Team 41932

Eradicating Ebola (Problem A)

February 5-9, 2015

Executive Summary

We distribute the world medical association's newly announced drugs and vaccines to needy areas in Sierra Leone, Guinea, and Liberia, countries worst hit by Ebola, by anticipating the number of infected individuals. That way, there is enough time for the drugs to be prepared and delivered. According to our predictive model, we update the number of the infected individuals in time steps. We observe that the number of people susceptible to Ebola decreases. Additionally, we encourage a vaccination protocol to be practiced. Among other things, we find that randomizing who first gets vaccinated is the optimal vaccination method. Furthermore, Ebola in Liberia can be eradicated within a year.

We then construct the architecture to produce delivery times. Using geographic data and infection rate data, we suggest that Monrovia, Liberia, Freetown, Sierra Leone, and Conakry, Guinea be the points where vaccines and drugs are first unloaded. We devise a way to determine the need for new Ebola treatment centers and we also show how to distribute the vaccines and drugs.

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Letter to the World Medical Association

To the World Medical Association:

We are confident that the number of Ebola cases will fall significantly given the implications of new drugs and vaccines from your previous announcement dated 5 February 2015. You may wish to quote the following statement:

"Research Team 41932 has developed a model that accounts for as many variables as possible related to the infection rates of Ebola, drawn from data easily measurable at the Ebola treatment centers and estimates from community centers, to predict future infection rates. The team's model highlights the importance of many factors, such as safe funerals.

There are constraints which affect the distribution of drugs and vaccines, like the amount of drugs which can be transported. By using our prediction model, doctors can use the predicted infection rates to determine the future number of patients. Consequently, they can prepare transport trucks for drugs in a timely manner and minimize waste, in case an unpredicted outbreak arises.

The vaccination program is the most effective component of eradicating Ebola; with sensible procedures like quarantines and thorough screening of hospital patients for Ebola, West African countries like Liberia will be rid of the menace of Ebola within a year. The researchers suggest constructing another treatment center in Guinea to increase the access to medicine and to shorten the distance locals and delivery trucks need to travel. To support the effort to stop the Ebola epidemic, the team also provides a way to visualize where the drugs and vaccines should be distributed.

Our research's value lies in the predictive function for future infection rates. The future infection rates can be used to determine the optimal allocation of doctors, for instance. Our model represents the whole process of how Ebola is spread, so the world medical association may be interested in tailoring our model specifically to decompose the spread of future diseases.

We created our models to help you understand and visualize what is happening. Thank you for giving us the opportunity to help you win the noble fight against Ebola.

Respectfully,

Team 41932

1. THE PROBLEM

We are tasked with eradicating Ebola. The solution we propose accounts for multiple considerations, such as the infection rate, the population susceptible to Ebola, quantities of drugs and vaccines, number of healthcare workers, and the time delay between the start of production for a vaccine and its delivery in West Africa to patients. We primarily focus on Sierra Leone, Guinea, and Liberia.

The world medical association claims to have found a medicine that "could stop Ebola and cure patients whose disease is not yet advanced." We interpret "medicine" as the combination of "drugs" (an umbrella term that encompasses anti-fever or anti-infection medication, as well as auxiliary materials like IVF tubing) and "vaccines" (which are specifically meant to provide immunity against Ebola).

To stop Ebola requires an immunization vaccine, whereas to cure patients already infected requires drugs. For the former case, there are two candidates, one of which the world health association may be referring to: GlaxoSmithKline's ChAd3-ZEBOV vaccine and NewLink Genetics' and Merck Vaccines' rVSV-ZEBOV. Curing patients whose disease is not yet advanced suggests some sort of combination of blood transfusions with an antiviral medicine like favipiravir [1]. To avoid loss of generality, our model arbitrarily chooses one of the vaccines and any potential antiviral on the market.

1.1 Essential Background Knowledge for Eradicating Ebola

Ebola is a virus which is spread from the bodily fluids of people who were infected or died from Ebola, and it is probably of animal origin (viz. fruit bats or primates). Mathematically modeling the spread of Ebola is simplified because only individuals who are in direct contact with those suffering or dying from Ebola are exposed; therefore, to understand the spread of infection, all one needs to consider are the ways a person may be in contact with an infectious person. Even if

Ebola mutates (as many viruses do), it is not expected that Ebola will become airborne in a human lifetime [2], so the intuition behind the model remains valid.

Although our model accommodates eradicating Ebola worldwide, it is most relevant to West Africa where poor infrastructure cannot support transporting medicine as effectively as in developed countries (so it is especially important to efficiently predict future needs). Since West Africa is experiencing an Ebola epidemic, our model strives to make as much of a positive contribution overall as possible [3].

Our model covers as many stages of the Ebola diagnosis and treatment process as possible, by accounting for delivering supplies to dedicated Ebola treatment centers and the quarantines at the district hospitals and transitional care facilities. A recent paper, the "Rapid Assessment of Ebola Infection Prevention and Control Needs in Six Districts, Sierra Leone, October 2014," informs our report [4].

1.2. Global Assumptions

Our report does not take any consideration of the financial constraints of conducting operations to eradicate Ebola. The reason being is that it is in the world's best interest to be rid of Ebola, and there is a precedent from past epidemics of pledges for large donations. As of February 7, 2015, $1.23 billion has been contributed to the fight against Ebola in Sierra Leone, Guinea, and Liberia [5].

We also assume that any frictional processes, such as politics or bureaucracy, are negligible, and do not significantly affect the delivery time of the drugs and vaccines.

Since West Africa is in the midst of an epidemic, we assume that steps such as producing risk communication messages are already being implemented [6]. Our model aims to establish the medical supply needs of localities where infection is already present.

We finally assume that any patients who have recovered from Ebola abstain from sexual contact with partners for 3 months, so that any remaining Ebola viruses in bodily fluids like semen will not be spread [2].

The World Medical Association may wish to note that the only assumption related to Ebola in our model is that it requires direct transmission of fluids for it to be spread. Therefore, our model can be applied to similar diseases.

2. PREDICTING THE NUMBER OF INFECTED INDIVIDUALS

Our goal is to address the needs of localities in Sierra Leone, Guinea, and Liberia as effectively as possible. We attempt to predict the infection rates in Sierra Leone, Guinea, and Liberia using a differential equation model whose inputs include other observable rates. Then, using the **Two-Step Adams-Bashforth** method of approximating differential equations, we solve for the predicted infection rate. We choose the Adams-Bashforth method because it saves information from two time steps ago as opposed to how Euler's method is forgetful after one step. This will reduce the amount of error in predicting future infection rates.

Furthermore, another motivation of why we decide to exploit the Adams-Bashforth method of second order is because the two equations we use in our model are both first order ordinary equations that clearly interact with one another, which behaves almost equivalently to a second order differential equation.

We purposely make our definitions only infection-specific, in the sense that observations from either large national datasets or from small towns can be imputed to produce a prediction for a particular area's infection rate. We suggest implementing our model in many towns so that a more detailed picture of Ebola's infection rate can emerge when seen at the national level.

2.1. Current Data

Using data from the World Health Organization, we produced maps which indicate the current numbers of infection [7]. In our simulations, we use these as initial conditions. To avoid biasing our model as much as possible, we seek to find coefficients for national data, rather than allow them to be left as variables for each regional treatment center, so that a greater amount of variability is captured and intrinsic in our equations.

2.2. General Form of Predictive Equation for Infection Rate

One modeling assumption is that the total number of those infected with Ebola is much less than that of the general population. This makes sense, since, for instance, the total population of Sierra Leone is roughly 6 million; the total number of Ebola cases in Sierra Leone is roughly 11 thousand, which is several orders of magnitude smaller [8]. Therefore, we do not consider any relationships which are of higher-orders. We keep in mind that in an ideal scenario, as with any infections with successful intervention, the number of people infected should decrease exponentially.

We break down the equation for the change in the number of infected individuals by place from living people and the corresponding death rates by place (community or hospital). We provide the general form of our model below:

$$\frac{dI}{dt} = r_C \cdot (I - Q) + r_Q \cdot Q$$

Notation:

- I is be the number of those infected in a given time.

- Q is the number of Ebola patients. In this paper we say "patients" to mean those infected individuals who are hospitalized (who are therefore under quarantine).

- $(I - Q)$ is the number of infected individuals in the community who are therefore not under quarantine.

- r_C is the rate of change of infected individuals observed in the community, per infected person in the community. We discuss r_C more thoroughly in section **2.4**.

- r_Q is the rate of change of infected individuals from a hospital environment, per person hospitalized. We discuss r_Q more thoroughly in section **2.5**.

After looking at several publications in the literature about modeling epidemics, we then chose what processes contribute to the spread of Ebola [9].

2.3. Vaccination and Quarantine Considerations

Once someone is sent to the hospital and displays Ebola symptoms, they should be quarantined. However, the quality of such quarantines may be dubious due to the stressful circumstances hospitals and Ebola treatment centers may be facing [4]. For this report, while quarantines are effective, at least relative to the no-quarantine situation, we consider the chance that infection may spread within a hospital.

Let $0 \leq v \leq 1$ be the ratio of the number of vaccinated people to the total population of interest. If individuals are vaccinated at random, then the probability that a random person is unvaccinated is $(1 - v)$.

But suppose that we have a prioritized vaccination scheme for those who must go to the Ebola treatment centers frequently, such as healthcare workers, the family/relatives of hospitalized patients, or local employees within treatment stations. Then, the probability that a random person near treatment centers/quarantine stations is not vaccinated yet, p_Q, should be smaller than $(1 - v)$.

We define:

$$q\ (quarantine) = \frac{Q\ (number\ of\ patients\ quarantined)}{I\ (total\ number\ of\ infected\ people)}$$

p_Q $(Probability\ that\ a\ random\ person\ near\ or\ in\ the\ Ebola\ treatment\ center\ is\ not\ vaccinated$

$$= \begin{cases} 1 - v & (Without\ Prioritizing\ Policy) \\ (1 - v)^{\frac{1}{1-q}} & (With\ Prioritizing\ Policy) \end{cases}$$

The reason why we come up with the exponent $\frac{1}{1-q}$ may not be immediately clear, and we do not claim that the relation is exact. However, the intuition is that as hospitals become better at quickly identifying patients with Ebola and quarantine them, p_Q will decrease even under the same vaccination rate, v. Therefore, as the ratio of the number of Ebola patients quarantined over the total number of those infected with Ebola goes to 1, p_Q tends to go to 0 (**Figure 1**).

On the contrary, people, who are just everyday members of local communities and not forced to interact with infect patients may be a slightly less priority for vaccination. In this sense, we define an analogous concept, p_C for everyday community members to be as such:

$$p_C \equiv (Probability\ that\ a\ random\ person\ in\ local\ communities\ is\ not\ vaccinated\ yet) = \begin{cases} 1 - v & (Without\ Prioritizing\ Policy) \\ (1 - v)^{1-q} & (With\ Prioritizing\ Policy) \end{cases}$$

The intuition is that as q increases, p_c reduces to 1, which makes sense in a perfect healthcare system.

For now, we hypothesize that prioritizing vaccines for those who are close to or within hospitals, such as first-line healthcare workers, is most effective. Therefore, we will use a model where the vaccination program is prioritized.

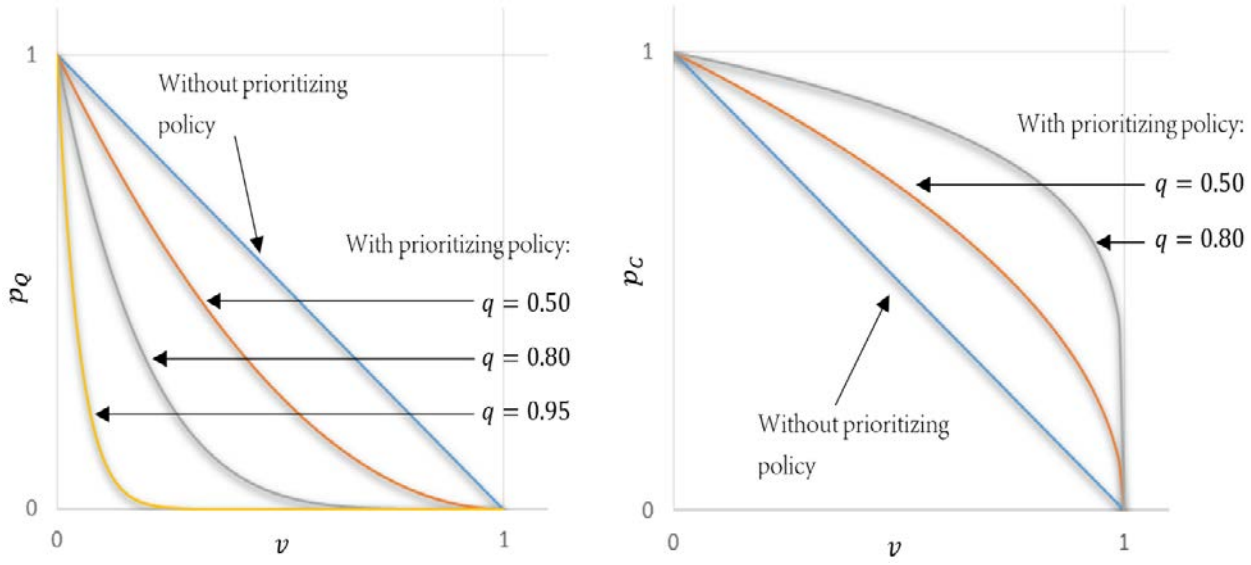


Figure 1 *The influence of the prioritizing policy on the effect of vaccination rate.*

2.4. r_C, the Net Infection Rate in the Community Per Infected Person in the Community

In the community, infection with Ebola can occur from infected individuals who are yet to be hospitalized and from individuals who died from Ebola but were not buried properly. All beta terms are constants that will be fitted later. We claim:

$$r_c = \underset{(r_{sc}),}{\beta_C p_C} + \underset{(r_F),}{\beta_F r_{DC} T_F p_c} - \underset{(r_{DC})}{\frac{m_C}{T_{DC}}}$$

Notation:

Term (r_{SC}) refers to the rate of secondary infection, i.e. infection caused from non-hospitalized victims of Ebola, per infected person in the community.

Term (r_F) refers to the rate of infections, per infected person from the community, resulting from improper funerals.

- r_{DC} is the death rate of Ebola within communities (per unit time).
- T_F is the average duration of funerals.

Term (r_{DC}) refers to death in the community because of Ebola, per infected person in the community.

- T_{DC} is the average time from infection to death in the community.
- m_C is the fatality rate of Ebola in the community.

We crafted this equation with the real world understanding that it is impossible for an infected member of the community to recover without medical intervention, hence why there is no "recovery" term. We also established early on to include the r_F term because of the recent news story where a traditional, but unsafe, funeral for an infected body in Guinea led to a resurgent outbreak [11].

2.5. r_Q, the Net Infection Rate in Treatment Centers Per Hospitalized Persons

In Ebola treatment centers and hospitals, quarantine protocols are in place and most of the healthcare workers are vaccinated. We subtract in this term the rate of recovery of individuals from the hospital per person in the Ebola clinic, and assume that infected patients cannot recover unless they are in the hospital environment. This makes sense, because our equation will be used to deliver medicine to Ebola treatment facilities only. We also subtract off the rate of deaths occurring in the hospital, per person in the hospital.

All beta terms are constants which will be fitted later. Accordingly, we have this relation:

$$r_Q = \underset{(r_{SC}),}{\beta_Q p_Q} - \underset{(r_R),}{\frac{(1-m_Q)hd}{T_R}} - \underset{(r_{DQ})}{\frac{m_Q}{T_{DQ}}(1-h\cdot d)}$$

Term (r_{SQ}) is the rate of new infections in the hospital per hospitalized Ebola- infected person. The presence of this term would suggest that the quarantine policy is not 100% effective.

Term (r_R) is the rate of recovery in the hospital per hospitalized infected person.

- T_R is the average time from being quarantined to recovery

- h is the degree of supportive health care offered by the Ebola clinic. $0 \leq h \leq 1$, where 1 is the best.
- d is the ratio between the amount of drugs we have now and the amount we need. We assume this is at unity, because the supply of antiviral medicines is not limited [12]-[13].

Term (r_{DQ}) is the rate of death in the hospital per hospitalized infected person.

- m_Q is the fatality rate of Ebola in the hospital setting
- T_{DQ} is the average time from being quarantined to death

Here, we do not include a term for the rate of change in those who are infected and just entering the hospital, 'r_H' (thoroughly described in section **2.6.**), because r_H is just a flow that goes from those infected in communities to those infected in hospitals. Since the goal of r_Q is to measure the rate of change in the number of those infected in treatment centers per hospitalized person, r_H should not appear in r_Q.

2.6. Predictive Model for the Rate of Change in Q

We define the functional form of the rate of change of those being quarantined as follows:

$$\frac{dQ}{dt} = r_H \cdot (I - Q) \; - r_O \cdot Q$$

Notation:

r_O: Rate of change in the number of hospitalized patients per hospitalized person who leave the treatment center. Mathematically, $r_O = r_{DQ} + r_R$.

r_H: Rate of change in the number of hospitalized patients per person, which comes from the people being sent to the treatment centers stations. Mathematically, $r_H = 1/T_H$, where T_H is the average time between developing an infection and being hospitalized.

Putting together this equation along with the equation in section **2.2.**, the model is complete:

$$\frac{dP}{dt} = \left[\beta_Q \cdot p_Q - \frac{m_Q}{T_{DQ}} \cdot (1 - h \cdot d) - \frac{1 - m_Q}{T_R} \cdot h \cdot d\right] \cdot Q + \left[\beta_C \cdot p_C - \frac{m_C}{T_{DC}} + \beta_F \cdot r_{DC} \cdot T_F \cdot p_C\right] \cdot (P - Q)$$

$$\frac{dQ}{dt} = -\left[\frac{m_Q}{T_{DQ}} \cdot (1 - h \cdot d) + \frac{1 - m_Q}{T_R} \cdot h \cdot d\right] \cdot Q + \frac{1}{T_H} \cdot (P - Q)$$

2.7. Fitting the Model in WHO data

There currently exist other models [9], [18], which make use of similar parameters, but we do not choose to borrow the values of their parameters to determine the values of our parameters that share the similar definition. Instead, to make our model self-consistent and robust, we chose to calibrate our parameters by ourselves to maintain the consistency of our definitions.

We calibrated our parameters with official historical data of the number of weekly reported cases from November 9, 2014 to February 4, 2014 [7]. It is highly probable for these parameters to vary by country (depending on the state of the Ebola epidemic), so we do not claim that these parameters are always applicable.

We used the least square fit method to fit the model the number of cases reported **in Liberia** over the weeks.

We illustrate the most successful curve fitting in **Figure 2.** The blue dots in **Figure 2** are data from the WHO Ebola Situation Report from 4 February 2015. Now, we set the vaccination rate, v, to be zero, because no vaccine was available during the time period of our historical data set. The solid orange line is the fit for our model. The shaded region shows how sensitively our model behaves over the values of parameters. We changed the value of fit parameters by ±5%. Since the number of cases corresponds to the number of courses of drugs we need, this model would be useful for determining the international allocation of drugs in Liberia.

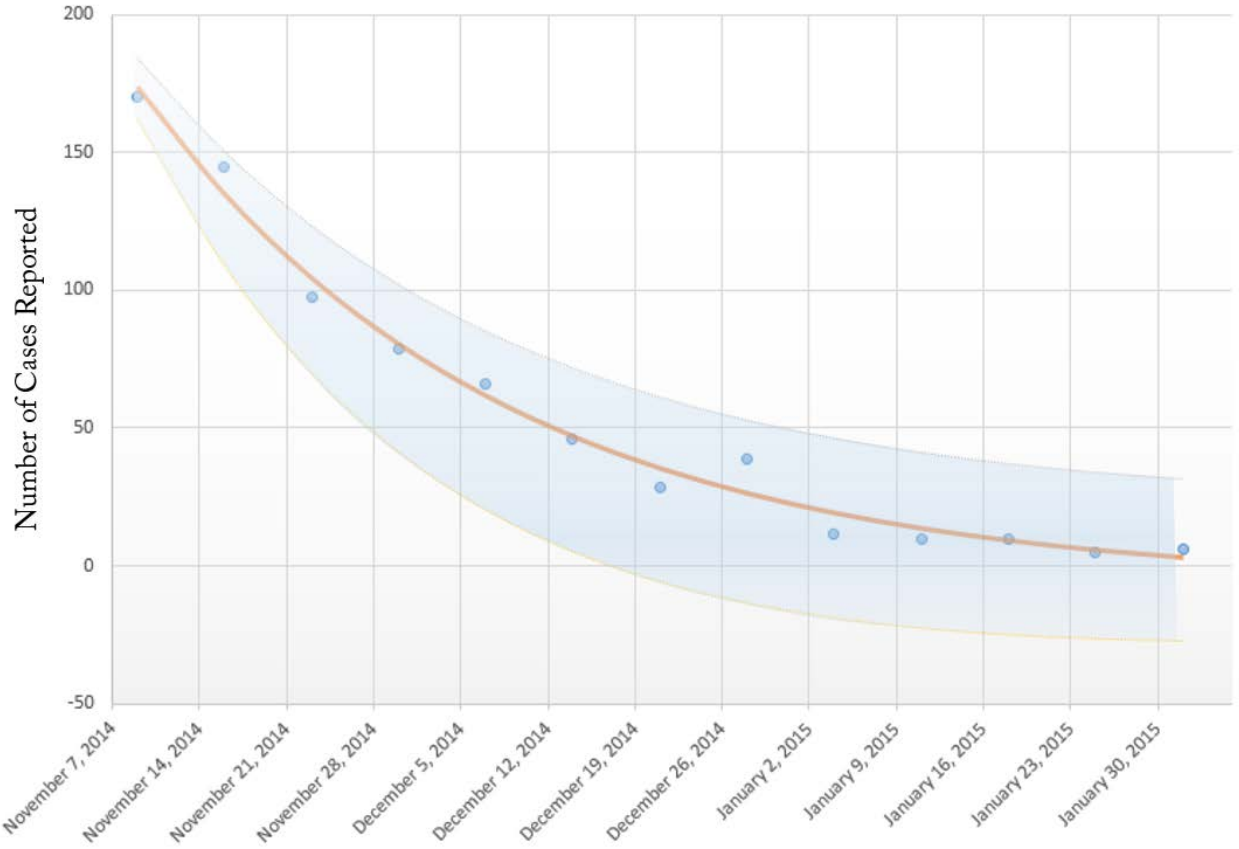


Figure 2 *Plotting the predicted number of cases over historical data.*

From the fitting, we obtained the values of fit parameters. (**Table 1**) These values are taken to be used for the prediction of the number of infected people.

Table 1. The value of fit parameters

Parameter	Implication	Value
$\boldsymbol{\beta_Q}$	Contact Rate, in Quarantine stations	0.0024 (/day)
$\boldsymbol{\beta_C}$	Contact Rate, outside of Quarantine stations (in Communities)	0.0851 (/day)
$\boldsymbol{\beta_F}$	Contact Rate, through Funerals	0.1271 (/day)
$\boldsymbol{m_Q}$	Fatality Rate, in Quarantine stations	0.6789
$\boldsymbol{m_C}$	Fatality Rate, outside of Quarantine stations (in Communities)	0.5000
$\boldsymbol{T_{DQ}}$	Average Duration from being Quarantined to Death	4611 (day)
$\boldsymbol{T_{DC}}$	Average Duration from Infection to Death	150.9 (day)
$\boldsymbol{T_H}$	Average Duration from Infection to being Quarantined	10.27 (day)
$\boldsymbol{T_R}$	Average Duration from being Quarantined to Recovery	5.990 (day)

$\boldsymbol{T_F}$	Average Duration of Traditional Funerals	2.122 (day)
$\boldsymbol{h}$	The degree of Intervention/Aid in Health care	0.3008

Analysis: We are fairly pleased with the parameters resulting from the curve fitting.

- $\beta_Q \ll \beta_C$, which makes sense since quarantining procedures, while not perfect, should substantially reduce the contact rate between Ebola patients and susceptible individuals.
- $m_Q > m_C$, which may strike one to be peculiar. However, there is a logical explanation. One would expect that infected individuals in the community would be sent to Ebola treatment centers, and depending on when dI/dt is defined to be calculated, those individuals' deaths would contribute to only m_Q, not m_C.
- We expect T_{DQ} to be large if the World Medical Association's drug is truly as effective as claimed, because then even the sickest patients can hope to survive. We interpret this large value (4611 days) as indicating that hospitalization is so effective that the patients hardly die within the hospital. Since our goal is to eradicate Ebola, the extremely large values of this parameter is uplifting.

Caveat:

The only immediate weakness of the curve fitting is that T_{DC} is rather high. This may be due to how the incubation period of Ebola is highly variable, between 2-21 days, which destabilizes the parameter.

On the other hand, since T_{DC} in the curve fitting is smaller than T_{DQ} by an order of magnitude, the relationship we meant to capture when defining the aspects of our model is very clearly preserved.

2.8. Eradicating Ebola with our Predictive Equation

A useful result is, since there is a one to one correspondence between the number of drugs and the number of patients at a specific time interval, the result of the Adams-Bashforth method with dI/dt produces the demand for drugs.

Using the same data set from section **2.7**, we also graph the time when the number of Ebola cases approach zero in **Figure 3** with the Adams-Bashforth method.

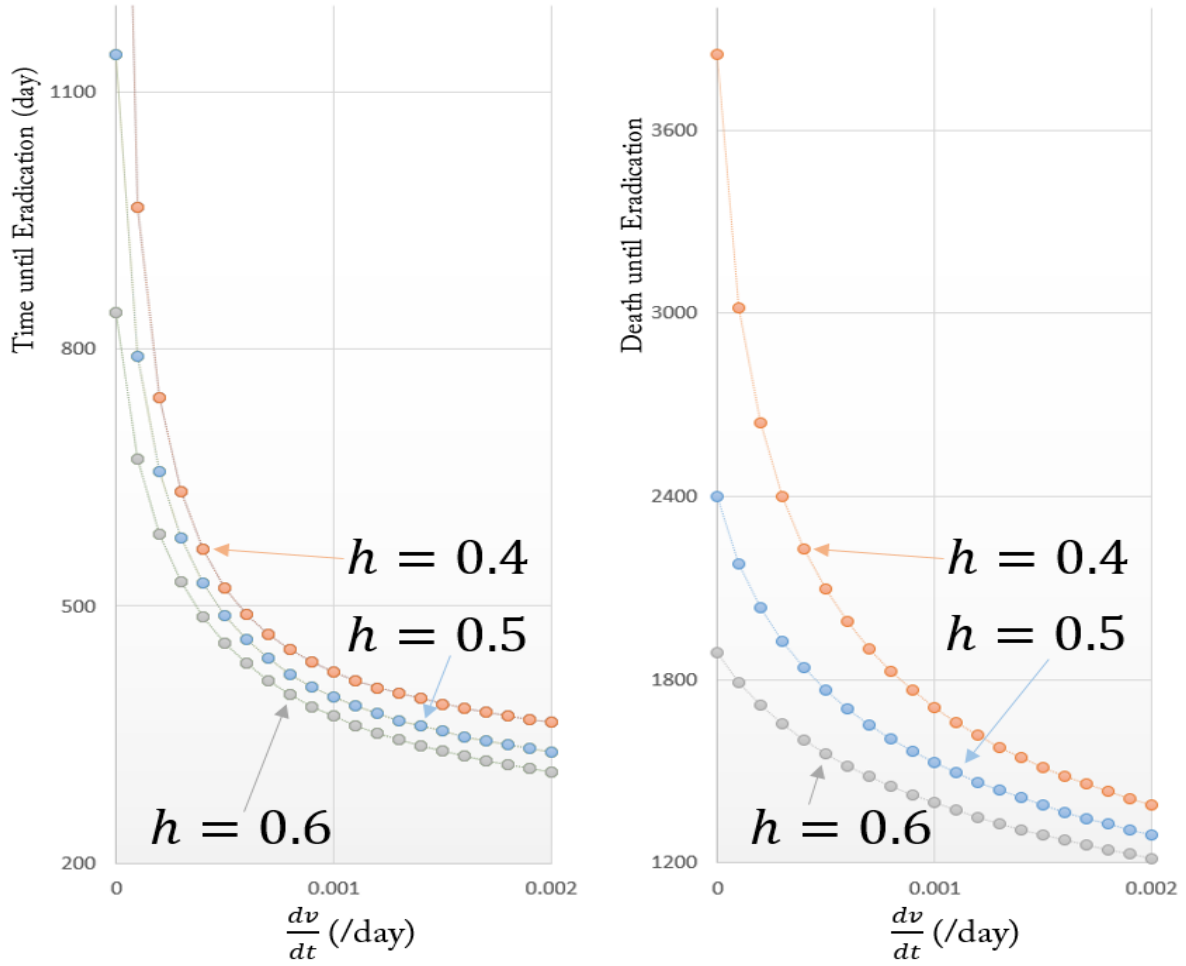


Figure 3 *Plotting the number of days it takes for Ebola cases to tend to zero, and the number of deaths our equation predicts before Ebola is eradicated, against the vaccination rate, while fixing the degree of intervention. We started from* I = *5000, and* Q = *1000, based off the 4 February 2015 WHO report.*

Our model therefore shows that, with a better degree of intervention (i.e. as h is closer to 1), both the time until eradication of Ebola and the death count decrease, which makes sense.

We note that the scaling of dv/dt seems small; however, the data set we used while fitting this particular usage of our dI/dt solutions is again from historical data, before the world medical association's announcement. Therefore, even the slightest change in the number of individuals vaccinated reduces the number of cases of Ebola.

Due to the asymptotic nature of the curve for the solutions of dI/dt, we define the time until eradication to be the time when I is ≤ 0.5.

The left graph in Figure 3 suggests that with even a limited vaccination policy in place and a relatively poor degree of intervention, Ebola will be eradicated in Liberia within a year.

If we execute a vaccination project with the rate of change of the vaccination proportion,dv/dt, set to 0.001, then the time it takes to eradicate Ebola in Liberia is roughly a year. Without any vaccines, Ebola will vanish within 3 years (given that $h = \sim 0.5$).

One important implication is that the influence of h on the number of deaths is exponential. When there are no vaccines, the number of deaths until eradication is roughly 4000 at h = 0.4. When h =5, the number of deaths is roughly 3000, but then it drops to only 2400 deaths at $h =$ 0.6. Policy makers should be aware that the faster and more intense the intervention for health care, the greater the chance that deaths are prevented.

Previously, we hypothesized that prioritizing vaccinations for healthcare workers before inoculating the rest of the population will reduce the number of infections. We tested this hypothesis and graphed the results in **Figure 4** using the same dI/dt solution.

The results actually show that the best results occur when vaccines are randomly distributed between both healthcare workers and members of the community. We explain this result by noting three facts:

- $Population_{Community} >> Population_{Healthcare\ workers}$. Therefore, an unaccounted term when representing $p_C$vs p_Q likely exists. Furthermore, as explained before, the forms of p_C and p_Q, as said before, are ideal for comparative purposes but are inexact and simplified.
- The parameters we used originate from when a vaccine protocol was not established.
- In probability and statistics, unbiased, random processes often end up reaching optimal solutions before biased strategies.

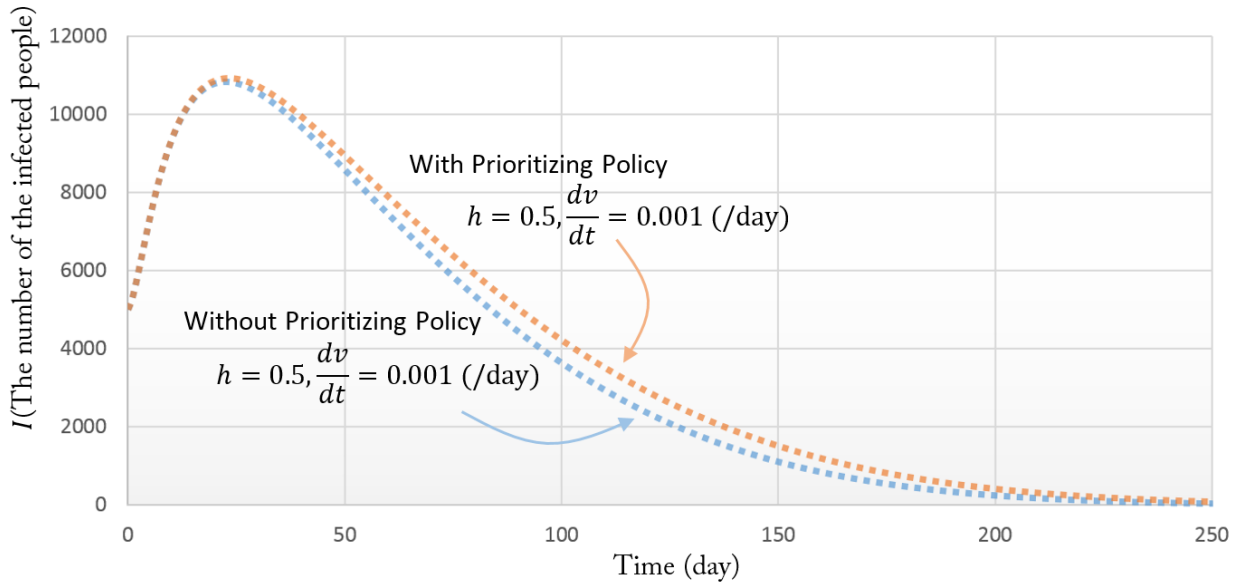


Figure 4 *Results concerning whether the number of infected people changes given a priority vaccination program. We fix the degree of intervention and vaccination rates, but we set* $p_Q = p_Q$.

Quick Summary of Part II

- The form of our dI/dt equation appears to be quite representative of the situation. When fitting values of our equation's solutions with historical data, we expected the observed determined parameters' values (or their relationship with one another).
- An unbiased vaccination protocol may be the best option to eradicate Ebola, but further research is required.

- We may be able to eradicate Ebola in Liberia within a year from now. One may follow the steps we took to make similar calculations for Guinea, Sierra Leone, and any other countries where the presence of Ebola is established.
- Our dI/dt equation's solutions can be used to model the amount of the drugs needed to cure patients with Ebola.

3. DELIVERY

So far, we can determine the necessary amount of drugs needed by each nation or treatment center. In this section, we examine the geography of West Africa and determine the waiting times to deliver medicine. We demonstrate how to determine the need to build another Ebola treatment center, among other things.

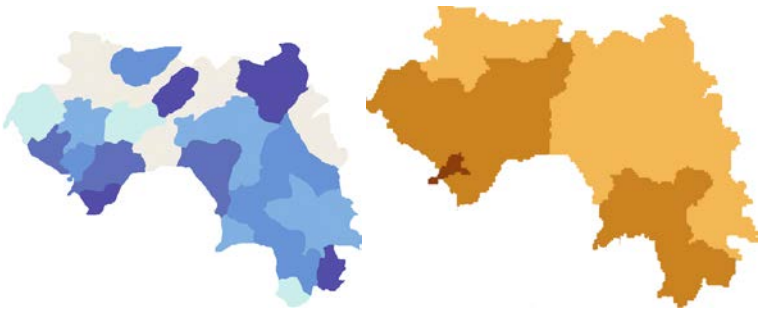
Delivering the medicine to forestall future outbreaks is enabled by predicting the time it takes to reach other Ebola treatment centers from Conakry, Guinea, Monrovia, Liberia, and Freetown, Sierra Leone. We choose these centers to first unload all drugs and vaccines because they are all near the sea and accessible to international aid workers.

3.1. Understanding the Initial Conditions

We have rendered the most recent data set to show how dI/dt, in this case at t = 0, relatively varies by area.

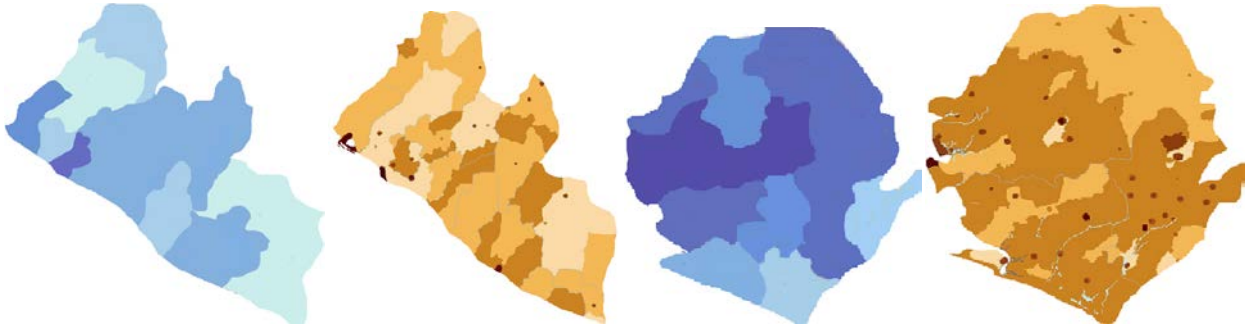
Areas currently plagued by Ebola (dark areas indicate recent record of cases)

Guinea



The left diagram is showing the relative dI/dt values in Guinea (technically, the map we rendered was based off the number of days since the last reported case). Darker areas indicate worse hit areas. The right diagram represents the population in Guinea, and darker orange indicates more population (and therefore areas which need more vaccines). We show similar renderings for Sierra Leone and Liberia.

Liberia Sierra Leone



These initial data values are immensely important. Since the total population in these countries is unlikely to drastically change by an order of magnitude, these maps say where the vaccines need to be delivered based off of the normalized population. This was determined after our dI/dt model predicted that a general, unbiased vaccination strategy can reduce the time of the Ebola epidemic.

We analyzed the terrains of each country to verify that even a slow average travel speed of 20 kph is reasonable.

Table 2. Terrain and Seaports of West African Countries

Country	**Terrain**	**Major Seaports**
Liberia	"Mostly flat… low mountains"	Monrovia, Buchanan
Sierra Leone	"Wooded hill country, upland plateau"	Freetown
Guinea	"Flat coastal plain, hilly to mountainous interior"	Conakry

Source: [14].

With these renderings and the assumption that any delivery vehicles travel at 20 kilometers per hour, we used Matlab to compute the average time from all the points in the map to travel to their closest Ebola treatment center. We also outputted the maximum time it takes to travel to closest Ebola treatment center.

Table 3. Finding the Average Time to the Closest Treatment Centers

Country	**Average time to closest treatment center (in hours)**	**Maximum time (in hours) it takes to reach closest center**
Liberia	3.2	11.6
Sierra Leone	3.0	8.6
Guinea	6.9	17.4

3.2. Assumptions

To repeat, we put an emphasis on time rather than the mode of transport, because the average time it may take to die from Ebola is much longer than the time it takes to travel across any of the countries at slow speeds (*viz.* 20 kilometers per hour).

In developing this model, we assume ability to fully use the existing Ebola treatment centers which are recognized by the World Health Organization. We state this assumption because if there are patients in any medical center, they require drugs and cannot be left out.

We also assume that a larger number of days where an Ebola case has not been seen implies that the number of infected individuals is decreasing.

We make final assumptions that the number of trucks is greater than the number of treatment centers and that the vaccines and drugs can be adequately loaded on said transport. Specifically concerning the first point, Denmark recently gave 262 vehicles (more than the number of treatment centers) to fight Ebola in Sierra Leone [15].

3.3. Determining the Effect of an Additional Treatment Center

We seek to understand how the number of Ebola treatment centers can affect travel times and consider the possibility that more Ebola treatment centers may need to be constructed.

To achieve this, we take points and weigh them with the normalized values for what we regard as the number of those infected (from the WHO's 4 February 2015 report) to predict the delivery time between two points.

New Center Construction Algorithm

For each point on the map

Include this point in the treatment center locations

Find out how much time will be shortened when going to closest center if we have this point as a treatment center

Update the longest time shortened and the best new center location

Output time difference matrix, largest time reduction, and the suggested new position

End For

We find the following results:

Table 4. Examining the Reduction in Average Time along with the Number of Cases

Country	Reduction in average time (hrs)	Number of Ebola Cases [16]
Guinea	2.47	2975
Liberia	0.65	8745
Sierra Leone	0.54	10740

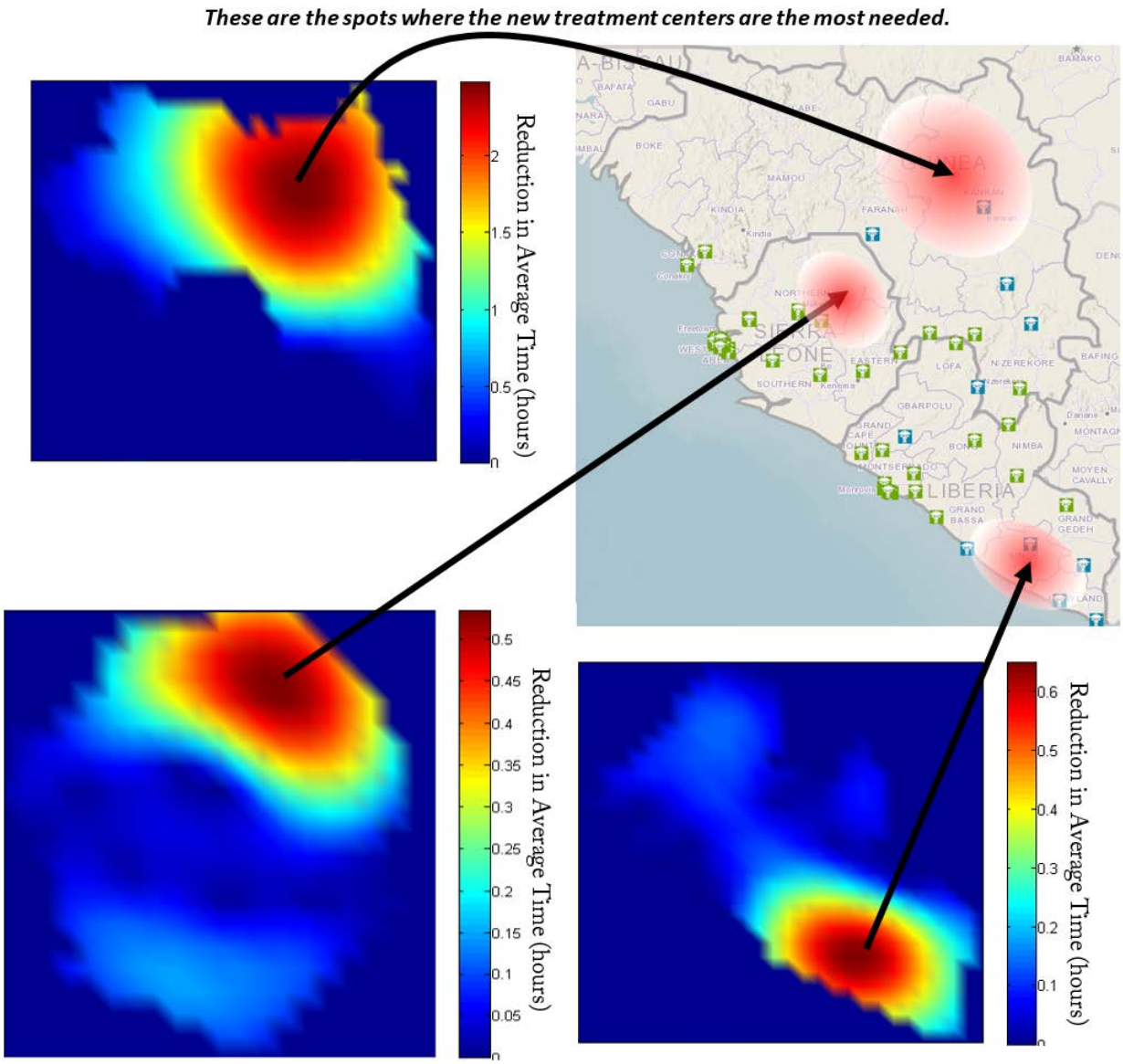


Figure 6 *We use a pseudocolor map to highlight the effect an additional Ebola treatment center, according to its position, may have for locals seeking treatment.*

As you can see in **Figure 6**, we conclude that there are enough treatment centers in Sierra Leone and Liberia, due to the small difference in the average time (weighted by the probability of a patient being infected) between any points to the closest treatment center. For a truck traveling 20 kph on average, an additional center does not reduce the overall average weighted time.

However an additional medical center can make a positive impact on Guinea, due to the relatively substantial reduction in the average time needed to access medical supplies.

3.4. Vaccine and Medicine Distributions

As we have mentioned before, it is important to know where and how many vaccines to distribute to the population. We can coordinate this goal with the normalized solutions of our $\frac{dI}{dt}$ model and map the exact drug and vaccine needs of the communities.

Back in **section 2.5**, we set $d = 1$, so that the demand for antiviral drugs is met by the supply. However, due to the finite space where the drugs may be stored (in trucks, etc) as well as the maximum possible loading times, one cannot stockpile an excessively large amount of drugs in West Africa. Since some drugs must still be delivered, one of the reasons we need dI/dt is so that officials can predict the exact amount of drugs needed. Otherwise, it is impossible to know what the future allocation requirements are.

Drug Distribution Algorithm

For each point on the map

> **Find** the closest distribution center from this point
>
> **Update** the distribution percentage of this treatment center with weighting by the probability that a patient occurs at this point

End For

Output the array that shows what percentage of drug delivery each treatment center should take

As stated before, we will vaccinate based off the distribution of population density weighted by the probability that a patient occurs at a specific location. The algorithm we implement is very similar to the drug distribution algorithm.

Vaccine Distribution Algorithm

For each point on the map

> **Calculate** the weight of this point by multiplying its probability of having a patient and the population density at this point

End For

Normalize the matrix and turn it into a probability matrix

Use similar methods of Drug Distribution Algorithm

Output vaccine distribution

We illustrate the implementation of these algorithms in **Figure 5.**

Figure 5 *We illustrate the implementation of the algorithms determining the optimal allocation of the drugs (medicine) and vaccines.*

4. EVALUATING THE MODELS

We reflect on the feasibility of both of our models' bases, and see if any improvements could be made.

4.1 Weaknesses of the Models

Mathematical modeling requires one to make assumptions or simplifications, and sometimes the machinery of the model may not reflect all situations. We provide some caveats and further details about our models.

The Predictive Model, dI/dt

This model treats populations of distressed villages as a whole unit, so individuals with Ebola cannot reasonably be tracked with the current equations. However, our model treats villages or nations in their entirety, so the person's movements would be reflected in the rates of spread of infection.

We also refer to a chosen constant h frequently. The value h means the degree of health care supports that are given to the country. But this definition is so abstract that it is hard to mathematically and realistically connect the parameter h with the actual indices such as the number of health workers, the density of Ebola treatment centers, or public hygiene of the country. However, we placed important emphasis on h since the quality of supportive healthcare is one of the major reasons why Ebola in developed countries like the United States of America has not gained a foothold [17].

If there are no infection rates to extrapolate from, our model cannot predict the start of an outbreak. This is just the nature of a differential equation, because one needs initial values. Since our methods would be implemented while the epidemic is occurring however, data to seed our model is readily available.

The Delivery Model

Our algorithms for the delivery model operate on the assumption that the minimum time to reach a destination is achieved with a linear route. In reality, roads may not follow a straight-line path. We compensate for this by choosing a very slow speed for the delivery trucks. Usually a truck might travel at "medium" speed, but we assume the worst case scenario, where the truck driver has to negotiate many turns. An improvement that could benefit the model may be considering other modes of transportation besides trucks, like by railroads.

4.2. Conclusion

Like our model, some examples we found in the literature use a similar first-order differential equations approach, but they typically consist of around six or seven equations. In particular, "Understanding the Dynamics of Ebola Epidemics" by Legrand et. al. uses six differential equations to account for the rate of spread of infection [18].

Our model is unique compared to other models in the literature, because we capture the relationships of the number of those infected and the number of those quarantined with respect to time in just two equations.

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