria 2015 and Sierra Leone 2014 to show the value of a quick reaction.

# 1. 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 model was used before in the same sort of experiment that we are trying to replicate. Although in the experiment before the research didn't go further into other outbreaks.

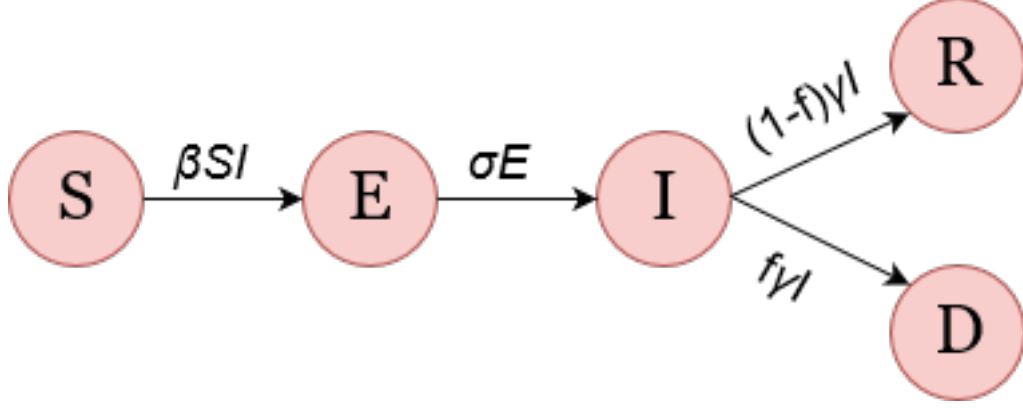


Figure 2: schematic model for EVD infection spread. Susceptible individuals  $S$  are infected by infectious individuals  $I$  at rate  $\beta$ . Then they go through a incubation period  $E$  at rate  $\sigma$ . After incubation individuals become infectious  $I$ . These infectious people either recover  $R$  or die  $D$  at rate  $\gamma$ . The fatality rate so how many people die or recover is given by  $f$ .

## 2. Materials & Methods

### 2.1. The Model

The model uses the following formula's:

- $B(t) = B_0 e^{(-k(time-t))}$
- $dS/dT = -B(t)SI$
- $dE/dT = B(t)SI - \sigma E$
- $dI/dT = \sigma E - \gamma I$
- $dR/dT = (1 - f)\gamma I$
- $dD/dT = f\gamma I$

The model itself is a rather simple SEIR (Susceptible-Exposed-Infectious-Recovered) model, as can be seen in figure 2. The people that are in the group of susceptible people  $S$  will move to the exposed group  $E$  after they get infected by the virus, if they are exposed to the virus they will go through a incubation period  $\sigma$ . After they went through the incubation period they will move to the infected group  $I$ . Here they will move through the infectiousness period  $\gamma$ . After this they will either move to the group recovered people  $R$  or the group dead people  $D$ . This will be calculated by using the fatality rate  $f$ , in the case of ebola it is 0.39. The differential equations will be solved using the  $ODE()$  function from deSolve, deSolve is a package in R. [1]

### 2.2. The data

The model was started with  $10^6$  susceptible people  $S$ , 1 infected person  $I$  and no people that were exposed to him  $E$ . This was done because the case that was simulated was with one index case that could be traced. We also started with 0 dead people  $D$  and 0 recovered people  $R^*$  because there can't be any dead people if there was nobody infected before the first day, this also goes for the recovered people. In the table below you can see the initial values of the model. [1]

Table 1: Standard initial values

	Value	Meaning
<b>S</b>	1e+06	Susceptible people
<b>E</b>	0	Exposed people
<b>I</b>	1	Infected people
<b>R</b>	0	Recovered people
<b>D</b>	0	Dead people

In the table below describes the parameters that where used. These parameters where based on the parameters used in the paper we are reviewing.

Table 2: Standard parmeters

	Value	Meaning
<b>k</b>	0.19	Rate at wich the control measures reduce transmission
<b>f</b>	0.39	<b>Fatality rate</b>
<b>y</b>	0.135	Duration of incubation
<b>sigma</b>	0.1063	Duration of infectiousness
<b>t</b>	3	Time at wich the control measures start to work
<b>Bo</b>	1.22e-06	<b>Transmission rate</b>
<b>e</b>	2.718	<b>Constante</b>

### 3. Results

#### 3.1 Simulating the model

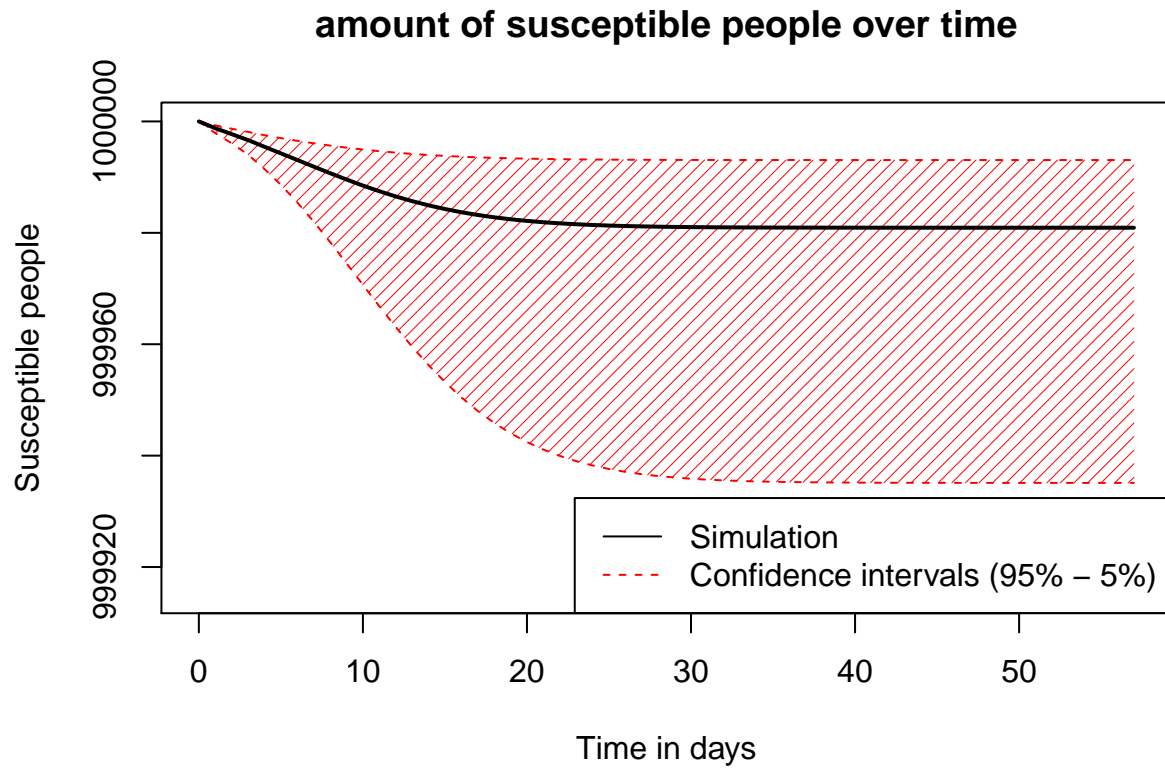


Figure 3: shows the amount of people susceptible to EVD infection with 95%-5% confidence intervals.

as shown with our model if control measures are implemented quickly the amount of people that are in danger of coming into contact with disease is minimal.

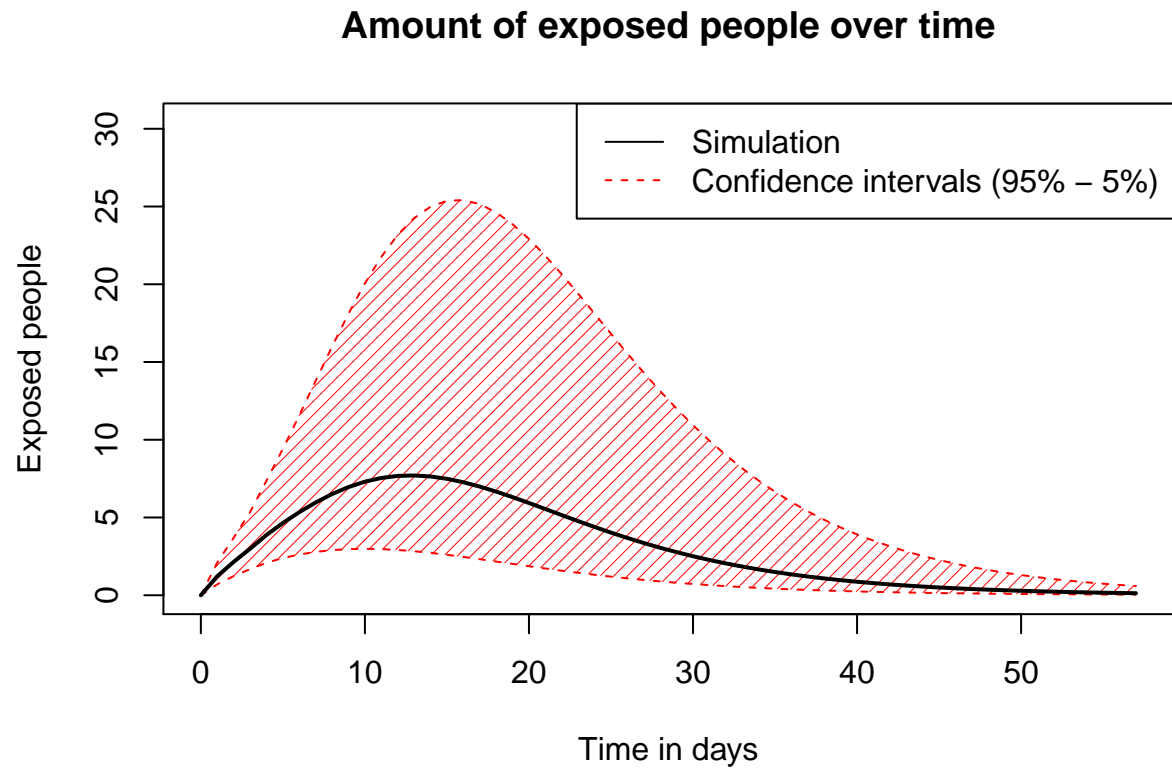


Figure 4: People exposed to a infected individual with 95%-5% confidence intervals

In this graph you can see the amount of exposed people over time, this plot uses the standard values over a timespan of 58 days.



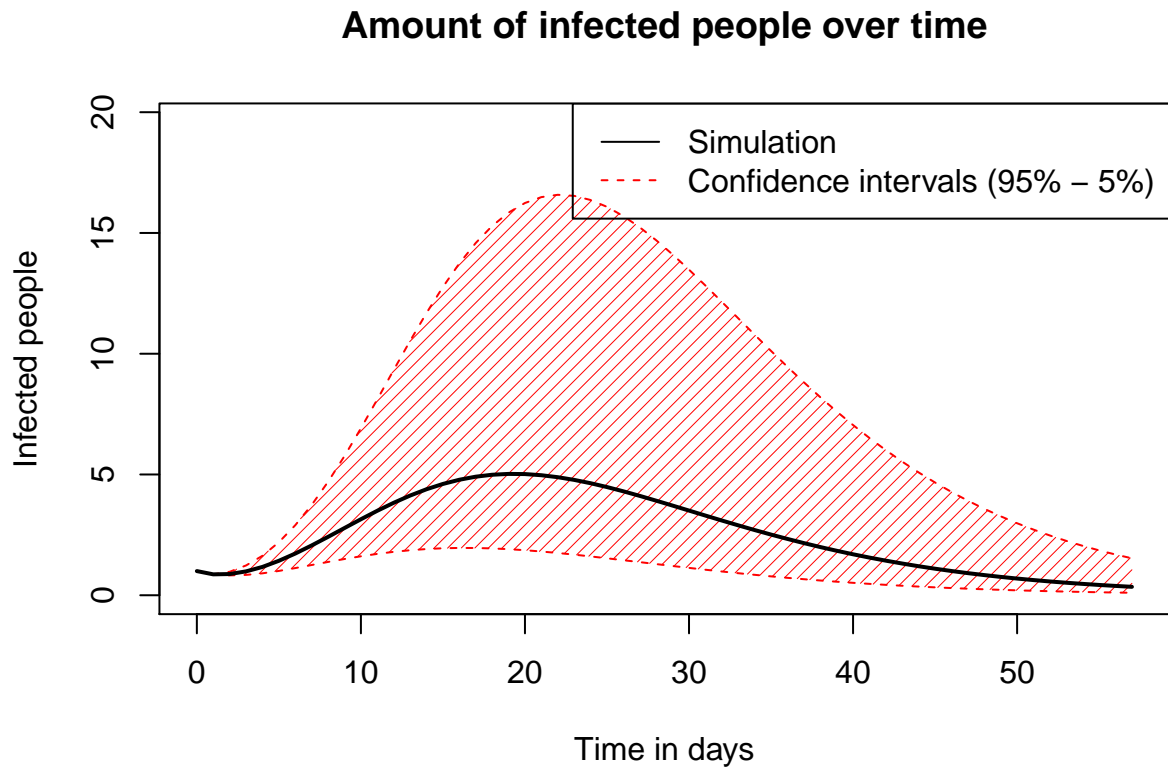


Figure 5: amount of people infected with EVD with 95%-5% confidence intervals

This plot shows the amount of people that were infected during the infection, the standard values were used over a timespan of 58 days.

## Amount of people that have recovered over time

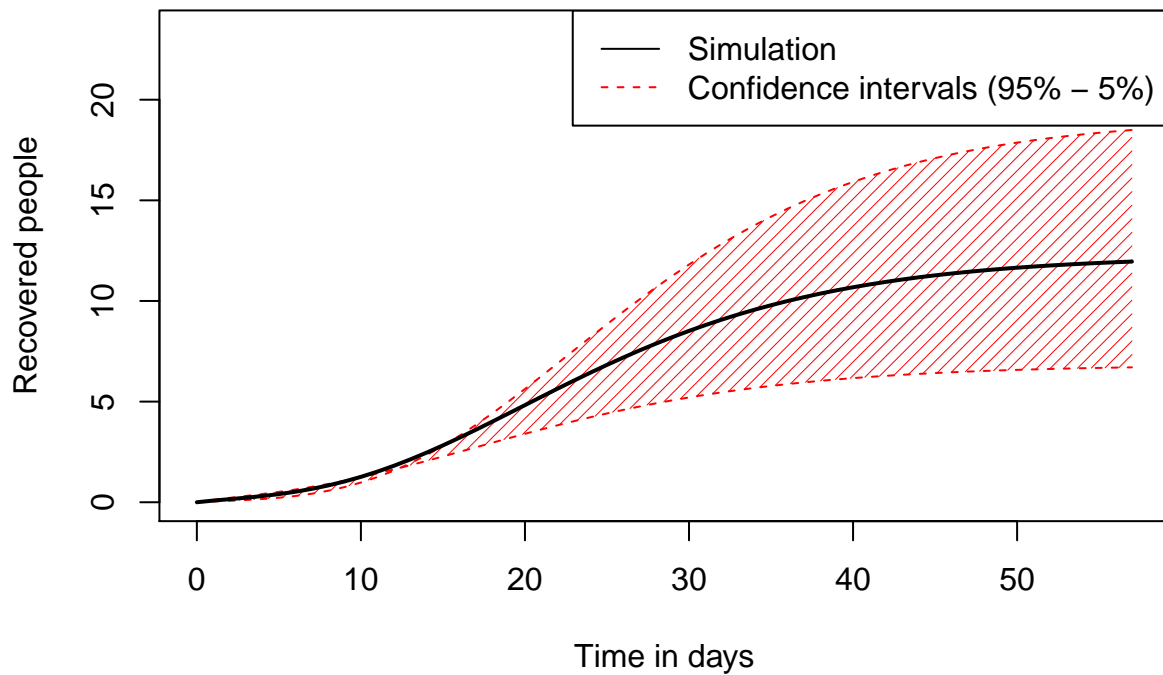


Figure 6: Total amount of people recovered from EVD infection, with 95%-5% confidence intervals.

The graph above shows the amount of people that have recovered from the EVD virus, these people will also be immuun for the Ebola virus, so they won't be added to the group of sucseptible people. This graph uses the standard parameters over a timespan of 58 days.

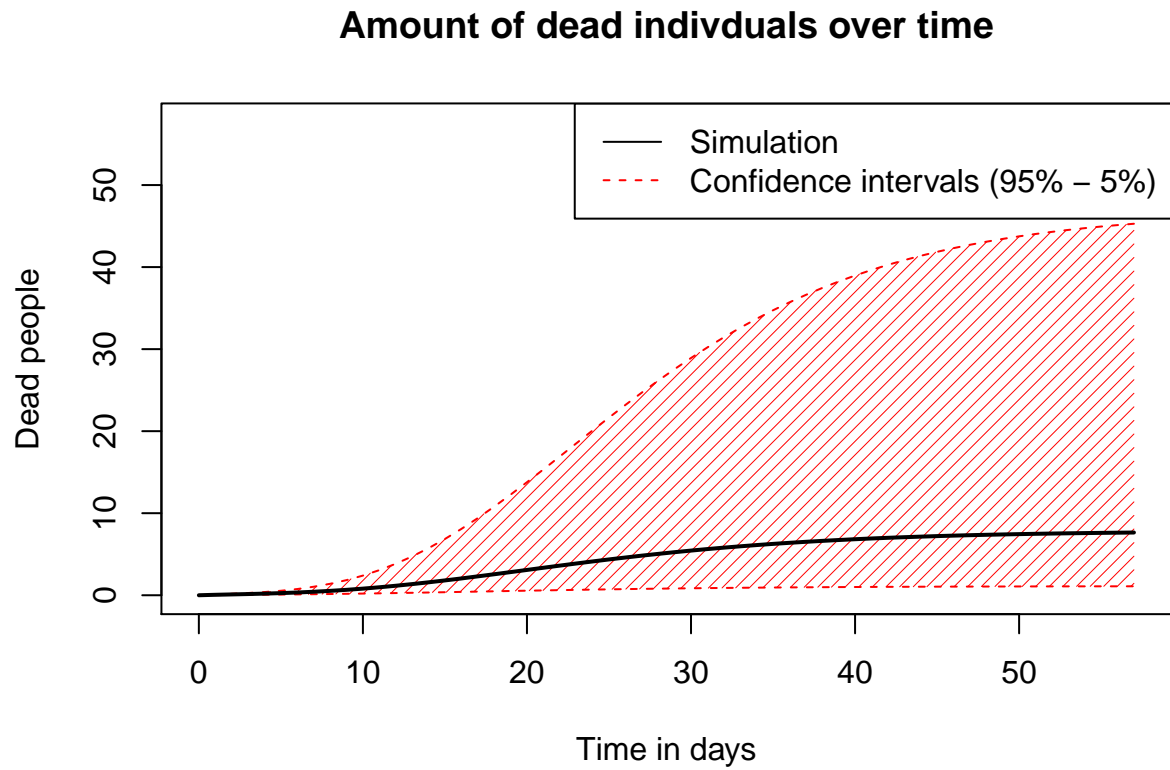


Figure 7: total casualties from EVD infection with 95%-5% confidence intervals.

The plot above shows the amount of dead people over the duration of the outbreak, the simulation in this plot used the standard values over an timespan of 58 days.

### Amount of recovered people per day

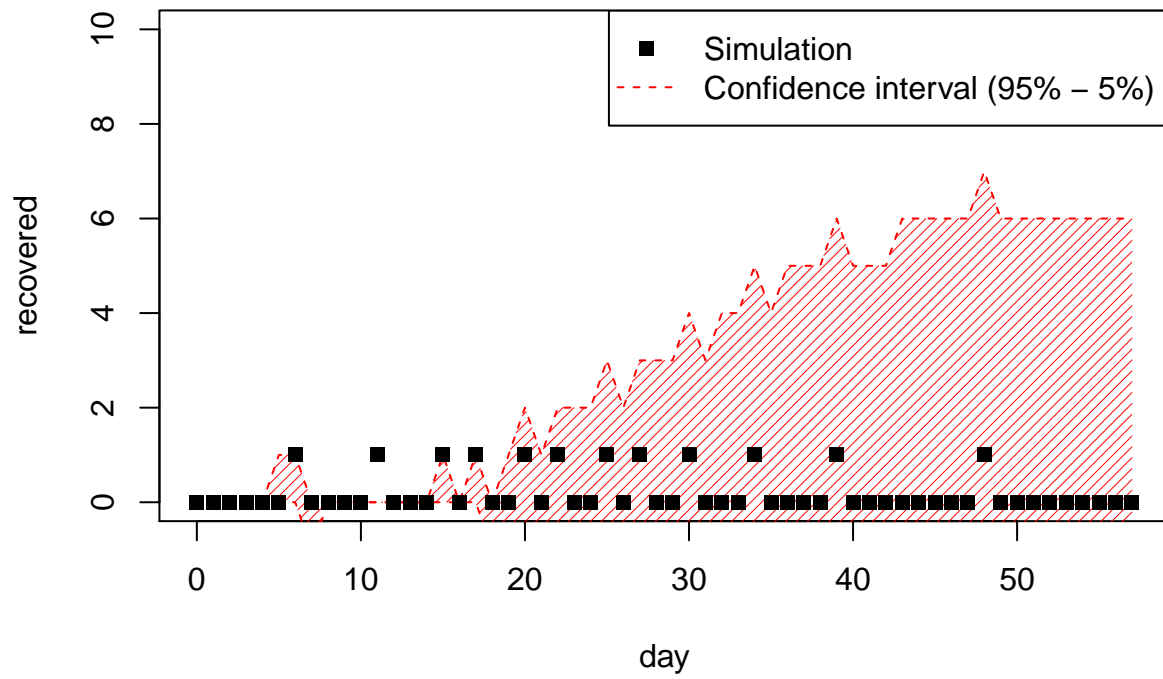


Figure 8: Recovered individuals per day with 95%-5% confidence intervals.

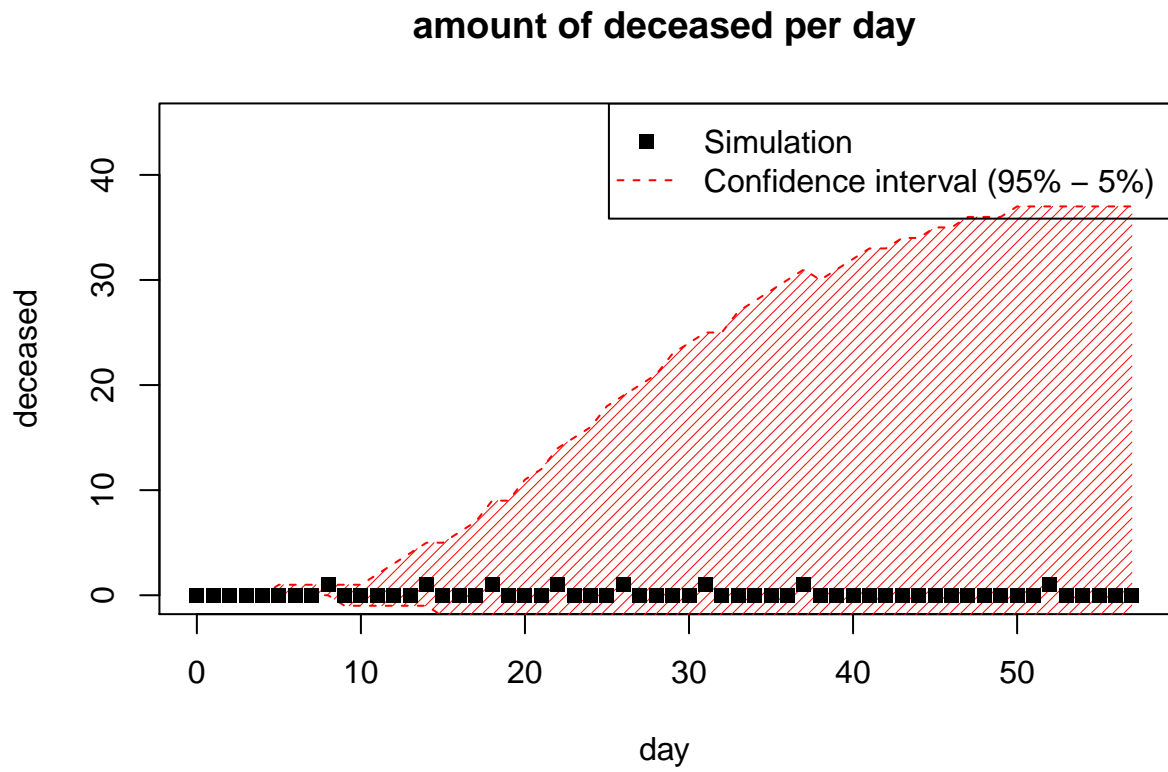


Figure 9: Diseased individuals per day with 95%-5% confidence intervals

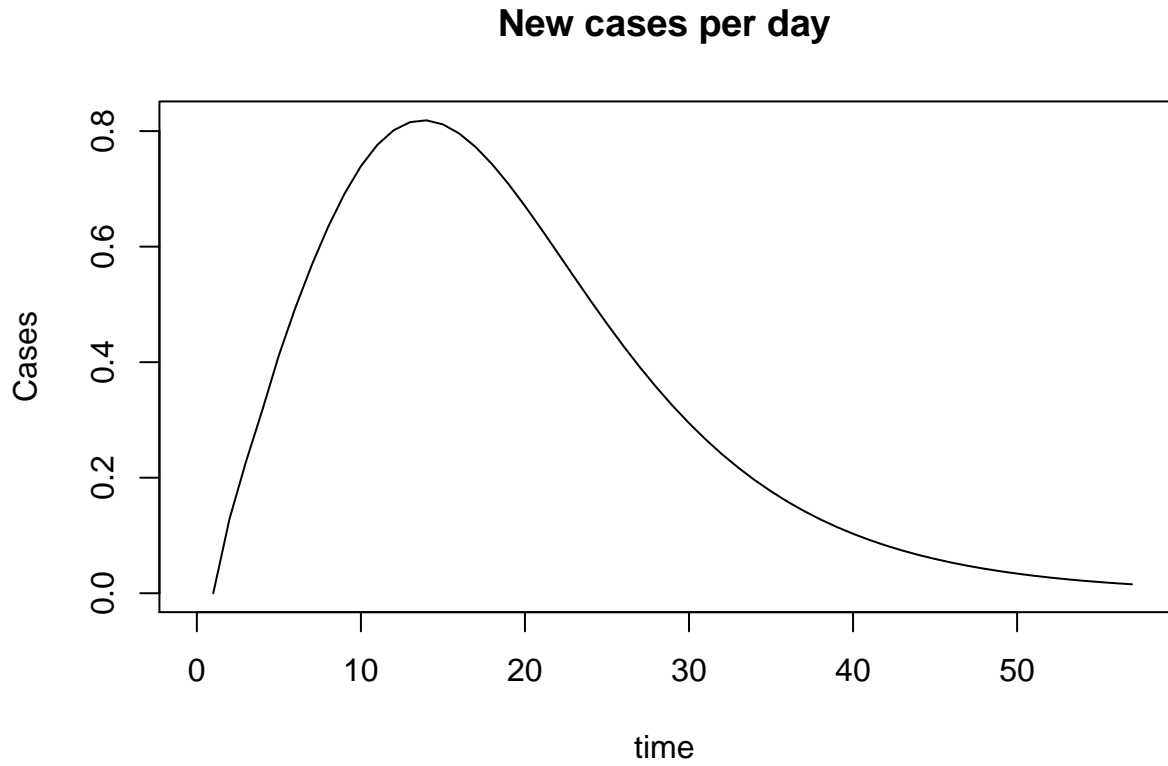


Figure 10: New cases shown per day

### 3.2 Matching the model to experimental data

Table 3: Changed initial values for the Sierra Leone outbreak

	Value
<b>S</b>	163675
<b>E</b>	0
<b>I</b>	1
<b>R</b>	0
<b>D</b>	0

Table 4: Chanced parameters for the Sierra Leone outbreak

	Value
<b>k</b>	0.011
<b>f</b>	0.39
<b>y</b>	0.135
<b>sigma</b>	0.1063
<b>t</b>	200
<b>Bo</b>	1.22e-06
<b>e</b>	2.718

## Model VS. Outbreak data Sierra Leone

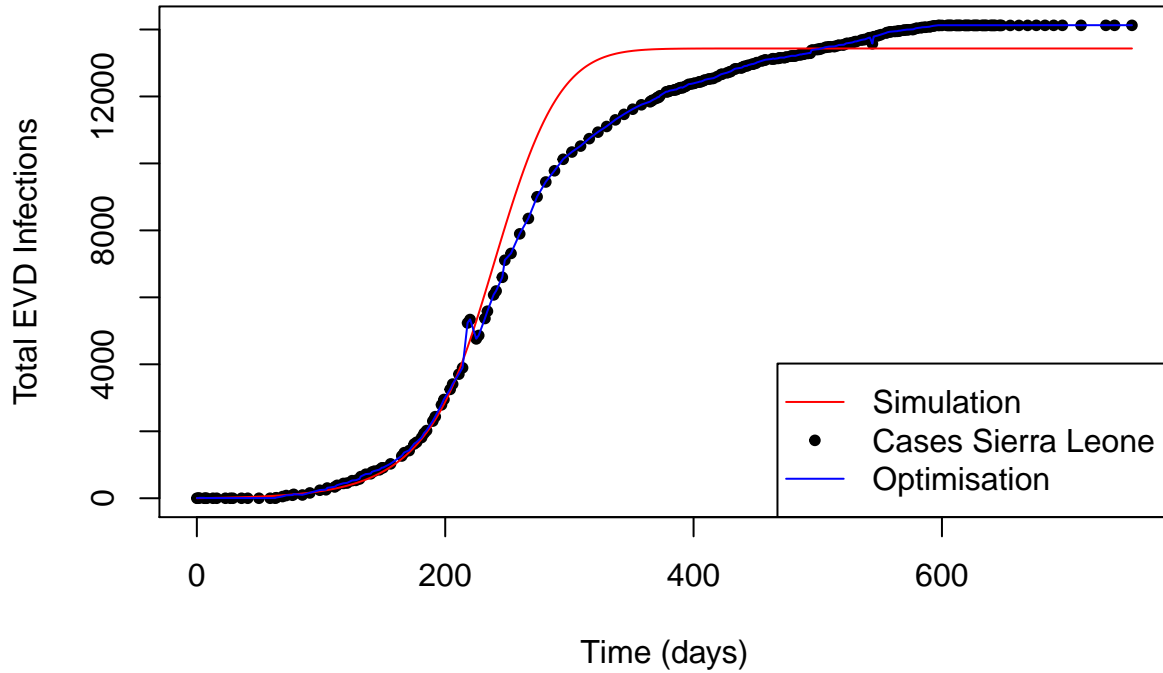


Figure 11: Model compared to other outbreak.

This plot shows the Simulation of the Sierra Leone outbreak, with the cases of the Sierra Leone outbreak next to it. The blue line in this plot is the optimisation done with the *optim()* function with the Nelder-Mead method. For this simulation was the transmission decay set to 0.011 and the time when the controlmeasures where implemented was at day 200 as can be seen in the table 4. The amount of sucseptible people was set to 163675 and we didn't change the amount of infected people at day 0. This can be seen in table 4 [4, 5]

## 4. Discussion

In the last graph the “k” variable, which stands for the rate that the transmission speed is decreased, is drastically different from our original assumptions as it was 0.19 and now 0.011. This was done because otherwise the simulation was drastically different from the outbreak data. A explanation could be that there was no real structured combatting of the infection spread in Sierra Leone. Also the time that measures were implemented were also changed from 3 to 200 days, this could just be that the outbreak wasn’t detected for a long time or just no measures were implemented.

Discussie: laat in het onderzoek kwam de fouten, optim(), review verslag was af en toe moeilijk te begrijpen, parameters, toekomst plan: andere data nemen (andere landen, andere tijden)

The model has some limitations. Firstly we can’t predict if a infected individual is maybe very outgoing and infecting lots or if that person isolates himself or gets isolated. Second we fitted our first simulations upon a very small outbreak of only 20 cases. Third we used the assumption that the infectiousness was equal over the whole period and not that there could be variations. Fourth the case location, as in hospital settings and whatnot in those quarantine locations spread would be minimal.

In our simulations we had some problems with the R code, firstly we later in the making we found that there was something wrong with the transmission decline, as the decline didn’t start at our given “t” but is started immediately which gave some weird results. Second in the paper we tried to replicate they used optim to fit the model to their data. We did try using optim but as seen by the blue line in the last graph figure: 11 it didn’t really do what we expected. Third the outbreak data from the other experiment was not available anywhere anymore so we had to judge by graph comparison and which parameters they used was also very unclear until the end.

What we’d like to experiment with further is more outbreaks in different places and times to see the differences and see if the model still applies, So that at a later date with other outbreaks this model can be used for damage assessment.



## References

1. Althaus, C. L., Low, N., Musa, E. O., Shuaib, F., & Gsteiger, S. (2015, 21 april). Ebola virus disease outbreak in Nigeria: Transmission dynamics and rapid control. Retrieved from <https://www.sciencedirect.com/science/article/pii/S1755436515000341> on 01-06-2018
2. Wikipedia, Ebolavirus. (2018, 29 mei). Retrieved from <https://en.wikipedia.org/wiki/Ebolavirus>, on 10-06-2018
3. Centers for Disease Control and Prevention (2017, 27 December). Retreved from <https://www.cdc.gov/vhf/ebola/history/2014-2016-outbreak/case-counts.html>, on 13-06-2018

# Appendix

Appendix A: The rmd file of the paper with all the code Appendix B: 2014 outbreak data