Extinguishing Ebola

An analysis of the spread and suppression of Ebola.

38707

Summary

Ebola is an aggressive, viral disease that is currently spreading through Western Africa. Assuming the existence of an Ebola vaccine, modeling the disease's behavior would be imperative to determine the most efficient strategy to exterminate the disease. To this end, we created a two-layer model to simulate the spread of Ebola within single populations and throughout a regional network. Using a system of differential equations, we created a robust SIR model that was insensitive for physical values for all parameters and initial conditions. The SIR model made up the first layer of our model and accounted for local vaccination, quarantine, death, and survival rates. After a series of iterations, we determined the best strategy for locally combating Ebola is through a combination of quarantines and oscillitory vacine production. Creating a network of nodes to simulate city connections, the second layer modeled spread of Ebola throughout a region. Applying several macro-level vaccination strategies, we determined vaccinating all adjacent cities and restricting travel between cities was the best response-based policy. However, taking preemptive measures and vaccinating proportional to the eigenvector centrality of a city network yielded the best results: saving on average 94.6% of the population per city.

Contents

Introduction

In August of 2014 the World Health Organization (WHO) declared an outbreak of Ebola in the West African country of Ghana. Since the outbreak, there have been 22,460 cases of Ebola around the world, and health organizations in every infected country are still striving to squelch the disease.[4] Conquering Ebola is a difficult task because it is a virus, and therefore drug based cures are ineffective and unrealistic.[7] The best hope for defeating a viral outbreak is vaccination, and recently there have been promising advances in the development of an Ebola vaccine.[3] Once a new, viable vaccination is developed, there will still be many issues to consider when creating an eradication strategy. In addition to the spread of the disease, an elimination plan must also account for the speed of vaccine manufacturing, rapidity of vaccine delivery, efficacy of the particular delivery method, and the effects of quarantining.

Model Overview

To build a strategy for suffocating an outbreak of Ebola, we used a system of ordinary differential equations (ODEs) to build a standard Succeptible-Infected-Recovered (SIR) model which simulated the spread of disease through a community of people. Simulating the dissemination of Ebola through a population should also include a macro model for the population level. We implemented a simple, second layer network model to simulate the spread between multiple communities and various vaccination strategies. The convergence of the straightforward SIR structure with the scalable network approach produced a robust model capable of providing a complete picture of the epidemic that will help inform public health officials about the best strategies to eliminate the spread of Ebola.

An Overgeneralization: The initial SIR model represented the way a disease spreads through a localized group of people. We made many generalizing assumptions to create a basic picture of what happens when an outbreak occurs. This was the foundation upon which our more realistic and complicated models were built.

A Realistic Approach: We expanded the first version of the SIR model to include a quarantine variable, more realistic rate of infection, and a

constant rate of vaccination. The result was a more practical model, with sensible growth and reduction of the infected population; however, it failed to consider the limitations of vaccination delivery and manufacturing.

Vaccination Strategies: Accounting for transportation and production restrictions led us to the third and final version of our SIR model. This is our most comprehensive assessment of the spread of Ebola through a localized populace, and is capable of evaluating the implementation of different vaccination strategies. While this version is an improvement upon the previous two, it does not account for the spread of Ebola between communities.

Scalable Quarantine & Vaccination: The SIR model is limited in scope to a single community, so we developed a network model that accounts for the rate of travel between communities, macro level vaccination tactics, and the spread of Ebola through a geographic region.

Succeptible - Infected - Recovered

The basic SIR structure is a three compartment ODE model that simulates the spread of a disease within a community. Each of our SIR models were solved using the numerical solver ODE45 in MATLAB. The behavior of each model is subject to specific parameters and initial conditions, which have values that are dependent upon assumptions. Figure 1 is a schema of the SIR model we used to simulate the spread of Ebola through a community. Susceptible individuals of a community, S, can become Infected, I, or Recovered, R, through the implementation of vaccinations. Infected individuals can either become Recovered after receiving extensive medical care[1] or die.

Version 1: An Overgeneralization

Assumptions

Our initial model includes many simplifying assumptions. First, due to the viral nature of Ebola, developing a drug-based cure for treatment after in-

[1] In the case of Ebola, there is no cure, but early hospitalization and treatment can lead to recovery.[5]

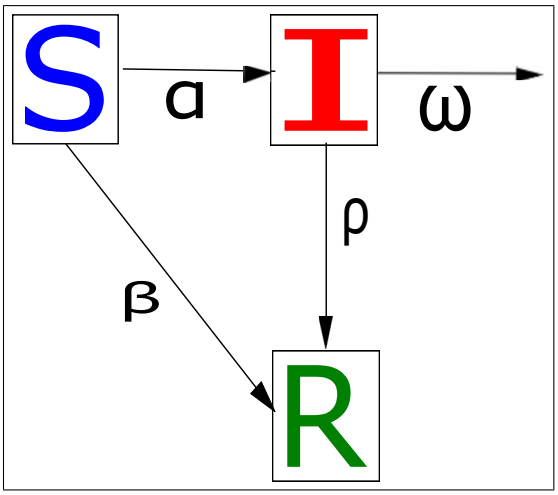


Figure 1: The simple SIR model

fection is impossible. Instead we must defend against a viral outbreak with vaccination.[7] Second, the birth rate and death rate of a community are equal, ensuring that there is no change in the population from any factor other than Ebola. While the Ebola virus is contractible from animals, we assume the animal-human interaction rate is negligible when compared to the human-human interaction rate. Therefore, susceptible individuals only become infected by interacting with infected individuals. The fourth assumption we made was that the use of personally protective equipment by healthcare workers is generally negligible when looking at the overall population, thus each person has an equal chance of contracting Ebola from any interaction with an infected person. Once contracted, the disease was assumed to last three weeks in the infected person before that individual died or recovered (three weeks is the average duration of infection [6]). The rate of movement from Susceptible to Infected was assumed to behave under the law of mass action, or proportionally to the product of the number of Susceptible and Infected peoples. For this first model we also assumed a constant vaccination rate throughout the epidemic and that the vaccination rate for an Ebola outbreak would be similar to a meningitis vaccination rate. The WHO estimates death rates of Ebola ranging from $50\% - 90\%$ depending on the strain[5]. To slow the dynamics of an Ebola outbreak and better visualize the spread of disease we assumed a less deadly strain. Because the definition of an outbreak is maleable, we defined an outbreak as being at least 5% of

the population being infected.

Model and Parameters

The rate of change of S, I, and R individuals within a community was represented with a system of differential equations (1). The units of time were all considered to be in weeks. The first was the rate of change in the Susceptible population. This rate was characterized by Susceptibles moving from S to I by an infection rate proportional to the product of SI. Susceptibles were also able to move directly into the Recovered compartment via vaccination. The rate of recovery was considered proportional to the number of Susceptibles. The compartment I grew with the same rate Infected individuals left S. Infected individuals left the I compartment either through death or recovery. Both the rates of mortality and recovery were proportional to I, and R grew at the same rate as S was vaccinated and I recovered.

$$\begin{aligned} \frac{\mathrm{d}S}{\mathrm{d}t} &= -\alpha IS - \beta S \\ \frac{\mathrm{d}I}{\mathrm{d}t} &= \alpha IS - (\omega + \rho)I \\ \frac{\mathrm{d}R}{\mathrm{d}t} &= \rho I + \beta S \end{aligned} \tag{1}$$

The parameters α, β, ρ, and ω in (1) represent the likelihood of infection, likelihood of vaccination, chance of recovery from infection and chance of death respectively. To ensure all differential equations are in the form of $\frac{\text{number of people}}{\text{week}}$ the units of each parameter are:

$$\begin{aligned} [\alpha] &= \frac{\text{proportion infected}}{\text{people} \cdot \text{week}} = \frac{1}{\text{people} \cdot \text{week}} \\ [\beta] &= \frac{\text{proportion vaccinated}}{\text{week}} = \frac{1}{\text{week}} \\ [\omega] &= \frac{\text{proportion of deaths}}{\text{week}} = \frac{1}{\text{week}} \\ [\rho] &= \frac{\text{proportion recovered}}{\text{week}} = \frac{1}{\text{week}} \end{aligned}$$

Realistic values for each parameter were researched and used during analysis [4, 5, 6] . The parameter α was estimated using the value of $\frac{r_0}{3} = \frac{2}{3}$, where

r_0 is the average number of new cases per case over an entire infection. The value was divided by three to get the average rate of infection per week assuming one infection lasts three weeks. While $\frac{r_0}{3}$ is not a perfect estimate for proportion of infected per person each week (due to poor estimation), it seemed adequate for our first model. The average vaccination rate per week during the meningitis outbreak was found to be 14.4%. Under the assumption that an Ebola vaccination rate would be comparable to a meningitis vaccination rate, β. To simulate a less deadly strain of Ebola we set $\omega = \frac{0.6}{3}$ and $\rho = \frac{0.40}{3}$ for the average death and recovery rate per week, respectively.

Performance

Figure 2 shows the population of each subpopulation over a year. The rate of infection was massive, showing nearly all individuals becoming Infected instantly. It only took four months for the disease to disappear; however, this is becausethe whole population had recovered or died. By the time the strain was exterminated only 2000 people remained in the city.

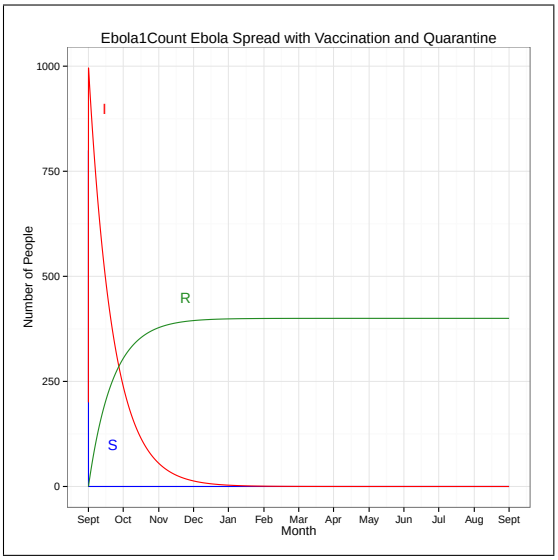


Figure 2: SIR model Version 1

Version 2: A Realistic Approach

Acknowledging the limitations of our ground level SIR model led us to consider the effects of quarantining infected and more accurately portraying rates of interaction between the Susceptible and Infected groups.

Assumptions

Our second version included many of the same assumptions made in version 1 with a few key additions. Instead of assuming mass action interactions between Susceptibles and Infected, we assumed the number of interactions with Infected individuals over a week would best be represented by a Poisson distributed random variable with probability mass function: $\frac{\lambda^k}{k!}e^{-\lambda}$. This is a reasonable assumption because Poisson random variables characterize a given number of events over a time period. To further improve realism in our model, we added the assumption that quarantining some infected individuals, a common practice during Ebola outbreaks, occurred within a community at a rate of one in five people. During an Ebola infection, individuals are only contagious after incubation, which accounts for half of the duration of disease.[5] At a given time, only half of the total infected population is actually infectious, assuming a uniform distribution of all severities accros the infected population.

Model and Parameters

To develop a model that considered quarantines and rates of interaction between Infected and Susceptibles, we developed the parameters q and μ. Quarantine measures were accounted for with q. Under quarantine procedures, Susceptibles are unlikely to interact with all members of the Infected population and q represents the proportion of non-quarantined Infecteds. This rationalization led to the development of μ, which represents the average number of infecting encounters per week. To develop μ, we looked at the average number of new cases per case per week, our modified r_0. Because we introduced a quarantine term, we modified R_0 again to reflect the decreased probability of an infectious encounter. We did so by multiplying r_0 with $\frac{qI}{2(qI+R+S)}$, the probability of encountering a non-quarantined Infected

individual in a community. Therefore, $\mu = \dfrac{r_0 qI}{2(qI + R + S)}$ represents the rate of infectious interactions per week. We let $\lambda = \mu$ in the Poisson random variable. Finding the expected value of the Poisson distribution told us that the average number of infectious encounters per week was μ. We then multiplied μ with S to determine the average number of infectious encounters between S and I. The previous αIS term in both $\dfrac{\mathrm{d}S}{\mathrm{d}t}$ and $\dfrac{\mathrm{d}I}{\mathrm{d}t}$ equations was altered to reflect this change. The value of q was set to $q = 0.8$ to reflect a quarantine rate of 20%. This value would likely vary depending on the geographic locations of an Ebola outbreak. In a society with strong healthcare infrastructure we expect much lower values of q whereas areas with weak healthcare infrastructure exhibit much larger values. All other parameters remained the same between Version 1 and Version 2.

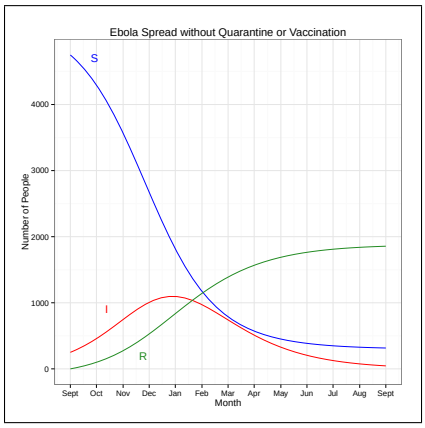
$$\begin{aligned} \frac{\mathrm{d}S}{\mathrm{d}t} &= -\frac{\mu S}{2} - \beta S \\ \frac{\mathrm{d}I}{\mathrm{d}t} &= \frac{\mu S}{2} - \frac{\omega I}{2} - \frac{\rho I}{2} \\ \frac{\mathrm{d}R}{\mathrm{d}t} &= \frac{\rho I}{2} + \beta S \end{aligned} \tag{2}$$

The units for the new parameter μ are $[\mu] = \dfrac{1}{\text{week}}$ where the units of qI and $2(qI + R + S)$ cancel each other out and we are left with just $[r_0] = \dfrac{1}{\text{week}}$. Therefore, all equations are in the appropriate $\dfrac{\text{number of people}}{\text{week}}$ form.

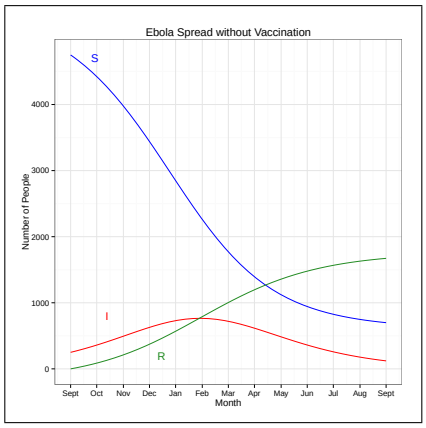
Performance

Version 2 showed much more realistic behavior than that of Version 1. Unlike Version 1, the growth curves are smooth and do not show an unexpected increase in any of the sub communities. Figure 3 shows the consequences of an unchecked infection without quarantine measures or vaccines. This figure provides a good baseline measurement for effectiveness of control measures: by the end of year only 2,171 (43.4%) people survived.
Figure 3 shows the effect of quarantining one out of every five individuals. The rampant growth of infection seen in Figure 3 is not present; however, the infection subsists for the entire year and shows signs of lingering throughout

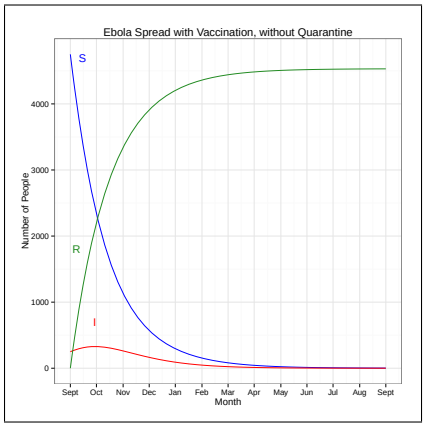
the second year. These results suggest even low-levels of quarantining aid in surviability: by the end of the year 2,371 (47.4%) people survived.
While small levels of quarantining made small improvements, vaccination was able to efficiently move Susceptibles into the Recovered group and essentially remove the infection from the population within half a year (Figure 3). Combining both light quarantine with vaccination slowed movement between Susceptible and Infected groups, and gave the best results both in terms of time until extermination and number of lives saved (Figure 3). By the end of the year 4,530 (90%) people survived. Running our model through multiple simulations, we found increasing β toward 1 and reducing q toward 0 resulted in increasing the number of survivors after an epidemic. Therefore, all measures should be taken to increase the amount of vaccination and quarantining during an epidemic. However, to aid in analysis between models, we will continue to use $p = 0.8$ and $\beta = 0.144$



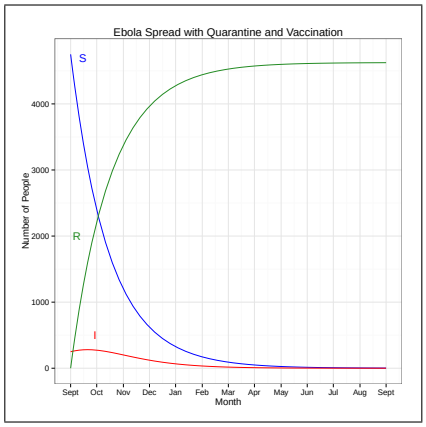
(a) without Quarantine or Vaccination



(b) with Quarantine



(c) with Vaccination



(d) with Quarantine and Vaccination

Figure 3: SIR Model Version 2

Version 3: Vaccination Strategies

While we were satisfied with the performance of our SIR model after the changes in Version 2, the assumption of constant vaccination was flawed. Although a constant rate of vaccination could account for quantity of medication under some circumstances, it is insufficient to account for the speed of drug manufacturing. Likewise, constant vaccination does not allow for different local inoculation strategies that could provide different methods for exterminating the disease. The best way to introduce factors for drug manufacturing, quantity of medication, and availability of medication was

to make β an oscillating function of time that represented the number of available vaccines.

Assumptions

While we are no longer assuming constant vaccination, we do assume the total amount of vaccination stays constant between models. This means any variation between Model 2 and Model 3 will be due to variations in vaccination strategy and not overal vaccination quantity. We also assume a one-to-one correspondance between number of vaccines available and proportion of vaccinated population over the unit time(e.g. if we have a single vaccine and a population of 100, we can vaccinate 1% of the population during the time interval).

Model and Parameters

To develop our new β we decided to look at two oscillating functions: the square wave and the negative sawtooth wave (Figure 4). The amplitude of the wave represents the available amount of medication (or because of the assumed one-to-one correspondence, the percent of the population vaccinated) at a given time t. The frequency of both waves represents the speed of drug manufactoring where longer periods result in longer production times. Contextualized, a sawtooth function with a period of one week would correspond to a single shipment of drugs being rationed off throughout the week. During the week the drug company would be able to produce another shipment of equal quantity and drop it off again at the end of the week. A square wave would be similar, however, there woud be a week of intense, constant vaccination followed by a week of drought. To ensure the total amount of vaccination between models remained the same, and to dissallow for negative vaccination proportion, we set the amplitude of each wave equal to the previous $\beta = 0.144$ and implement a vertical shift by 0.144 as well. Thus, the resulting function for β was:

$$\beta = 0.144 - \frac{0.144}{\pi} \sum_{k=1}^{\infty} \frac{\sin\left(2\pi k f t\right))}{k}$$

Where f changes depending on the speed of drug manufacturing. With the exception of the new β function, the structure of Model 3 remains the same:

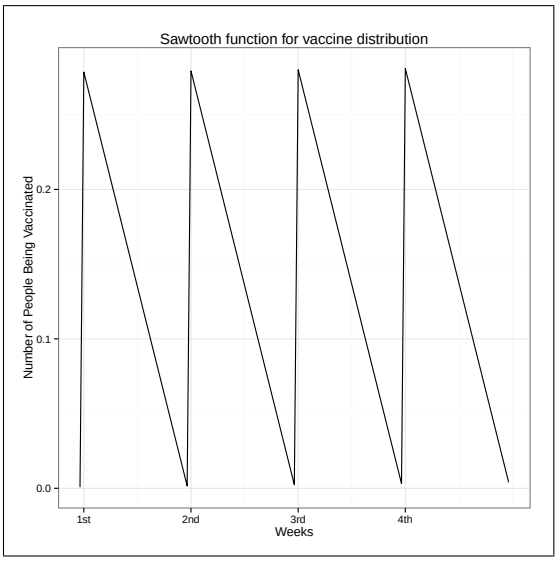


Figure 4: Sawtooth Distribution of Vaccinations

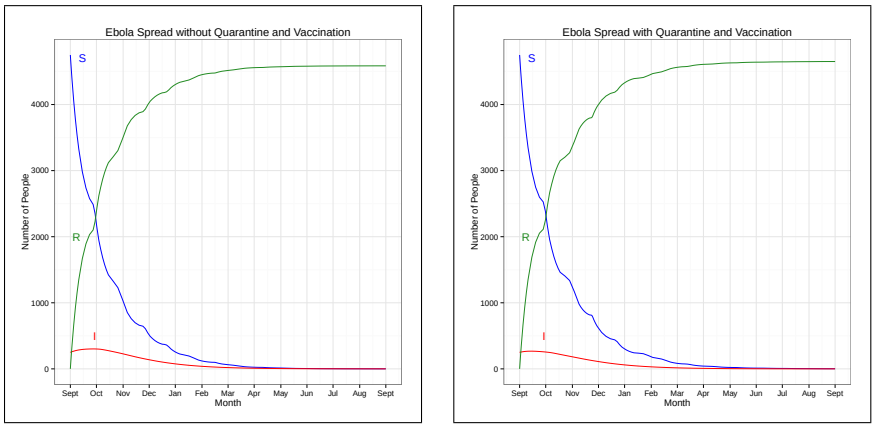
$$\begin{aligned} \frac{\mathrm{d}S}{\mathrm{d}t} &= -\frac{\mu S}{2} - \beta S \\ \frac{\mathrm{d}I}{\mathrm{d}t} &= \frac{\mu S}{2} - \frac{\omega I}{2} - \frac{\rho I}{2} \\ \frac{\mathrm{d}R}{\mathrm{d}t} &= \frac{\rho I}{2} + \beta S \end{aligned} \tag{3}$$

Likewise, because of the assumed one-to-one correspondance between number of vaccines and proportion of vaccinated population per unit time, the units of β remain the same and $[\beta] = \frac{1}{\text{week}}$. Again, ensuring the proper unit structure for our system of equations.

Performance

Performance of the third model showed the importance of early vaccination and the benefit of rationing vaccines over a time period. In general, a sawtooth distribution of vaccines outperformed a square wave pulse (saving 4655 to 4628 people). Likewise, distributing vaccines according to a sawtooth distribution showed marked improvement over constant vaccination (Figure 5). In general, decreasing the frequency of the distributions also showed increase performance compared to high frequency distributions of vaccines (1 week,

4377; 2 week, 4428; 3 week, 4458; 4 week, 4655). Experimenting with the square wave distribution showed even though total amount of vaccination remained constant, failing to vaccinate within the first three weeks resulted in more loss of life and spread of the disease when compared with vaccinating within the first three weeks (4,369 people compared with 4628). Model 3 suggests in order to best combat the spread of Ebola, vaccine suppliers should focus on producing a large supply over extended periods of time (4 months in our model). Once the supplies are dropped off, production should begin again. Medical workers should focus on rationing the vaccines, but also deliver more vaccines during the initial vaccine drop-off phase. Figure 6 shows substantial improvement across each iteration of our SIR model with a sawtooth dissemination of vaccines outperforming other delivery methods.



(a) with Quarantine and Vaccination (b) with Vaccination

Figure 5: SIR Model Version 3

Sensitivity and Robustness

To analyze the sensitivity and robustness of our model, we conducted bifurcation analysis at equilibria and simulated 20 Ebola infections using different parameter values. The simulations selected random parameter values from a realistic range and ran over a one year time period. From research the ranges allowed were: $r_0 = (1.5 - 2.5)$, $q = (0.2 = 0.8)$, $\beta = (0.05 - 0.25)$, $\omega = (0.50 - 0.90)$, $\rho = (0.50 - 0.10)$ [4, 5, 6].

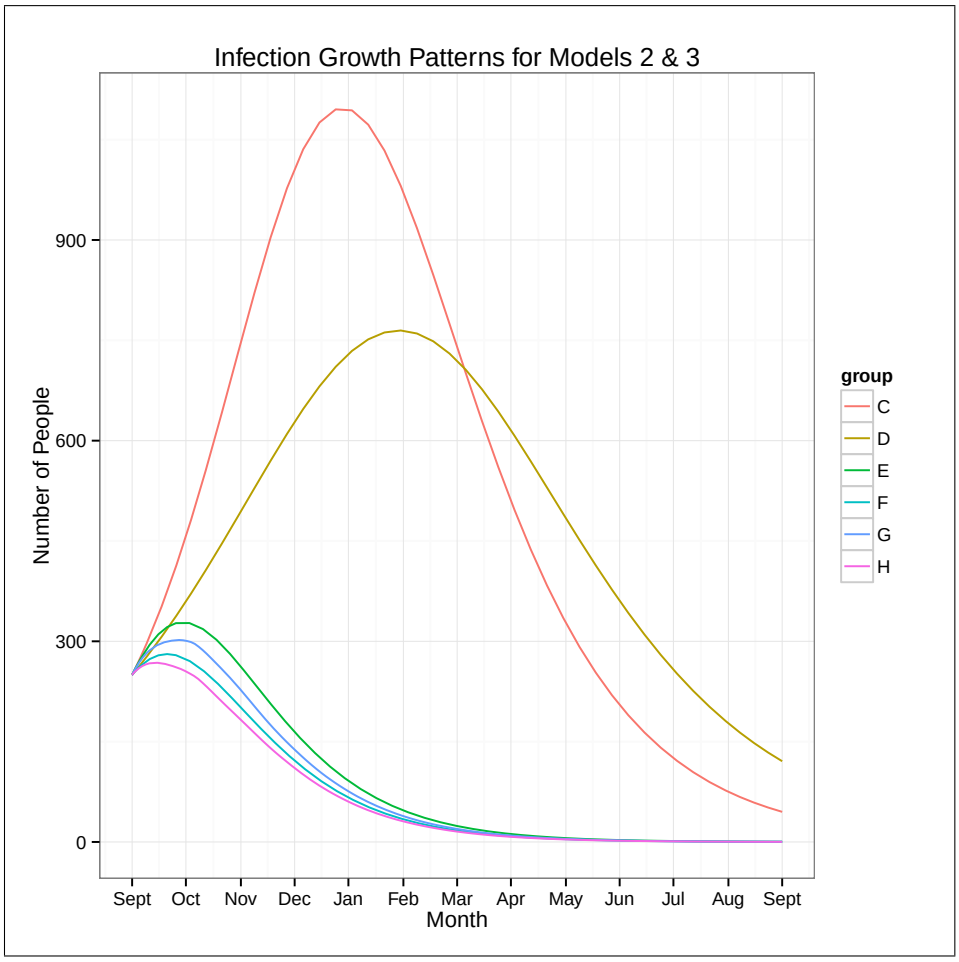


Figure 6: Infection Rate for Models 2 & 3

Bifurcation Analysis

Bifurcation was done by finding the equilibria of the model, linearizing the system using the Jacobian, and finding the Eigenvalues of the Jacobian. Solving equilibria in Model 3, substituting μ in and letting β represent the sawtooth function from Model 3:

$$\frac{\mathrm{d}S}{\mathrm{d}t} = \frac{-r_0 qSI}{2(qI+S+R)} - \beta S$$
$$\frac{\mathrm{d}I}{\mathrm{d}t} = \frac{r_0 qSI}{2(qI+S+R)} - \frac{-\omega I}{2} - \frac{\rho I}{2}$$
$$\frac{\mathrm{d}R}{\mathrm{d}t} = \frac{\rho I}{2} + \beta S$$

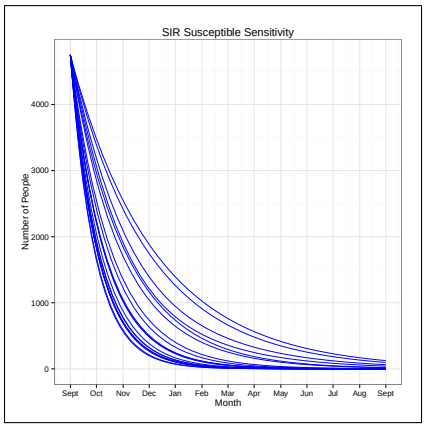
Setting each rate equal to zero and solving for S, I, R gives the physical equilibria at $I = 0$, $S = 0$. Finding the Jacobian of the system then gives:

$$J(S,I,R) = \begin{bmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ \beta & \frac{\rho}{2} & 0 \end{bmatrix}$$

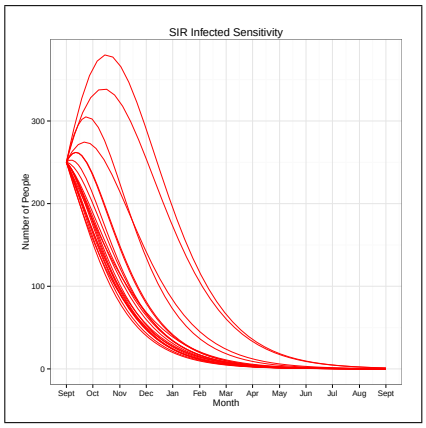
Thus, the only Eigenvalues of the Jacobian are $\lambda = 0$ and the equilibrium is non-hyperbolic: suggesting a non-robust equilibrium.

Randomized Simulations

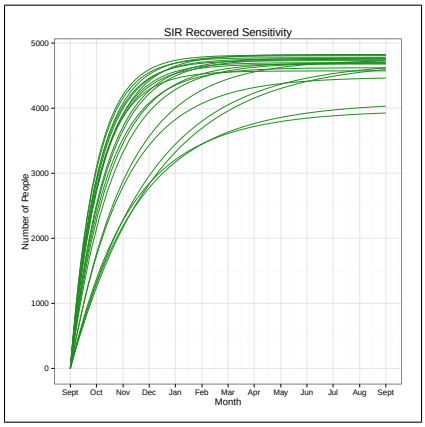
While bifurcation analysis shows instability and a non-robust system, we were confident our model showed similar qualitative behavior when using physical values for parameters and populations. In order to explore strength of our model using realistic values, we ran 20 different simulations with randomized parameter values. In all cases, the qualitative behavior was the same: in all cases Susceptible and Infected populations grew toward zero (Figure 7). The number of Recovered did change in each iteration, but this is to be expected because the death rate of Infected varies with each iteration. Simulations were also ran for a variety of initial conditions, again without a change in qualitative behavior. We conclude our model is robust for physical systems and demonstrates the same qualitative behavior across simulations. Therefore, the SIR model allows for a useful tool to measure the spread of Ebola within a community.



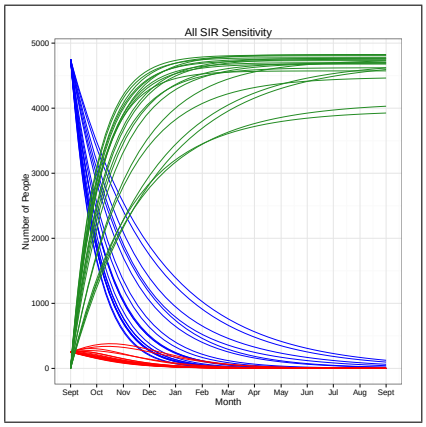
(a) Randomized Simulations for Susceptible



(b) Randomized Simulations for Infected



(c) Randomized Simulations for Recovered



(d) Randomized SImulations for all Subpopulations

Figure 7: SIR Model Version 2

Network Model and Regional Spread

While our SIR model explained and modeled Ebola outbreaks within a single community, most efforts to prevent the spread of the disease focus around multiple communities (e.g. villages, cities, countries, etc). In an attempt to focus on macro-level strategies for fighting Ebola, we created a simple, second-layer network model to simulate the spread of the disease between nodes. Simulations started by choosing a starting node, beginning infection, and tracking the infection and population sizes as Ebola spread between

nodes. We then focused on three different strategies of vaccination (vaccination of adjacent nodes, quarantining infected nodes while vaccinating adjacent nodes, and vaccinating proportional to the eigenvalue-centrality of each node) to determine which strategy saved the most lives and best contained the disease.

Assumptions

To begin, we assumed each node represented a city with a starting population of 5000. This decision was arbitrary and initial tests showed starting size did not effect the qualitative preformance of the model. All 5000 individuals were considered Susceptibles. Next, we assumed an equal basal likelihood to spread the disease between cities. This means we made no distinction between travel distance or travel densities when transfering a disease between cities. We also assumed the we were modeling an outbreak as it was starting, so only one started the simulation as infected.

Model and Parameters

When builidng the network, we chose an arbitrary network represented by (Figure yeaaah). We chose a network of 10 nodes for simplicity, but again the model is scaleable to larger nodes. To simulate spread of the disease throughout the network, we essentially ran a random walk. The simulations started by choosing a random seed city where the infection would begin. Spread throughout the network was modeled over the course of two years with $dt = 1week$. At each timestep, the probability of infection spread from an infected city to a non-infected city was calculated. A random number between zero and one was found to determine whether the infection spread. If the infection spread to a new city, a random value between $0\% - 5\%$ (again reflecting our definition of an epidemic) was chosen. This percentage would then represent the proportion of the newly infected population. This process was repeated for all infected cities. After determining newly infected cities, Model 3 was run for infected cities to simulate the spread of the disease within each city. Ending populations were taken from SIR output and used at initial conditions for the next iteration. If a city was not infected, the number of Susceptibles stayed constant at the initial starting population of 500. The process was repeated for two years.

To calculate the probability of spread from city i to city j, we derived the formula $\frac{q_i \cdot I_i}{2(q_i \cdot I_i + S_i + R_i)} \cdot \frac{S_j}{q_j I_j + S_j + R_j} \cdot a_{ij}$. Where $q_{i,j}$ are the proportion of non-quarantined Infecteds in their respective cities and $I_{i,j}, S_{i,j}, R_{i,j}$ are the number of each disease group in their respective cities, and a_{ij} is the entry of the adjacency matrix at row i and column j representing the basal likelihood of spreading disease between the two cities. The default value for all entries in the adjacency matrix were 1. Therefore, the first quantity represents the proportion of accessible Infected over the total population of accessible individuals in city j; the second term represents the proportion of Susceptibles over the total population of accessible individuals in city j. Therefore, their product with a_{ij} represents the probability of infecting susceptibles in city j from city i.

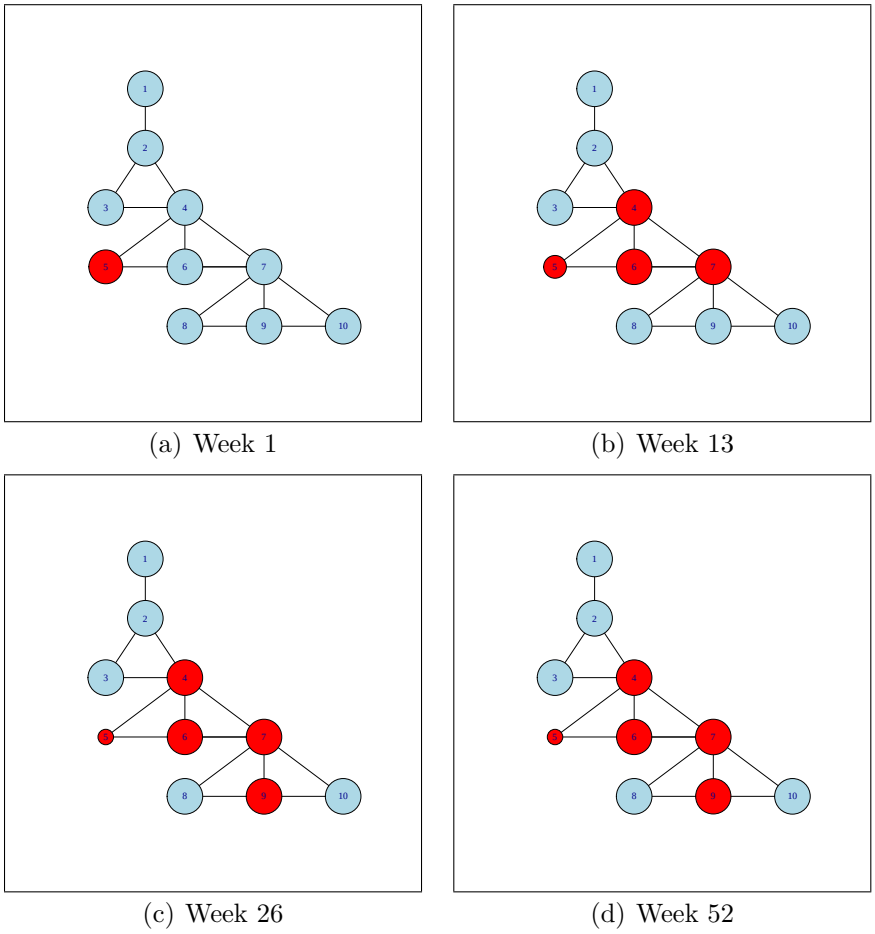
For SIR analysis during network simulation, basal parameter values were set to $r_0 = \frac{2}{3}, q = 1, \beta = 0.144, \omega = \frac{0.6}{3}, \rho = \frac{0.4}{3}$. We chose to set $q = 1$ to best determine how vaccine strategies varied performance without confusing vaccination effects with quarantine effects. After setting up the basic network, we decided to focus on our three different, macro containment strategies. For each strategy we ran 100 simulations with random starting nodes.

Strategy 1: Adjacent Vaccinations

The first strategy we implemented was to vaccinate only cities adjacent to infected cities. In this simulation, once a city became infected, any city with a connecting edge would be vaccinated. The total amount of vaccination was held constant, so the vaccines were split evenly between all adjacent cities. The logic was that the immunized population in adjacent cities would prevent the disease from spreading to other parts of the network.

Performance

This strategy proved to be a very effective way of keeping the infection from spreading throughout the network. This simple strategy was on par with our most sophisticated system. However, it relies on knowing exactly where the virus originates and so this strategy is only a containment model. Figure 9 is a representation of what happened to the network at various stages of infection over the course of one year.



(a) Week 1 (b) Week 13

(c) Week 26 (d) Week 52

Figure 8: SIR Model Strategy 1

Strategy 2: Quarantine with Adjacent Vaccinations

After testing adjacent vaccinations only, we decided to test adjacent vaccination with a quarantine between cities. This strategy seemed realistic as, again, quarantines are often used to restrict the spread of disease between regions. To do this, we altered our assumption that all cities have equal basal likelihood of spreading disease. This means for all edges connected to infected cities, travel was restricted and $a_{i,j}$ was altered to relfect the decreased flow

between cities. We ran the simulation for two different quarantine levels where $a_{i,j}$ was reduced to 0.60 and then to 0.40. These numbers were arbitrarily selected but do showcase the effect of differing rates of quarantine.

Performance

We added a twist to the Adjacent Strategies by creating a dynamic flow of vaccine and accounted for quarantine measures. The Dynamic Adjacent Strategies send vaccine to all cities that are or become adjacent to any infected city. These strategies end-up not performing as well as their non-dynamic counterparts. We theorize this was due to the fact that the infection was unlikely to spread out of the vaccinated cities adjacent to ground zero all together, so reducing the amount of vaccine available to the original adjacent cities only increased the number of infected in those cities and gave vaccine to cities that were unlikely to be infected in the first place.

Strategy 3: Vaccination Proportional to Eigenvector Centrality

After results from Strategy 2, we decided come up with a different approach for regional vaccination that did not rely on vaccinating adjacent cities. For this strategy, we found the eigenvector centrality of each node in the network and vaccinated proportional the that number. The motivation behind this strategy was to prioritize cities with a large amount of connections to other important cities. This would create an immune population at hub cities where the disease could travel easily to other cities. The immune population would then act as a buffer and stem the flow of the disease through the rest of the network.

Performance

We theorized that distributing the total amount of vaccine among nodes proportional to their eigenvector centrality score would be a very strong preventative measure. The eigenvector strategies performed almost identically to the adjacent strategies, however, the eigenvector strategies can be employed prior to any outbreak because they highlight the best locations for vaccination before the outbreak. We felt that this makes it our most promising strategy because it performs just as well as our best containment strategy,

but would perform even better as a preventative measure.

Sensitivity & Robustness

To test the robustness of the network level of our model we ran simulations of an outbreak for our variety of containment strategies. For the first battery of tests we simulated outbreaks originating from three types of nodes chosen for their position in our network: remote nodes, which have only one connection; medial nodes, which have two connections, and central nodes, which have three or more connections. For each combination of node type and containment strategy we ran 100 simulations of a two-year outbreak with each SIR parameter randomized within a range of plausible values every iteration. Our outcome measure for these simulations was the average number of healthy (Susceptible + Recovered) individuals in the network across all simulations. The Dynamic Adjacent Strategy was most effective for the remote node condition.

The second battery of tests was the same as the first, but each iteration of the simulation started with a randomly selected node as the origin of the disease. This tests the power of our strategies as preventative measures in addition to containment protocols.

		Adj. Vac.	Dyn. Adj. Vac.	Eigen Cent.
Av. Healthy After	No Q	4464	4176	4483
2 Yrs (from 5000)	20% Q	4746	4688	4731

Conclusion

While our base level SIR model contained flaws, it was nonetheless an effective footing to build a more realistic and effective model. Through multiple iterations and tests, we were able to determine high quarantine rates and oscillatory vaccination distributions were the most effective at eliminating the spread of Ebola. Designing a model that accounts for only the micro level spread of Ebola neglects the macro level dynamics of an Ebola outbreak and would have limited effectiveness. To this end, we developed an additional layer. The second layer focused on the iteractions between infected and noninfected cities by representing the cities as nodes in a network. Both parts of the model were effective at simulating the spread of Ebola, the capability of vaccination, and the effectiveness of quarantine in their respective layers. The first layer of our model showcased the importance of localized quarantines and distributing vaccines according to a sawtooth distribution. The model also indicated that the first three weeks of an outbreak are the most crucial for mitigating mortality rates. In every case where vaccinations were delivered, the number of Infected individuals was greatly mitigated, but there were certain strategies that resulted in the maximum number of lives saved. In our second layer, network analysis showed using eigenvector centrality and implementing quarantine measures between cities saved 4730 out of 5000 people on average. Therefore, if health officials wish to eradicate Ebola as quickly as possible, vaccinations should be distributed to cities depending on their relative connectedness with other cities. From there, vaccination within the cities should focus on vacinating a large proportion quickly, and slowly reducing the amount of vaccinations until the new shipment arrives.

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