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T2	_____		F2	_____
T3	_____		F3	_____
T4	_____	Problem Chosen	F4	_____
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2015 Mathematical Contest in Modeling (MCM) Summary Sheet
(Attach a copy of this page to your solution paper.)

Type a summary of your results on this page. Do not include the name of your school, advisor, or team members on this page.

The ongoing Ebola outbreak is the worst in its history. It is spreading exponentially and threatens economies and populations of numerous countries that are currently or could be exposed to it. Unfortunately, little is known about the virus and even with the efforts of multiple countries actively fighting to stop it from spreading, the results are still weak. Fortunately, a vaccine to cure Ebola was discovered for the purposes of this paper. We are now attempting to aid the efforts of the world to fight the deadly virus in the most effective manner. One of the hardest parts of the ongoing fight against Ebola is to identify where to put the most effort of fighting the virus and identifying how it is going to affect the overall spreading of the virus. Therefore, our aid comes from the methods of identifying and targeting the most infectious regions during the outbreak. Moreover, our models predict how a certain region will progress in its fight against Ebola when it will receive a certain amount of medication. We provide the minimum number of vaccines needed to suppress the outbreak and to eradicate the Ebola virus within a certain region. To predict the spreading of the virus in a particular area, we use a system of ordinary differential equations. Furthermore, to predict how the virus will spread to other areas, we use networking and Markov chains to weigh how infectious each region is to its neighbors and use that data to identify the stationary solution, which will represent a ranking of the most infectious regions. Finally, we merge those two methods to make a simulation of how the infection is going to spread and what the future most infectious regions will be. Such approach allows to spend the supplies of vaccine effectively, predict the spreading of the outbreak of the virus, and to suppress it. Therefore, we provide a toolbox for optimizing the eradication of Ebola.

Eradication of the Ebola Network

Team #34691

February 9, 2015

Contents

1 An Introduction to the Mathematics of Epidemiology

In terms of literature on this subject, there seems to be a lot of research on how diseases are spread, but not nearly as much as on how to use these models to stop disease from spreading. Additionally, we found that most people modeled disease spreading through sets of ODEs; although we did find some literature on graph theory as well. Through the remainder of the paper we will explore both types of models, what they say about how we can stop Ebola, and a possible way to merge the two together. The first model analyzes the spread of the disease as well as the quantity of the medicine needed within a region. It applies 6 essential ODEs (Ordinary Differential Equations) describing how the Infection will progress in the conditions of given parameters such as numbers of people being: S (susceptible), E (having Ebola in latency stage), I (infected and infectious in that region), R (dead or immune to the virus). We applied this model to Guinea at the beginning of Ebola outbreak and found the reproduction rate of the virus to be 1.2. The reproduction rate was found by optimizing the average amount of people one gets in contact in a day and the probability of those people getting infected. By optimizing the distribution rate and the amount of vaccine, we have identified the number of vaccines to be given out per day in order for the Ebola infection to stop spreading and to start converging to zero. Our second model focused on the possible delivery systems and the locations of delivery that would be most advantageous to eradicating the Ebola infection. We have constructed a network of infected and nearby regions in Africa. Using a Markov matrix in which every entry (i,j) is the likelihood of region i to spread the decease to region j, we were able to find the ranking of the most infectious regions of Africa in its current state. Therefore, to minimize further spreading of the Ebola virus, we advised to deliver medicine based on the ranking found. Our third model combined our first and second model. A set of ODEs from the first model was modified to account for a small amount of infected people travelling or visiting from bordering countries. We then read in parameters of each region and input them for the modified set of ODEs that is applied to each region. Then, the simulation proceeds and calculates the new parameters for each region, as the time progresses. Such an approach will allow us to identify and to predict what the most infectious regions will be with the current state of the network.

2 SEID Deterministic Model

2.1 Development

In this report, we develop three models to simulate the evolution of the current Ebola outbreak in West Africa with the goal of eradicating the disease as quickly as possible and with a reasonable amount of resources. Ebola is a highly contagious and lethal disease that was first observed in humans in 1976 when a small outbreak erupted in Central Africa [9]. In March of 2014, Ebola cases began to appear in Guinea. These few cases rapidly spread throughout West Africa, causing the most damage to Sierra Leone and Liberia. This outbreak is severe, causing more fatalities than all other outbreaks of the virus combined. The limited history of the disease makes Ebola even more dangerous; little research has been performed on the virus and no effective vaccines have yet been deployed. There are, however, two developed vaccines undergoing extensive testing. [8, 9]. The goal of our models is to determine how to optimally distribute a potential vaccine to eradicate the virus.

Our first simulation is an SEIR deterministic model, which we use to model relatively small infected populations (the size of a single country). SEIR models are standard in the field of mathematical epidemiology, dating back to the early twentieth century when Ronald Ross and William Hamer used similar models to study malaria and other infectious diseases [7]. This approach partitions a given population into four groups, S, E, I, and R: people who are susceptible, infected but not infectious, infectious, and recovered. The behavior of these partitions is governed by a system of coupled ordinary differential equations. Figure 1 graphically explains this process, Table 1 identifies the population partitions, and Table 2 defines the parameters that appear in Figure 1.

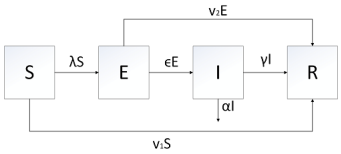

Figure 1: SEIR Model of Disease

Group	Definition
S(t)	Population susceptible to disease
E(t)	Population in latency period
I(t)	Infected population
R(t)	Recovered population
N(t)	Total population

Table 1: SEIR Model Population Partitions

Parameters	Definition	Interpretation
$\lambda(t)$	$\lambda = \frac{r\beta I(t)}{N(t)}$	Rate of Contraction of the Disease
ϵ	ϵE is the Movement of Population from E to I per Unit Time	$\frac{1}{\epsilon}$ is the Average Latency Period
r	Average Number of Contacts Between one Person in I and one in S per Unit Time	Rate of Contact
β	Probability of Contracting the Disease per Contact per Unit Time	Transmissivity of the Disease
γ	γI is the Movement of Population from I to R per Unit Time	$\frac{1}{\gamma}$ is the Average Recovery Period
A	Percentage of Infected Who Perish	Death Rate
α	αI is the Death due to Disease per Unit Time	$\frac{1}{\alpha}$ is the Average Time to Death
V	Amount of Readily Available Vaccine	One Vaccine Can Be Used per Person
v_1	$v_1 DV$ is the Movement of Population from S to R per Unit Time	Fraction of Vaccine Distributed to Population in S
v_2	$v_2 DV$ is the Movement of Population from E to R per Unit Time	Fraction of Vaccine Distributed to Population in E
D	Length of Time to Distribute Available Vaccines	Distribution Rate
m	Length of Time to Make a Vaccine	Supply Rate
R_0	$R_0 = \frac{r\beta\epsilon}{(a+\gamma)(\epsilon+v_2 DV)}$	**Basic Reproduction Number**–Average Number of People Infected by an Infected Individual

Table 2: SEIR Model Parameters

The basic reproduction number, R_0, will be especially important in our analysis. As this number shows how many people get infected from an infected individual, if $R_0 > 1$, the infection will spread exponentially (this scenario is called an **epidemic**, if $R_0 = 1$, the disease will stabilize in the population (this scenario is called an **endemic**), and if $R_0 < 1$, the disease will be eradicated. We will discuss this value much more in Section [OPTIMIZATION]

Using the information above, the differential equations that describe this system are easy to derive. The population change for each partition is simply the rate at which people enter the partition minus the rate at which they leave. This is described quantitatively on the next page.

$$\frac{dS}{dt} = -\lambda S - v_1 DV \quad (1)$$
$$\frac{dE}{dt} = \lambda S - \epsilon E - v_2 DV \quad (2)$$
$$\frac{dI}{dt} = \epsilon E - (\alpha A + \gamma(1 - A))I \quad (3)$$
$$\frac{dR}{dt} = \gamma I + (v_1 + v_2)DV \quad (4)$$
$$\frac{dV}{dt} = m - D \quad (5)$$

Before applying this model to simulate actual outbreaks of the Ebola virus, it is necessary to highlight the main assumptions we made in its development.

- The natural death rate and natural birth rate within the population are negligible.
  - None of our models simulate more than a year of an outbreak. Over this time-period, natural deaths and births are negligibly small compared to the country's total population.
- The basic reproduction number is constant when no interventions are made to slow the spread of the disease.
  - This is almost always true, except at the very beginning and end of an outbreak. [2, 3]
- Parameters represent average behavior of the disease, and individual variations are negligible.
  - Because all parameters are independent and identically distributed, probabilistic variations have no effect on average values for large populations. This is a general assumption for all deterministic models. [5]
- Recovered individuals are indefinitely immune to the disease.
  - This is almost always true for Ebola survivors. [8, 9]
- Individuals in the latent period of the disease are not contagious.
  - Again, this is usually observed to be true in Ebola. [8, 9]

- A vaccine will immediately and perfectly cure a person in E and immunize a person in S.
  - This is valid by hypothesis.
- The simulated population is homogeneous and mixed–everyone interacts with everyone else with the same probability.
  - This assumption is hard to justify because it is generally not true for large populations. However, we find empirically that this assumption does not drastically effect our results for for the 2014 Guinea outbreak. This assumption will be discussed in Section [STRENGTHS/WEAKNESSES] as a weakness of this model, and our next model will address it.

2.2 Testing

To test our model, we researched the behavior the Ebola virus to determine the correct values for our parameters and compiled data from the recent outbreak in Guinea that began in March 2014. We then calibrated our model by finding an approximate value for the product $r\beta$ from the empirical data, initialized our simulation with the total population of Guinea as our susceptible population and the first number of recorded cases as our latent population, and then, finally, we compared the simulated behavior of the epidemic to the actual data. The outbreak in Guinea began about nine months ago, so we ran our simulations for 270 days. The parameter values we used are contained in Table 3 below, and our initialization values are contained in Table 4 on the following page.

Parameter	Value
$r\beta$	0.096
ϵ	$\frac{1}{7}$ (Average Latency Period is One Week) [8]
γ	$\frac{1}{20}$ (Average Recovery Time is Two-Three Weeks) [8]
A	$\frac{3}{5}$ (Outbreak has 60 Percent Death Rate) [8, 9]
α	$\frac{1}{10}$ (Average Time from Symptoms to Death is Ten Days) [8, 9]
$\lambda(t)$	$\frac{12I(t)}{25N(t)}$
v_1	0
v_2	0
D	0
m	0

Table 3: Parameter Values in Simulating the Guinea Outbreak

Group	Initial Value
S(0) = N(0)	11474383 (Total Population of Guinea)
E(0)	27 (First Recorded Infections)
I(0)	0
R(0)	0
V(0)	0

Table 4: Initial Conditions for the Simulation of the Guinea Ebola Outbreak

Most of our simulation and analysis is performed using MATLAB. Its structured format is conducive to managing and plotting our five functions. We used MATLAB's ode45 to numerically solve and plot the solution to this system. It is extraordinarily difficult to estimate the values of r and β, so instead we ran several simulations with reasonable values for r and β and chose the values that yielded the most consistent results. This is a common practice to calibrate a mathematical model when empirical data is available [3]. Using the data from the recent Guinea outbreak, we determined $r\beta = 0.096$. On the following page, the plot of our simulated data is on top and the actual data we collected is on bottom. Note that we are comparing cumulative cases of the disease, which is the yellow line on our simulated data plot.

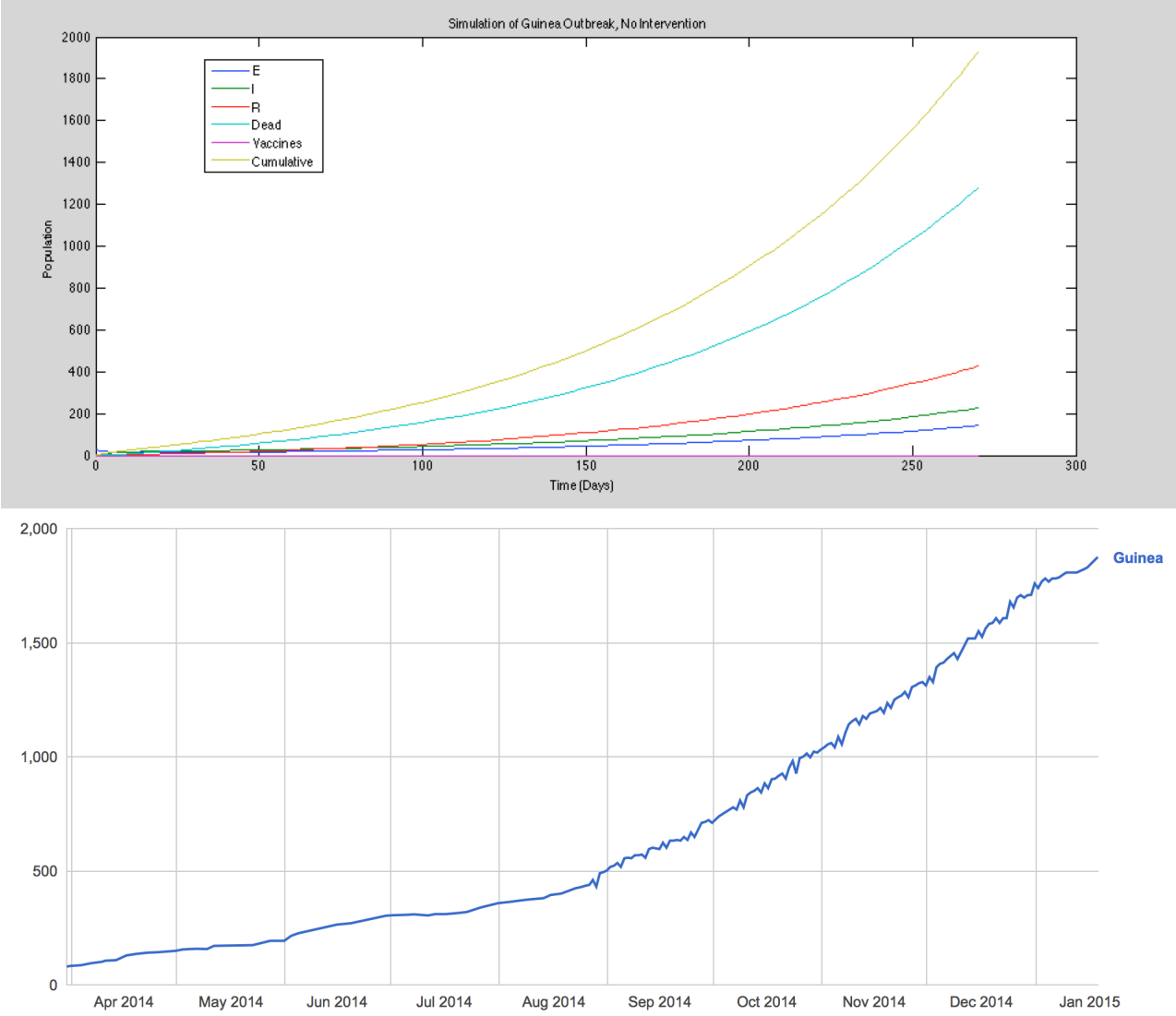

Figure 2: SEIR Model of Disease

Our simulated data fits the collected data well. Both the simulation and the actual data represent an exponential growth in the number of recorded cases of Ebola. Furthermore, the cumulative number of predicted cases at the end of the nine months (1,928 cases) closely matches the recorded value (1,875 cases), with a 2.7 percent error.

The biggest discrepancy between our simulation and the actual data is the R_0 value. Using the equation in Table 2 to calculate the R_0 value in our simulation, we find that R_0 is about 1.2. The R_0 value in the actual outbreak, however, was estimated to be closer to 1.5 [8, 1, 3]. This example highlights a general weakness of this model, and will be discussed in Section 2.4.

2.3 Optimization

Our main goal is to eradicate the disease using as few resources as possible, in other words, with as slow a supply and creation rate as possible and with as few vaccines as possible. To begin our search for the optimal eradication of Ebola, we will investigate two avenues toward achieving that goal. Eradication of the disease will occur if $R_0 = \frac{r\beta\epsilon}{(a+\gamma)(\epsilon+v_2DV)} < 1$ as we discussed earlier, so one way to eradicate the disease is to adjust v_2, D, and $V(0)$ until R_0 is stabilized around a value less than one. Also, according to [14], herd immunity will occur if the number of vaccinated people exceeds an estimated critical population ratio, defined as $p_c = 1 - \frac{1}{R_0}$. On the other hand, the first scenario directly adjusts reproduction number as the disease progresses. In the first scenario, we would want $v_2 = 1$ i.e. the maximum of vaccine being distributed to the E group and no vaccine going to the S group. This would have the greatest effect on lowering the R_0 value. In the second scenario, it does not matter which part of the population is vaccinated, so it follows that all available vaccine should be distributed to the E group.

Considering the second scenario, our simulation predicts an R_0 around 1.2, so the second scenario would imply that the disease would be eradicated if $\frac{1}{6}$ of the population is vaccinated. Guinea has a population of more than 11 million, so it is not feasible to quickly and cheaply implement this program. However, combing the two ideas of focussing our efforts on the population in E and estimating a critical vaccinated population ratio, we developed a closely related strategy that is feasible and effective.

Our model exhibits a strong sensitivity to the number of infected people in its initialization. Increasing the initial infected population causes an observable increase in R_0. This sensitivity, which is discussed more extensively in Section STRENGTH AND WEAK, led us to believe that if a certain pro-

portion of the infected and treatable population could be vaccinated, the R_0 value could be made arbitrarily small. This is the population in E. Assuming $m = D$ so $\frac{dV}{dt} = 0$, we used MATLAB's Optimization Toolbox to find the minimum distribution rate and initial number of vaccines need to eradicate the disease in the Guinea simulation. MATLAB found that $R_0 < 1$ when $DV(0) < 3.76$. In terms of the current state of the Guinea population, $R_0 < 1$ when $DV(0) < \frac{E(0)+I(0)}{100}$, where $E(0) = 141$ is today's population in the latent period and $I(0) = 235$ is today's infected population. Figure 2 on the following page shows the predicted behavior of the Guinea outbreak for the following year for the following situations: with no vaccines, with an immediate adjustment so $DV(0) = 3.76$, and for an immediate adjustment so $DV(0) > 3.76$.

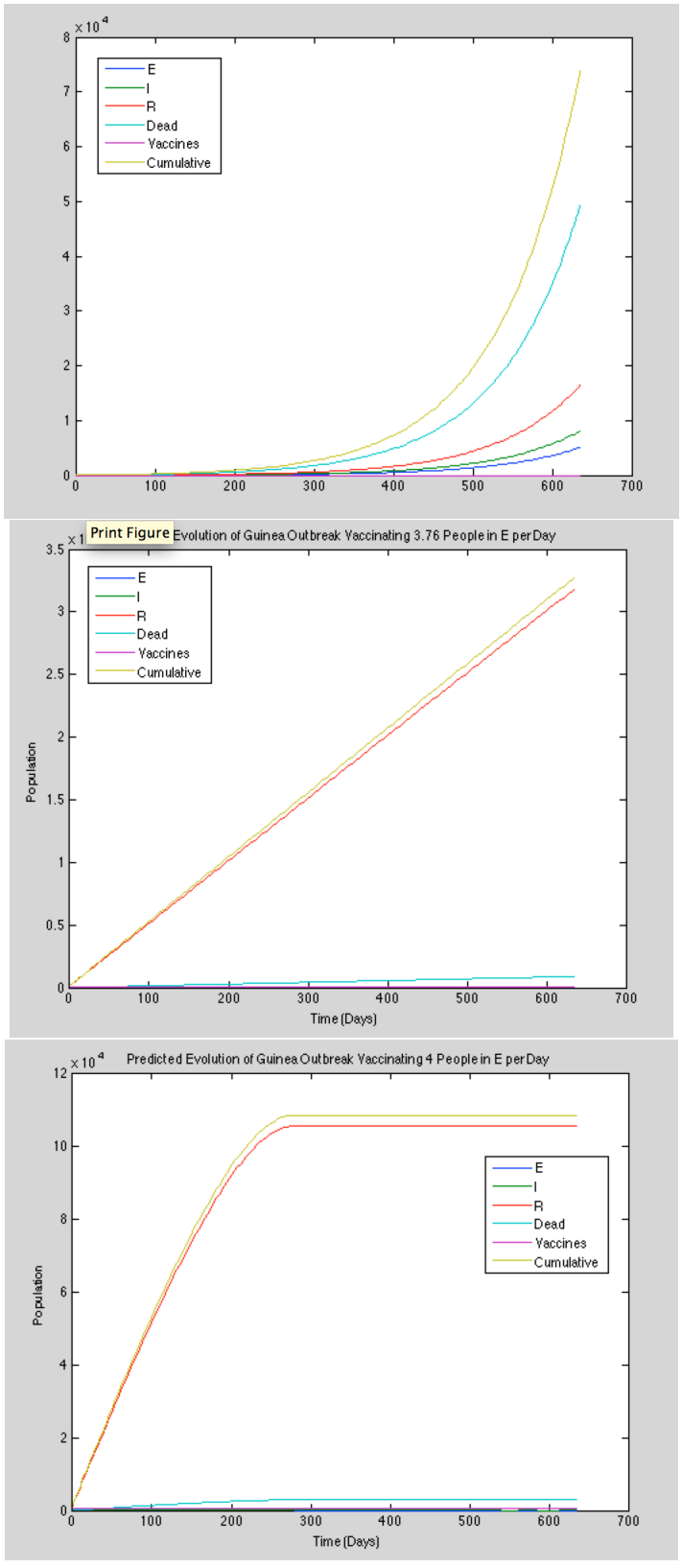

Figure 3: Simulation of the Following Year of the Guinea Outbreak. Note: $DV(0)$ is the number of vaccines distributed per day.

The above figures show a simulation, from top to bottom: without intervention, given 3.76 vaccinations per day, and given 4 vaccinations per day. They also show that this strategy optimizes the treatment of the ongoing Guinea Ebola outbreak. This strategy is a bit difficult to generalize because only the population in E can be vaccinated, but the estimation $DV(0) < \frac{E(0)+I(0)}{100}$ gives an excellent estimate. This result hints at the importance of identifying an outbreak quickly. As the infected population grows, the rate at which vaccines are distributed grows linearly, which means that the number of vaccines needed to stop the outbreak grows exponentially. We suggest that education programs are implemented to teach locals how to identify the beginnings of an Ebola infection, so that they know to seek treatment quickly. Also, we suggest that the reporting of all suspected cases is made mandatory.

Optimizing the location of the distribution of the vaccine will be performed using our next two models.

2.4 Strengths and Weaknesses

The biggest strength of this model is that its predicted number of cumulative cases of Ebola closely matches the number of recorded cases in Guinea's recent outbreak. This suggests that the conclusions we derive from this model can be applied to real outbreaks with similar results. Also, it is worth noting that

The biggest weakness of this model is that it predicts the disease to be remarkably more volatile than its behavior suggests. As our predicted value for R_0 is increased from 1, the disease begins to proliferate much faster than it does in reality. Similarly, as our R_0 value is decreased from 1, the disease is eradicated much faster than is observed. This weakness is most likely due to the fact that we are assuming our population is homogeneous and well-mixed. This is not actually the case. It is impossible that over 11 million people interact with the entire population constantly and for the same amount of time. This assumption causes our simulated infectious people to meet and infect many more people than they would in real-life. For the same reason, when R_0 is less than one, our simulation cannot account for the virus perpetuating in small communities for an extended period of time before it is eradicated. This explains why our simulated $R_0 = 1.2$ looks like a real-world $R_0 = 1.5$. This logic also shows that our model becomes weaker the further the basic reproduction number deviates from one.

Along these same lines, this model is extremely sensitive to initial conditions. Initializing the simulation with 27 people in the latency period yields

much different results than initializing the model with 35, even though they are almost the same percentage of the total population of Guinea. This is because the rate at which new people are infected grows exponentially as the number of infected people increase. Also, it should be noted that it is rare for a large number people to immediately become sick at exactly the same moment. [NEED REFERENCE] This mirrors the behavior of an actual outbreak, though, so it is not a weakness in the model unless an unreasonable number of people are initialized to be sick. It is rare for a large number people to immediately become sick at exactly the same moment. In this situation, it is more likely that the outbreak began with just a few cases, but they were not observed.

In fact, the behavior of our model reveals how important it is to spot an outbreak early in its development. The amount of resources needed to treat an outbreak grows exponentially as the number of initial cases grows. Therefore, we reiterate our suggestion to educate the population of West Africa about the symptoms of Ebola so they know to seek treatment immediately, and to enforce mandatory reporting of all suspected cases.

Parameters	Definition	Interpretation
v_i	The i^{th} Vertex	The i^{th} Country
$P_{i,j}$	The Weight of the Edge from Vertex i to Vertex j	How Infectious Country i is to Country j
N	The Set of All Vertices	The Countries in West Africa
R_i	The Set of All Vertices Connected to v_i	The Countries that Share a Border with Country i
S_i	The Susceptible Population in v_i	The Susceptible Population in Country i
I_i	The Infectious Population in v_i	The Infectious Population in Country i

Table 5: Parameters for Network Model

3 Network Model

3.1 Development

One question we have not yet addressed is where these vaccines should be distributed. The shortcomings of our previous model would not allow us to answer this question; the necessary conditions of homogeneity and perfect-mixing imply that the method is not scalable for large populations. In order to determine where in West Africa the vaccine would have the greatest effect, we must use a model that takes into account the formation of subpopulations, and it must allow certain subpopulations to be less "social" than others. With these ideas in mind, we developed network and a Markov matrix model to simulate Ebola outbreaks in West Africa.

Our network spans over most of West Africa. We treat each region (as defined by the WHO) as a subpopulation, a vertex in the network. Each country is connected to another vertex by a weighted edge, where the weight represents how connected, or infectious, one country is to the other. We calculate these infectiousness numbers for each edge and store them in a large matrix, à la Markov. Once this is done we generate a random vector of initial states and continuously multiply the vector and the Markov matrix together.

We know from the theory of Markov chains that this process will eventually converge to a steady-state vector, which represents how infectious each subpopulation is to the rest of the network. Distributing all the vaccines to the most infectious regions (using the techniques learned from the SEIR Model) will optimally slow the spread of the virus, leading to eradication.

Because this model is significantly different than our first, we need to take the time to define some new parameters and assumptions,

The crux of this model is calculating the parameter $P_{i,j}$. We have defined this parameter to be

$$P_{i,j} = \begin{cases} \left(\frac{S_i}{\sum_{k \in R_j} S_k}\right)\left(\frac{I_j}{\sum_{q \in R_i} I_q}\right) & i \neq j \\ 1 - \sum_{k \in R_i} P_{i,k} & i = j \end{cases}$$

Qualitatively, right-most term in this equation is saying that any given region is more likely to be infected by its most infectious neighbor. More subtly, the other term in this equation states that any given node is more likely to be infected by a neighbor who considers the region to be the most susceptible. These values can be interpreted as a probability of infection for v_i. This interpretation and the fact that the values are stored in a Markov matrix require that $0 \leq P_{i,j} \leq 1$, and that the sum of the probabilities belonging to each node is equal to one. This is also why a probability must be defined for the case when $i = j$. This condition simply states that any "left over" probability goes to maintaining the vertex's status quo.

This model also relies upon some key assumptions:

- The area of the region is not accounted for nor how the people are distributed within it.
- It assumes that people go to surrounding counties with the same probability.
- It assumes that the disease will only be spread to adjacent counties.
- It assumes that the Si and Ij have the same relation to the probability as each other.

3.2 Results

Using the aforementioned probability distribution for weighting the edges of the network, we can now construct a Markov matrix using 58 different counties and districts from Guinea, Sierra Leone, and Liberia. Furthermore, we can construct a visual representation of what this network looks like as seen below.

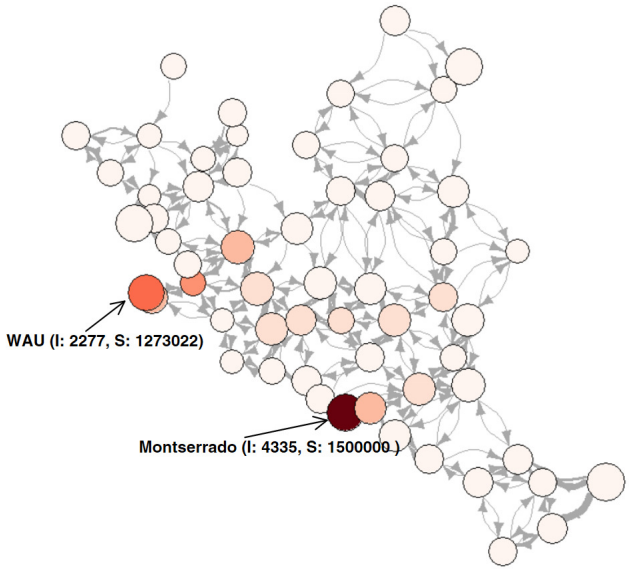

Figure 4: Current State of Infected Regions of Africa

As one can see in the network above, each of the territories is represented by a circle where the size of the circle indicates the population of the territory, the color of the circle represents how many infected there are, and the width of the edge indicates that magnitude of the value.

Now that we have this Markov matrix and its visual representation, we can find stead-state vector as previously mentioned. Once this is done, another visual representation can be constructed where instead of the colors representing amount of infected, they will represent amount of threat to spreading the virus.

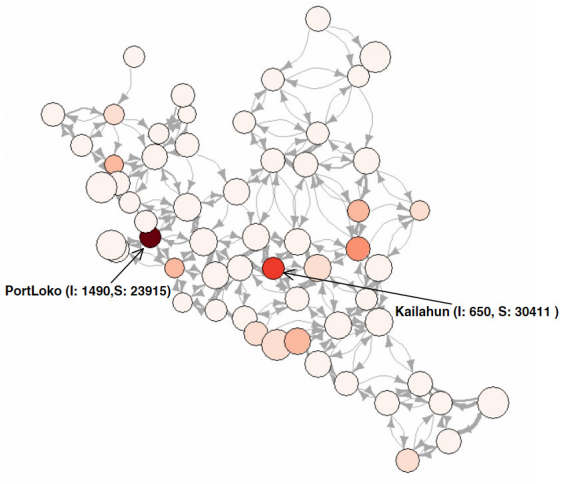

Figure 5: Ranking of the Most Infectious Regions-Denoted by Color

As seen above, the two territories that the algorithm identified as having the most risk to other territories are Port Loko and Kailahun. There are several key attributes of our model that is demonstrated through this result. For one thing, note that the territories selected to have the most risk of spreading are not the territories with the most infection; this is due to the fact that the territories with the most infected people often do not have many connections or are surrounded by territories that are already themselves infected with a lot of people. Another thing to note is that the territories identified by the algorithm are not only some of the more infected territories, but they are the territories that would have the most devastating effect if they were to spread their disease to surrounding territories. Because of this, they hold the most danger for spreading the virus and thus should be some of the first territories to be treated.

3.3 Evaluation

Overall, this model holds many key benefits that can be used when deciding where to apply the vaccine first. As previously discussed, it can identify which territories have the greatest risk of becoming an epicenter for the disease. This is invaluable for eliminating Ebola in the most contained manner possible. In other words, although this may not be the fastest way of eradicating the disease it is the safest in terms of preventing the disease from spreading to more places.

That being said, the model has some drawbacks that inhibit the accuracy of the model. For one thing, the model assumes that population in each territory is uniformly distributed and neglects any idea of area within each territory. In future models this could possibly be amended by splitting the territories used above into even smaller territories; thus, the error introduced from neglecting area and population distribution is reduced to an even greater amount. In a perfectly ideal situation, the model could be expanded down to such a fine level that the vertices in the network represent people rather than territories.

Another weakness of the model is its assumption of uniform conditions throughout all territories. This is harmful to the model because poor conditions in areas can lead to a greater likelihood of becoming sick, thus skewing the probability for that disease to spread. Likewise, a territory may have exceptional medical facilities which would make it less likely for the disease to spread to this area. This could possibly be addressed by researching health conditions and adjusting the probability distribution used for finding edge weights correspondingly.

Furthermore, the model does not discuss the probability of the disease spreading in a non-contiguous manner (spreading in a way other than crossing a border). For example, a diseased person could travel by sea, could travel by air, or could even just drive across multiple territories to infect others. An extension of this limitation is that the model only considers West Africa and does not explore the idea of the disease spreading outside of this area. Given more time and resources, a probability distribution could be made that connects all vertices in the network in the graph and considers the distance between the two nodes and the likelihood of traveling to that specific vertex.

Lastly, this model only considers initial conditions of the disease and fails to identify nodes to target as time progresses and the virus spreads or dwindles. However, this shortcoming will be addressed in the following model.

4 SEIR-Networking Model

4.1 Development

Now that we have established two separate methods of modeling Ebola outbreak, we will attempt to merge the two together in order to get benefits from both. Not only will this new model be able to show how the virus spreads or dies off over time because of the SEIR model, but it will also be able to show how the infection spreads geographically because of the Markov model. We start by reconstructing the network found with the Markov model. This time, we make sure to record each territory?s S, E, I, and R population. After the network has been found the ODEs of the first model can be applied to each vertex in the network for a given time step. However, we must now also account for infections spreading between vertices and find a way for that to be reflected in the ODEs. To do this,

$$\lambda_i = \frac{r\beta \sum_{R_i} I_i + P_{i,j} I(t)}{N_i(t)}$$

To demonstrate we will first start with the network that reflects the initial conditions of the different territories of West Africa. Note that this will be the same network found in the previous section of this paper; additionally, the same cities are chosen for treatment. However, now we can advance time on the network to see how the virus progresses.

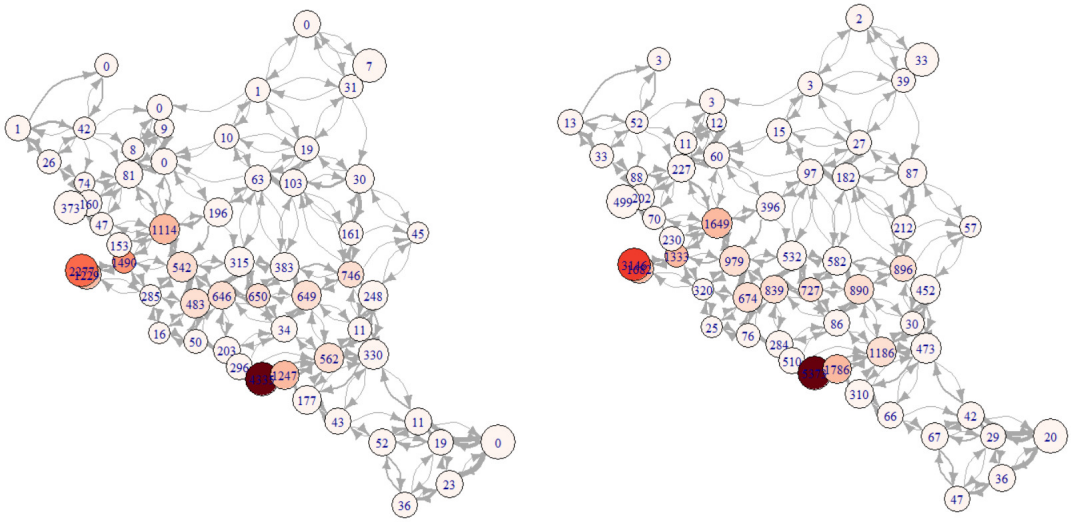

Figure 6: Ranking of the Most Infectious Regions-Denoted by Color

Looking at the numbers of infected at each vertex, one can see that each territory has become more infected. Even territories that initially had no infected population become more infected, indicating that infection is actually spreading through the edges of the network as well as within a given vertex. Ideally, this progression of the outbreak could be calibrated with actual information found from how the virus progressed in the past; however, those past resources seem to be unavailable; thus, we would have to wait until future data is released to calibrate the spread of the disease. Likewise, now that we have a different geographic distribution of the virus we can re-rank the territories as we had done for the initial condition.

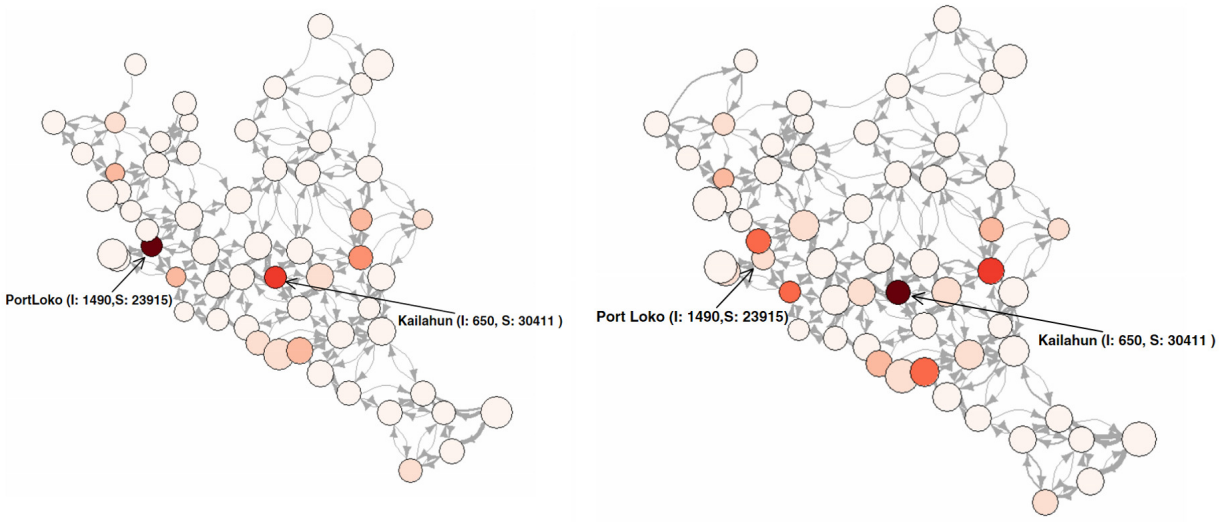

Figure 7: Ranking of the Most Infectious Regions-Denoted by Color

One can easily observe that after the disease has progressed some amount the most dangerous territories in terms of spreading the virus have shifted. This is because as the situation evolves, the disease spreads and creates new epicenters that need to be dealt with.

4.2 Evaluation

This model becomes a useful tool for identifying which cities to target because, like in the previous Markov model, we can identify which territories are vital for treatment; then, time can advance and new potential threats can be found. This is essential for eradicating Ebola because it is almost certain that Ebola will not be eradicated after only a few territories have been treated. Instead, Ebola will be eradicated through a number of phases, each corresponding to a different geographical distribution of the virus. Because we have a tool to model each phase of those geographical distribution, we can better plan out the full process for eradicating Ebola. In the future, this model can be expanded to include how the virus spreads once vaccines have been distributed to key cities. In this way, we would have an even better understanding of how to distributed vaccines in the future since it would account for the virus reacting to our intervention. One weakness of this

model is that it treats the probabilities (i.e. the edges between the vertices in the network) as rates in the differential equations rather than probabilities. Although this may approximate the actual situation for large amounts of time, there exists a discrepancy nonetheless. Furthermore, we have no way of telling whether those probabilities are accurate to the real world situation because we do not have access to resources revealing that information. Perhaps, given access to more information the model could be optimized to reflect an even more realistic progression of the disease. Furthermore, this model shares many of the weaknesses of the pure Markov model. For example, the model fails to account for the area and population distribution of each territory, the conditions of each territory, and other possibilities of the disease spreading. Likewise, given more time and resources, this model can be expanded in similar ways to minimize the effects of the weaknesses in the graph.

5 Conclusion

In summation, through these three models, we have learned valuable information needed for stopping the spread of Ebola and ultimately eradicating it. For our first model, we used differential equations to model how much vaccine we would need to stop Ebola in a given community with respect to the number of people in latency for that area. Next, we moved to a network model and used a Markov matrix in order to model which territory was the most likely to spread disease to other territories. As a result, we identified Port Loko and Kailahun as territories to treat so that the virus does not spread any further. Lastly, in our third model, we paired the two models together so that we could predict how the virus would spread geographically over time. This allows us to make a more extensive strategy for eliminating the illness as we can predict the shape of future situations. Overall, while the models explored in this paper undoubtedly have setbacks and leave room for future improvement, the information that they provide about the current situation with Ebola would be a great help in eradicating Ebola.

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