

Expediting the Eradication of Ebola

Team #38722

February 9, 2015

Contents

1	Introduction	2
1.1	Outline of Our Approach	2
1.2	Assumptions	2
2	Estimating the Amount of Medicine Needed Using the SEIR Model	3
2.1	Estimates on Current Interventions	4
2.2	Fitting the model to data	4
2.3	Ceasing the Spread	5
2.4	Prioritizing the Distribution	5
3	Delivering the Medicine	5
3.1	Route Optimization Using Prim's Algorithm	6
4	Case Study on Sierra Leone	8
4.1	Model predictions for Sierra Leone	8
4.2	Delivery Method	9
5	Weaknesses and Improvements of Our Model	10
5.1	Fruit Bats and Future Outbreaks	10
5.2	Effects of Population Mixing	10
5.3	If the Cure is a Vaccine	10
6	Conclusion	10
7	Executive Summary	10
	References	12

1 Introduction

The Ebola outbreak in West Africa has been a problem for much of the last year. Now the world medical association has announced that there is a cure available for Ebola. In this paper, we present a computerized model to optimize the eradication of Ebola with a cure developed. Our goal is to present a model for the eradication of Ebola focusing on these points:

1. Cease the spread of Ebola.
2. Determine a minimum amount of the cure required to eradicate Ebola.
3. Choose reasonable locations to deliver the cure.
4. Develop a feasible and efficient delivery system for the cure.

1.1 Outline of Our Approach

The first part of our paper will devote on the theoretical framework of the model and the implementation on a computer. The remaining part of our paper will discuss the implication of our model on one of the major infected country Sierra Leone and will assess the validity of our model. In our case study, we will perform the followings:

- **Calculate the minimum amount of medicine needed** from the SEIR Model in ceasing the spread of the disease. This will also give some information on severity of the infection throughout the districts in Sierra Leone.
- **Find a quickest path** using Prim's algorithm in distributing the medicine to needed districts once the medicine arrives.
- **Determine how the resources will be distributed** accordingly with the constraints such as the number of patients in each districts, quantity of medicine produced, or number of available trucks.

1.2 Assumptions

Our relatively simple model relies on several reasonable assumptions that we believe will not change the result much:

- **The new medication that the world medical association announced is a treatment, not the vaccine.** So the cure will only affect people who are infected and showing symptoms of Ebola.
- **Deceased people by Ebola are buried or cremate immediately and safely.** Thus the deceased does not affect the spread of Ebola. Currently, there has been great efforts being taken to safely dispose of corpses. [?]

- **People in infected areas are not allowed or able to travel outside of West Africa.** Anyone who contracts Ebola outside of Sierra Leone, Guinea, and Liberia will be isolated and given medical care quickly such that Ebola will not spread outside of the three countries listed. Until now, only those three countries have shown a lack of ability to contain and eradicate Ebola [?], so we do not need to worry about Ebola spreading outside of those countries so long as the surrounding areas remain vigilant for potential outbreaks.
- **Curing one person requires one dose of medicine per day.** Also, the cure will increase patients' recovery speed and chances of survival. Quantifying these will let us make estimates for how much of the cure is needed, how it will affect infection and fatality rates.

2 Estimating the Amount of Medicine Needed Using the SEIR Model

The transmission of the Ebola virus follows a Susceptible-Exposed-Infectious-Recovered (SEIR) stages. The SEIR model is a deterministic compartmental model with its compartments providing an accurate abstraction of the various stages of some diseases. Ebola is one such disease amenable to the SEIR model. Those stages can be described through following set of ordinary differential equations: [1]

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta SI}{N}, \\ \frac{dE}{dt} &= \frac{\beta SI}{N} - \sigma E, \\ \frac{dI}{dt} &= \sigma E - \gamma I, \\ \frac{dR}{dt} &= (1-f)\gamma I.\end{aligned}$$

where β is the transmissibility of a disease, N is the size of the total population under consideration, σ is 1 over the incubation period, γ is the recovery rate, and f is the fatality rate.

Once an individual contracts Ebola and eventually becomes infectious, all other population become susceptible S to catching the virus. The individual who contracts Ebola undergoes an incubation period E where symptoms are not apparent and he/she is not yet infectious. Then the individual enters a infectious stage I . Finally, the individual either recovers (R) and survives or dies. Individuals belong to the compartment R are no longer susceptible to the virus.

Unlike many compartmental models, Ebola has a strong potential to cause death. Thus, in many models N remains constant, but for Ebola N decreases at a rate of $f\gamma I$. This is the death rate and can be written as dD/dt . The rate of change of cases of Ebola will be modeled by $dC/dt = \sigma E$.

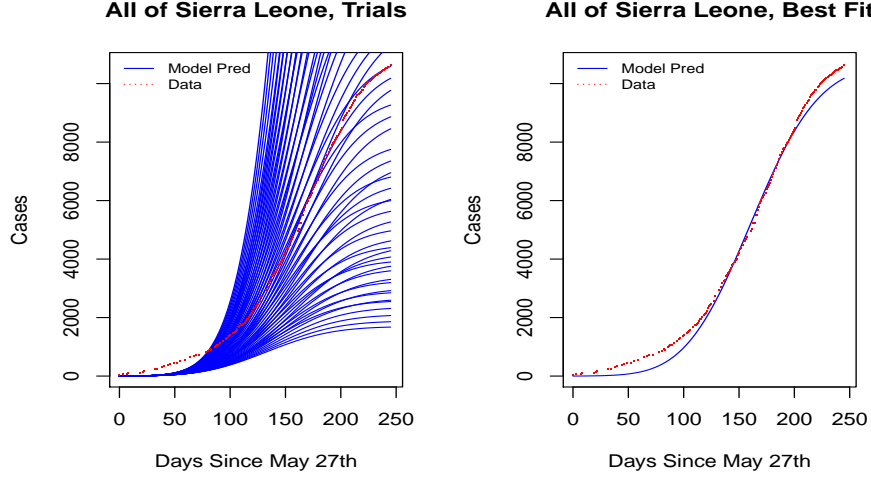


Figure 1: Best fit function of cases in Sierra Leone

2.1 Estimates on Current Interventions

There has been quite an effort trying to contain the spread of Ebola in many countries. For those countries with interventions, it is known that the transmission rate β for a disease decays exponentially. [2] Thus, we will assume the rate is of the form

$$\beta(t) = \beta_0 e^{-\kappa(t-\tau)}$$

where β_0 is an initial transmission rate, τ is the time that the intervention begins, and the decay rate κ scales the intensity and effectiveness of the intervention.

2.2 Fitting the model to data

We used the statistical computing language R in solving above four ordinary differential equations and find a best fit for the parameters. First, we use the average duration of the incubation and infectious period from the paper with similar Ebola case in Congo in 1995: $1/\sigma = 5.3$ days and $1/\gamma = 5.61$ days. [7] Then, our model determines the parameters β_0 , κ , and f .

We allowed β_0 , κ , and f to vary depending on the specific population being modeled. To determine β_0 and κ for a given population, we minimized the sum of the squares of the differences between our model and the data for the *total number of cases of Ebola* based on a large sample of different β_0 and κ values to see which values gave the best fit. To get the value for f , we employed a similar minimization of the sum of squares, but compared to the data for the *total number of deaths from Ebola*. See figure 1, which shows the model estimation for data in Sierra Leone.

2.3 Ceasing the Spread

From our SEIR model, in order to cease the spread of Ebola, we need to reduce the magnitude of

$$\frac{dS}{dt} = -\frac{\beta SI}{N}.$$

In other words, we would like to reduce the rate of susceptible people getting infected. In order to achieve this, we need to

1. decrease the β , the rate of infection, and
2. decrease the I , the number of infected people.

Increasing the intervention level such as more doctors and precise detection method in will decrease the β .

The effective way to decrease I is to make closer to

$$\frac{dI}{dt} = \sigma E - \gamma I < 0,$$

which we can achieve it by increasing γ , a recovery rate. However, notice that the recovery rate will naturally increase if we distribute the cure to infected people.

Therefore, the efficient methods in distributing the medicine will solve the large part of problem of halting the spread.

2.4 Prioritizing the Distribution

The key parameter describing the spread of an infection is the effective reproduction number

$$R_e = \frac{\beta}{\gamma} \frac{S(0)}{N} \approx \frac{\beta}{\gamma}$$

which is defined as the average number of successful transmissions per infected person. [5] If $R_e < 1$, the epidemic eventually stops. [6]

We can prioritize the cite of distribution accordingly by calculating each R_e values separately and comparing. Higher R_e value represent the higher average number of successful transmission, so if we have constraints on the supply of medicine, we need to prioritize the delivery to the places which have a higher R_e value.

3 Delivering the Medicine

In this section, we will describe how the medicine will be distributed in a most efficient manner. We will assume that every Ebola treatment centers has a capacity to hold certain amount of medicine. Also, we will assume that there are roads connecting each districts and health facilities.

Sine we will not be able to deliver the cure individually, we will send the cure to existing Ebola treatment centers. These are typically located near existing Ebola outbreaks, so it is an excellent position to make use of the cure.

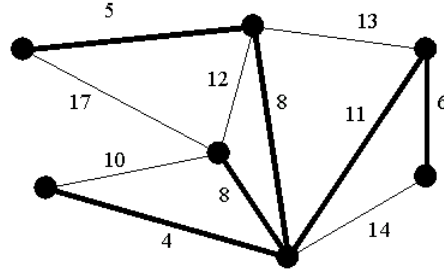


Figure 2: The bold line is the route that minimize the cost of traveling

3.1 Route Optimization Using Prim's Algorithm

The point of route optimization is to expedite distribution of the cure, get an estimate of the resources required to distribute the cure, and to make it cheap. Our primary resource for distribution is truck hours: the time spent driving for trucks distributing the cure. Due to differing road conditions between highways and the roads connecting district capitals to Ebola treatment centers, we decided to break the route up into those two components to make estimating the travel time. We assume that the cure is delivered to the district capitals via the highways, and from there the cure is distributed to the treatment centers.

Our chosen method of constructing a fast route for delivering the cure to the district capitals is to treat the target area as a graph, and make a minimum spanning tree of the graph that represents the route. The district capitals are treated as vertices and the roads between them as edges. The weighting of an edge is best done in truck hours required to drive along the edge as this is the prime resource we are considering. Minimum spanning trees have a couple of nice properties. See Billey for details.

The first is when the weights of the edges of the graph represent Euclidean distances between the vertices; the total weights of the edges of a minimum spanning tree form a lower bound for the fastest possible route through the graph. A full traversal of the minimum spanning tree starting from a certain vertex and returning to it is, at worst, half as fast as the best possible route through the graph. While in practice the roads between cities are not straight, the time it takes to travel between cities by truck are frequently approximately linearly related to the Euclidean distance between them. Because of this a minimum spanning tree makes a pretty good route for distribution.

The second property is that there exist algorithms that generate minimum spanning trees in polynomial time. We used Prim's algorithm, and its worst case run time is $O(N^2 * \log(N))$ [Billey].

Due to a lack of good information on local roads in districts, getting an optimized route to distribute the cure to the Ebola treatment centers within each district is not something we try. Instead, we aim to get a reasonable estimate of the truck hours needed to distribute the cure within the districts. To do this the

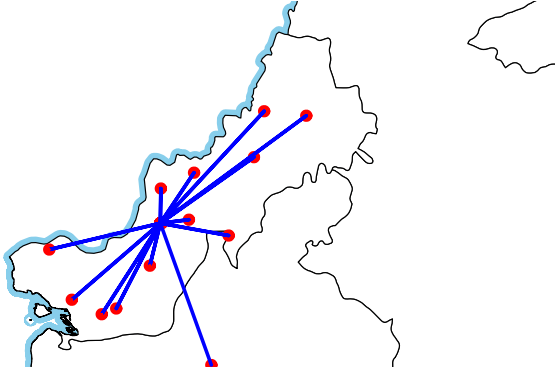


Figure 3: Using Euclidean distances within the district

locations of the treatment centers and district capitals are needed. It is easy to get the locations of the capitals from Google Maps. The locations of most of the treatment centers can be found from <http://data.hdx.rwlab.org/dataset/travel-distance-and-time-chart/>. Our estimate of truck hours is based on the assumption that the average time it takes a truck to get from the district capital to a treatment center is based on the Euclidean distance separating them. Because the locations are given in latitude and longitude, the differences in these measurements between the individual treatment centers and district capitals are converted into kilometers, summed up, and multiplied by 2 because the roads will not be straight. To convert this distance into truck hours multiply the total estimated distance of treatment centers to district capitals by 2 times the average hours required to travel one kilometer on highways by trucks. The factor of two is in there because the trucks probably will not be able to travel at highway speeds along the roads that connect district capitals to Ebola treatment centers. This gives us the total truck hours needed to distribute the cure within the districts.

Combining twice the sum of the edges of the minimum spanning tree with the total truck hours needed to distribute the cure within the districts produces the total number of truck hours needed to fully distribute the cure. This can be used to calculate the number of trucks needed to distribute the cure.

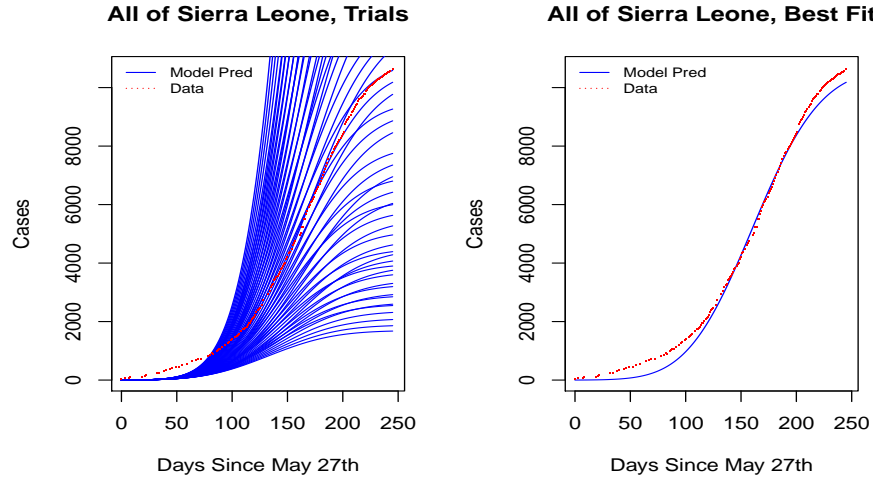


Figure 4: Best fit function of cases in Sierra Leone's district

4 Case Study on Sierra Leone

In this section, we apply the models presented in previous sections to Sierra Leone which is one of the seriously affected country in the West Africa.

4.1 Model predictions for Sierra Leone

We now suppose that we have a cure for Ebola. It would be foolish to assume that though this cures Ebola at a 100 percent efficiency rate, distrust of the government and other factors are still prevalent in Sierra Leone and hospital beds can be in limited supply. Thus, we assume the medicine has effectiveness c , which we incorporate into our model by adjusting the recovery rate $\gamma \rightarrow \gamma + c$. We can then use our model and integrate the number of future infections out to infinity, obtaining the following results:

Model forecasts based on c -values ($c = 0$ assumes no cure is being used)

c -value:	0	0.1	0.2	0.3	0.4	0.5
Expected future cases:	3549	3194	2836	2484	2129	1775

Thus, a medication that works only half the time, will reduce the total number of cases by half by the time the disease dies out.

Our model also predicts the effective reproductive number R_e to be 0.6710 in Sierra Leone. This would imply that Ebola is already on the decline. This means that our medication may not be necessary for the eradication of the disease, but would no doubt speed up the process and save many lives.

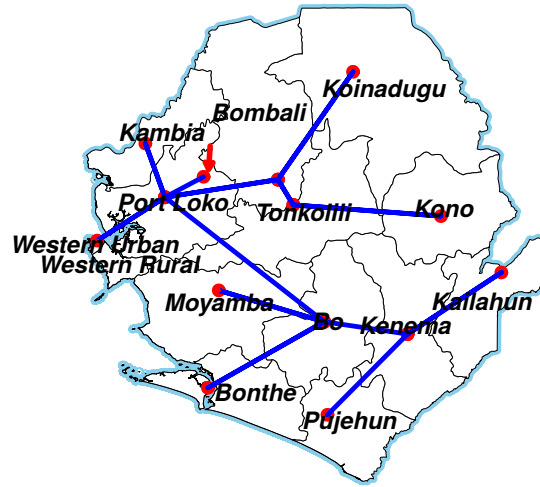


Figure 5: The optimal route between districts in Sierra Leone

4.2 Delivery Method

To determine an estimate for the number of truck hours required to make a full distribution of the cure for Sierra Leone we used the method described in the Route Optimization section. We were fortunate to have found a table of truck hours required to travel between the districts, as well as a corresponding table of distances [citation needed]. Using capitals in each districts as nodes on the graph and this data as weight on the vertices, we can find a minimum spanning tree using Prim's algorithm described in Section 4. Double the sum of the truck hours corresponding to the edges gives us 49 truck hours needed to distribute the cure throughout the district capitals from Lungi International Airport. From the location data of the Ebola treatment centers and the district capitals we got an estimate of 207 truck hours needed to distribute the cure within the districts. Thus a total of 256 truck hours are required to fully distribute the cure to all the Ebola treatment centers in Sierra Leone.

A price estimate for total fuel cost of doing a full distribution is done by converting truck hours into kilometers, dividing by an estimated 35 kilometers per gallon of diesel, and multiplying by the price of diesel. The result is \$1,107.31. Converting truck hours into kilometers was done by comparing the table of truck hours to the table of distance.

5 Weaknesses and Improvements of Our Model

5.1 Fruit Bats and Future Outbreaks

Fruit bats are thought to be a natural host for Ebola [www.who.int]. This means that future outbreaks can occur in human populations when there is contact with an infected bat instead of an infected human. Our model does not consider the possibility of a population being infected multiple times. This will not make a large difference in how the population is dealt with so long as people are alert to the possibility, and new cases are watched for. It will also help if people avoid contact with bats.

5.2 Effects of Population Mixing

Population mixing was something we wanted to use in our model, but did not due to a lack of data and time. Currently our model predicts the spread of Ebola within a population as a number of cases, but with a good model of population mixing we could predict where new cases are likely to appear. That would help by giving us a better idea as to where the cure should be sent.

Quarantines, border closures, and bad roads or lack of vehicles limit population mixing. All of these things are significant in West Africa. Although we did not use population mixing in our model, β from our model incorporates the effects of population mixing to some extent.

5.3 If the Cure is a Vaccine

It is possible that the cure may be a vaccine instead of a medicine used for treatment. If the cure is a vaccine we will leave γ alone, multiply the mortality rate by something less than 1 but great than zero, and take vaccinated people out of the S and E groups and put them into R. In English this means that using a vaccine will reduce the number of people getting Ebola by make people immune.

6 Conclusion

Modeling real world epidemiological data has proven to be a very difficult. It is impossible to account for all of the intricate interactions at the individual and community level. While we were able to fit the data reasonably well, the variability was too high to make confident predictions about the future.

7 Executive Summary

The Ebola outbreak in West Africa has been a newsworthy problem for much of the last year. Now the world medical association has announced that there is a cure available. In this paper, we present a model to optimize the eradication

of Ebola using the cure. The focus will be on: Halting the spread of Ebola. Determining a minimum number of the doses of the cure required to eradicate Ebola. Choose reasonable locations to deliver the cure. Develop a feasible and efficient system for delivering the cure.

Our model of choice for predicting the spread of Ebola is the SEIR model. It models a population by splitting it into Susceptible, Exposed, Infectious, and Recovered stages, and calculating how the individuals in the population move through these stages as time passes. The flux of the population through the stages depend strongly on how easily Ebola is transmitted, the rate people recover from being ill represented by γ , and how many people are infectious.

How the cure interacts with the SEIR model is an important assumption. We are assuming that the cure is a medicine that is used on a sick person to cure them of Ebola. It is not a vaccine, but a method of treatment that requires one dose per day that greatly improves recovery speed and strongly reduces the mortality rate. This means the cure will aid in the extermination of Ebola by rapidly reducing the proportion of the population that is infected so that fewer people will be exposed to Ebola.

Spatial spread of the disease is not something the SEIR model calculates. That would make it very hard to predict where Ebola will spread to. However, because Ebola is so widely spread in Guinea, Sierra Leone, and Liberia while the surrounding countries have managed to suppress and eradicate Ebola within their own borders, we will assume that most of the spread of Ebola will be within already infected areas. Thus, while being able to account for spatial aspects of spread such as population mixing would improve the model, it is good enough to make useful predictions as it is.

In our cases study of Sierra Leone our model we predict 3,549 future cases of Ebola when $\beta = 0.178$, which is its baseline value without the cure. If we assume the cure increases the value of β to 0.378 then our model predicts there will be 2,836 future cases, and if β becomes 0.678 with the cure there will be only 1,775 future cases.

As for determining how to distribute the cure, we recommend using trucks to distribute the cure within afflicted countries. The truck routes can be made fast by creating a minimum spanning tree of the roads between distribution points. We recommend using currently existing Ebola treatment centers as the distribution points as they are typically near existing Ebola outbreaks.

References

- [1] Chowell G, Hengartner NW, Castillo-Chavez C, Fenimore PW, Hyman JM. (2004) The basic reproductive number of Ebola and the effects of public health measures: the cases of Congo and Uganda. *J Theor Biol*, 229(1):11926.
- [2] Lekone PE, Finkenstädt BF. (2006). Statistical inference in a stochastic epidemic SEIR model with control intervention: Ebola as a case study. *Biometrics*, 62(4):1170–7.
- [3] Billey, Sara. Discrete Mathematical Modeling: Math 381 Course Notes, University of Washington, Winter Quarter, 2011.
- [4] <http://www.cdc.gov/vaccines/programs/vfc/awardees/vaccine-management/price-list/index.html>
- [5] Vynnycky E, White RG (2010) *An Introduction to Infectious Disease Modelling*. Oxford: Oxford University Press.
- [6] Althaus CL. Estimating the Reproduction Number of Ebola Virus (EBOV) During the 2014 Outbreak in West Africa. *PLOS Currents Outbreaks*. 2014 Sep 2. Edition 1. doi: 10.1371/currents.outbreaks.91afb5e0f279e7f29e7056095255b288.
- [7] Chowell G, Hengartner NW, Castillo-Chavez C, Fenimore PW, Hyman JM. (2004) The basic reproductive number of Ebola and the effects of public health measures: the cases of Congo and Uganda. *J Theor Biol*, 229(1):11926.