How Vaccination Coverage Level Impact Cases Observed During Ebola Outbreak in Guinea, Sierra Leone, and Liberia

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1 Introduction

Ebola, a highly infectious and deadly virus, has severely impacted various regions in Africa, highlighting the urgent need for effective epidemic management. This study examines Ebola outbreaks in Sierra Leone, Liberia, and Guinea, focusing on the basic reproductive number (R_0) and vaccination efforts. Essentially, R_0 indicates how contagious an infectious disease is.

The 2014 Ebola outbreak in West Africa was a major public health crisis affecting Sierra Leone, Liberia, and Guinea. The basic reproduction number (R_0), which indicates the average number of secondary infections produced by a single infected individual, was used to gauge the virus's transmissibility in each country. According to Aylward et al. (2014)[1], Guinea had an R_0 of 1.71, Liberia had an R_0 of 1.83, and Sierra Leone had an R_0 of 2.02. These values suggest that the virus was most transmissible in Sierra Leone.

Takahashi et al. (2015)[3] explored the impact of reduced vaccination rates due to the Ebola outbreak. They reported that the effective reproduction number (R_t) for Liberia and Sierra Leone was between 1.0 and 2.0, indicating that control could be achieved by preventing more than half of the secondary transmissions per primary case. This finding emphasizes the importance of maintaining vaccination efforts to control infectious diseases after Ebola.

Mathematical modeling and optimal outbreak control were considered essential for understanding the epidemic dynamics and developing effective containment strategies. The key research question here is: How does the implementation of the same vaccination program affect the number of infections and the spread of Ebola disease in different settings?

2 Methods

The method used here is the SEIR model that was proposed by Oduro et al. (2016)[2] using vaccination as the intervention to control the spread.
Where S are susceptible populations, E are the exposed populations, I are infectious populations, and R are recovered populations at time t.
The transmission rate due to contact with an infected human is given as β, ρ is the transmission rate due to contact with a dead human that had Ebola, μ is the mortality rate, ν is the birth rate, σ is the average incubation period, ψ is the vaccination rate, α is the rate at which the recovered lose immunity thereby becoming susceptible and γ is the recovery rate.

We also used the following parameters for the model given by [2]

Parameter	β	ρ	σ	γ	ν	μ	α	ψ	μ_I
Value	0.710	0.089	0.083	0.1	1.7	0.073	2.57	0.5	0.1

Table 1: Parameter values for Ebola model

2.1 SEIR Model with Vaccination

The representation of this model is shown in Figure 1.

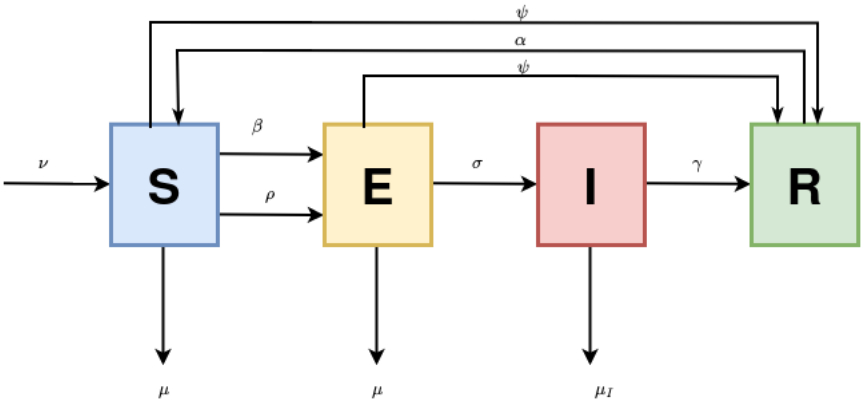

Figure 1: SEIR model of Ebola with vaccination

The equations below represent the SEIR model of Ebola with vaccination

$$\frac{dS}{dt} = -\beta SI - \rho SR - \mu S + \alpha R - \psi S + \nu \quad (1)$$

$$\frac{dE}{dt} = \beta SI + \rho SR - \sigma E - \mu E - \psi E \quad (2)$$

$$\frac{dI}{dt} = \sigma E - (\gamma + \mu_I)I \quad (3)$$

$$\frac{dR}{dt} = \gamma I - \alpha R + \psi E + \psi S \quad (4)$$

The following assumption was also used in this analysis:

- The population size is constant.
- The number of Exposed and Infected people will reduced due to the vaccination.
- The vaccination was assumed to be 100% effective.

Disease-free equilibrium point of SEIR model: At disease-free equilibrium the assumption made is that there is no disease in the population, that is $E = 0$ and $I = 0$
Setting Equations 6-9 to Zero and solving for the equilibrium state we have that the disease-free equilibrium states are

$$S^* = \frac{\nu}{\mu},\ E^* = I^* = 0,\ R^* = \frac{\psi\nu}{\mu\alpha}$$

Basic reproductive number R_0 of SEIR model: We also used the basic reproductive number as calculated by Oduro et al. (2016) given as

$$R_0 = \frac{\sigma\beta}{(\gamma + \mu_I)(\sigma + \mu + \psi)}$$

$$\beta = \frac{R_0(\gamma + \mu_I)(\sigma + \mu + \psi)}{\sigma}$$

3 Results

We used the "deSolve" library in R to simulate the solutions of the ODE in Equations 1-4 and the "tidyVerse" library in R to organize the results in a data frame. Below are the results from the SEIR model.
Below is an example of the epidemic cases in Liberia

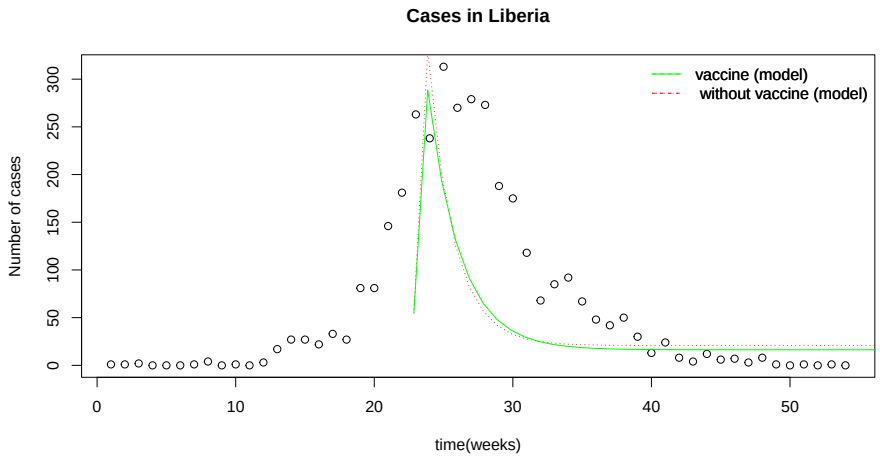

Figure 2: Model of the cases in Liberia with and without vaccination

Using the parameters estimates in Table 1 and the R_0 values for the different countries and using different infectious rates that is, σ = 0.099 for Sierra Leone, σ = 0.069 for Guinea, σ = 0.078 for Liberia we have the following plots in Figures 3 and 4.

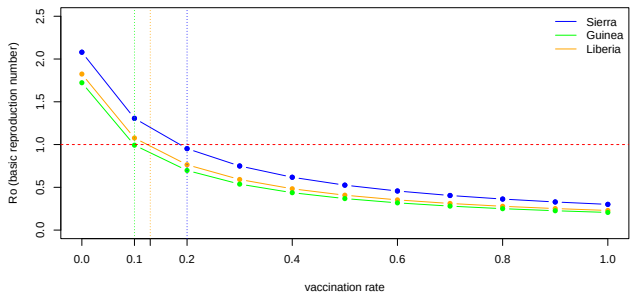

Figure 3: Variation of R_0 with vaccination rates for three countries

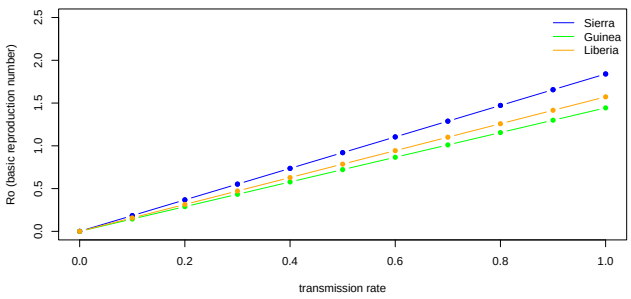

Figure 4: Transmission rate vs R_0

Also, we showed that a high vaccination rate and low transmission rate results in low R_0 and that a low vaccination rate and high transmission rate results in high R_0 as seen in Figure 5.

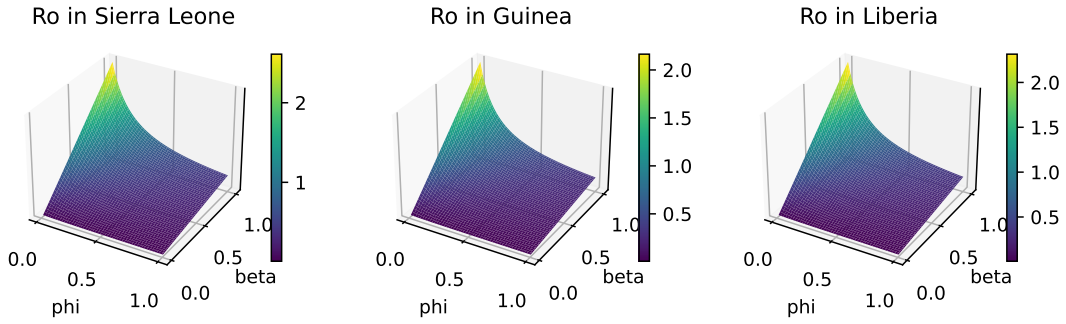

Figure 5: Variation of R_o with vaccination rate(ψ) and transmission rate(β)

Using vaccination coverages of 20%, 60%, and 90% for each country, we obtain the following plot in figure 6.

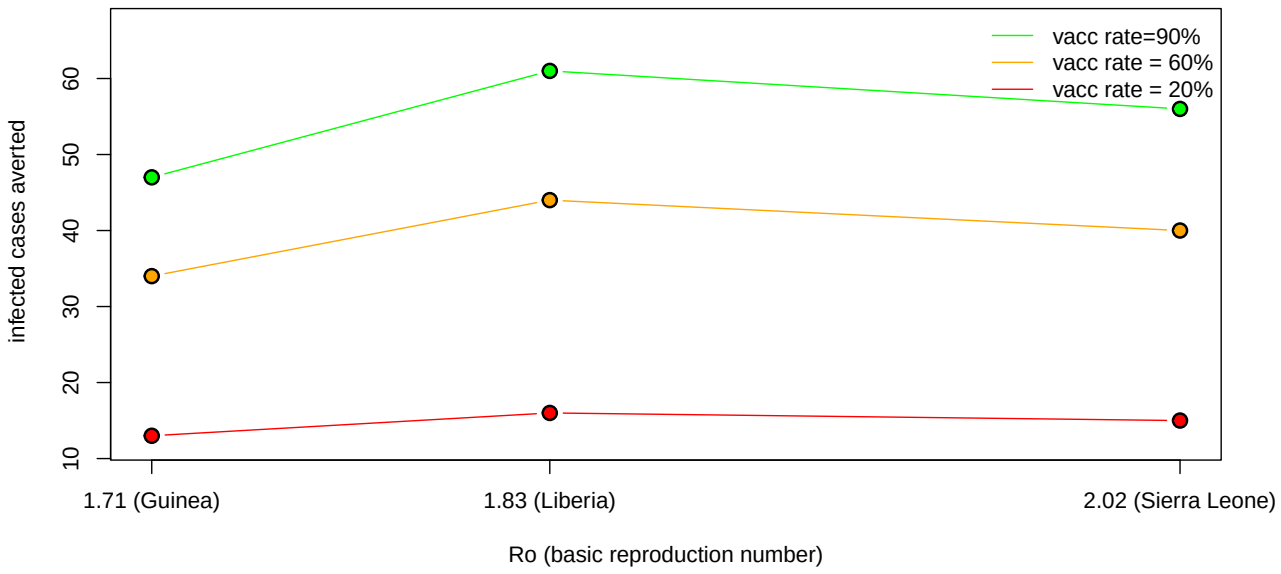

Figure 6: Variation of number of averted cases with different vaccination coverages.

4 Discussion and Conclusion

From the epidemic data from Sierra Leone, Liberia, and Guinea, we have seen increases in cases averted with increasing vaccination coverages (20%, 60%, and 90%), as shown in Figure 6.

We also showed that as vaccination rates increase, the basic reproduction number R_0 decreases exponentially across the three countries as shown in Figure 3. This indicates that vaccination effectively reduces the disease's transmission potential by lowering the number of susceptible individuals.

Figure 3 demonstrates the relationship between vaccination rates and the basic reproduction number (R_0) across the three countries. The plot shows a clear direct relationship: as vaccination rates increase, R_0 decreases. This trend is consistent across Sierra Leone, Guinea, and Liberia, indicating that vaccination is a highly effective intervention in reducing the transmissibility of Ebola.

The data suggests that even fair increases in vaccination treatment can significantly lower R_0. For instance, with a vaccination rate of 20%, the R_0 values drop below the critical threshold of 1 for all three countries. This threshold is crucial as an R_0 below 1 indicates that the disease will eventually die out in the population. Therefore, achieving and maintaining high vaccination rates is essential for controlling and eventually putting an end to Ebola outbreaks.

References

[1] Aylward B. et al. Ebola virus disease in west africa - the first 9 months of the epidemic and forward projections. *New England Journal of Medicine*, 371(16):1481–1495, 2014.

[2] F. T. Oduro1 et al. Optimal control of ebola transmission dynamics with interventions. *British Journal of Mathematics Computer Science*, 19(1):1–19, 2016.

[3] Takahashi et al. Reduced vaccination and the risk of measles and other childhood infections post-ebola. *Science*, 2015:347, 2015.

5 Appendix

5.1 Contributions

Comfort Jones
I assisted Pontsho in writing, editing, and proofreading of this report, poster, and presentation slides for this research. I also worked with Herman and Wisdom on the R Codes used for the analysis.
Nkateko Pontsho
I worked with Comfort on the literature review, introduction for the slide, poster, and research project. I also worked on typing parts of the slides, poster, and research project.
Herman Franclin
During the first two days of the week, we collaborated as a group to read papers and discuss in order to formulate a research question. Thereafter, I primarily focused on the coding aspect to implement the workflow we had established, and generate the illustrative graphs necessary to support our final statement.
Wisdom Aduah
I wrote the code to prepare the dataset into a form that is appropriate for our analysis. I also refined the final version of the report.

5.2 Data and Code Accessibility

The datasets used for this research were obtained from the MMED 2024 website which was culled from "Humanitarian Data Exchange" and the R code for this analysis can be accessed Here.