1 Executive Summary

In this paper, we present a computational model that evaluates both the spread of Ebola in discrete geographical regions as well as the delivery and transport of Ebola to the afflicted regions of interest. To model the spread of Ebola, we utilize a system of ordinary differential equations (ODE) to evaluate the change in three distinct population categories: those who are susceptible to the Ebola virus, those have just contracted the virus (i.e. individuals who are curable) and those who have Ebola in its advanced stage (i.e. individuals who are incurable even with proper medication). We model the transmission rate of Ebola as a function of the inhibitory effects of crowding out and individuals' changes to behavior in a given region. We numerically solve the system of ODEs using the Forward Euler Method to evaluate the spread of the disease from initial conditions.

In order to determine the optimal delivery method, we take a combinatorial approach and represent the producers of the specified Ebola medication as sources and the regions that require the medication as sinks in a directed flow network graph. We represent the routes of medicine delivery as edges, which correspond to possible paths of delivery. We then define capacities on the edges that represent the quantity of medication that can be transmitted from one destination to another, which reflect the different quantities of medicine that different modes of transport (i.e. helicopters or trucks) can deliver. We then compute maximum flow on our transportation network to evaluate the distribution of medicine from the sources that create medicine to the discrete regions that demand Ebola medicine. We merge both the SRI model with the network flow model to introduce a unified framework that couples the transmission of disease with the human delivery of medicine to effected regions. By using the output of the SRI model to specify the demand of the effected regions for the flow model, and likewise using the output of the flow model, the medicine delivered, to update the SRI model to take into the account the individuals cured, we are able to incorporate both problems into a solution that considers both disease epidemiology and human transport of medicines.

We then compare this model with a cellular automata model that takes into account spatial factors in the spread of disease. We evaluate both models, and highlight advantages and disadvantages of both. Our model also illustrates the changes in the three categories of population over a period of time for different inputs of parameters and initial values, thus emphasizing flexibility while maintaining the ability to generate useful results. Our model not only determines which regions require the most immediate medical attention, but also answers the question of the most efficient delivery method of the Ebola medication. Our model is extensible, by adding terms to the ODE that introduces stochastic processes to the spread of disease, or by developing different network topologies that reflect each specific Ebola epidemic more closely.

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Contents

2 Introduction

In this paper, we develop a computational model that evaluates both the spread of Ebola in specific, discrete regions and the transport of drugs to the regions most in need, while considering geographical, time and cost constraints.

2.1 Interpretation of the Problem

In order to properly eradicate Ebola, our first priority was to determine which regions require the most medical attention. Because proper medication would only help those individuals who are in the earliest stages of Ebola, we deemed it appropriate to stratify our infected population into those who had just contracted the virus and those who were experiencing Ebola at its most advanced stages. After determining which regions showed the greatest density of infected individuals with curable symptoms (i.e. individuals in the early stages of the virus), we consider the most efficient way to deliver the medication, where we define most efficient as globally maximizing medicine distribution. We consider the multitude of paths that transportation vehicles can take from a factory, where the medication is produced, to the regions that need the most medical attention. We represent these paths on a network flow and using maximum flow, we optimize the total number of medicine delivered to these villages. We then compare the results of our ordinary differential equation model to an alternative cellular automata model in order to explicate our model's strengths and weaknesses.

2.2 Interpretation in a Mathematical Framework

Here, we discuss the aforementioned interpretations of Problem A in a mathematical framework.

1. **Determine how much medication is demanded by each region**.
   We develop an ordinary differential equation (ODE) model that determines within a bounded region, the quantity of susceptible individuals, the quantity of individuals who have contracted Ebola and are in its early stages and the quantity of individuals who have an advanced form of the Ebola virus.

2. **Ensure a maximal distribution of medicine among villages.**
   We approach this problem combinatorially with a flow network. Given a graph where vertices represent discrete locations (such as factories that produce medicine and discrete regions afflicted with Ebola that demand medicine) and edges that represent the rate at which medicine can be delivered, we solve the maximum flow problem on a directed graph to optimize the total number of medicine delivered to these villages. In doing so, we ensure that given our constraints: the capacities of our transport routes and amount manufactured at factories, we are delivering as much medicine as possible.

3. **Merging the ODE model and Maximum Flow network**
   Whereas the maximum flow model in a flow network models the distribution of medicine, the ODE model simulates the behavior of the disease in each discrete population. Thus, we merge the two seemingly disparate models, one combinatorial, one continuous, by

modeling the delivery medicine to each region with medicine flow, and evaluating the subsequent epidemiological response with ordinary differential equations. As a consequence, we are able to evaluate the effect that different medicine flow has on the epidemiology of Ebola in our model.

As one can see, there are several assumptions that were necessary to be made in order to allow our interpretation of the problem. In the next section we address these concerns.

After we generate data from our MATLAB code that explicates which paths optimize the amount of medicine being delivered, we evaluate our model's potential under different parameters and at loss of certain assumptions. In addition, we simulate a Cellular Automata model using Java and compared its results with our ODE model to provide further insight into our model's strengths and weaknesses.

3 Assumptions of SIA and Delivery Models

We divide the general population affected by the Ebola epidemic into three disjoint categories:

- Those susceptible to the Ebola virus.
- Those infected with the Ebola virus in its earliest stages (i.e. curable with proper medication).
- Those infected with the Ebola virus in its advanced stage (i.e. incurable even with proper medication).

We also make several assumptions about the dynamics of the population:

- Fixed population size on a bounded region. This implies no birth, death, immigration, or emmigration. This reduces the complexity of our model and only simulates the spread of disease and the effect of medicine in the current population.
- No individuals can die from the Ebola in its earliest stage and must first transition to a state where Ebola is well-advanced in order die.
- The demand of specified medication is equivalent to the number of individuals who have Ebola in its early stage and have the potential to be cured.
- No one can be cured of Ebola without the specified medication.
- Anyone in the bounded region who has not contracted the Ebola virus is susceptible to it.
- The specified medication produced by the world medical association will immediately cure the patients after administration.
- Any cured person gains immunity to the virus and so can no longer be infected. In other words, cured people will not be considered as part of the susceptible population.

4 SIA Model

We develop a compartmental model in order to illustrate the stratification of a given population in a bounded region. We divide the population under speculation into three subpopulations:

1. S: the number of individuals in the population who are **susceptible** to the Ebola virus.
2. I: the number of individuals in the population who have been **infected**/contracted the Ebola virus and is in its earliest stage (i.e. curable with proper medication).
3. A: the number of individuals in the population who are currently infected with an **advanced** form of the Ebola virus (i.e. incurable even with proper medication).

For each subpopulation, we define an ordinary differential equation that represents its change in quantity with respect to time. We denote this system of ordinary differential equations as the SIA Model and is as follows:

$$\begin{aligned}\frac{\partial S}{\partial t} &= -g(S, I, A)\\ \frac{\partial I}{\partial t} &= g(S, I, A) - rI\\ \frac{\partial A}{\partial t} &= rI - dA\end{aligned}$$

where

1. $g(S, I, A)$: the transmission rate of the Ebola virus as a function of S, I, A.
2. r: the rate at which infected individuals enter an advanced phase of infection that is incurable even with proper medication.
3. d: the death rate of the Ebola virus.

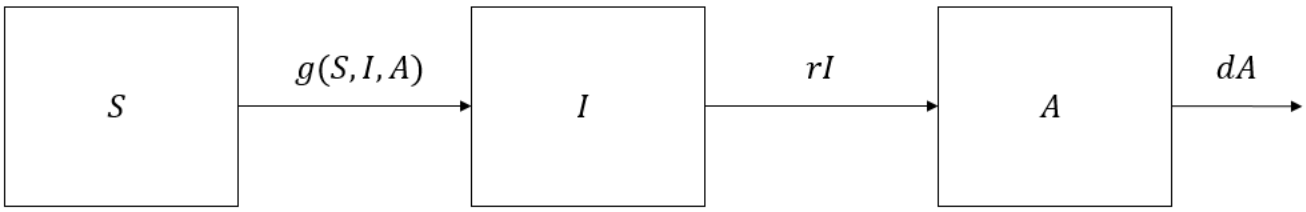

Figure 1: Schematic Diagram of SIA Model

4.1 Transmission Rate

There are several choices for $g(S, I, A)$. One simple option is the density-dependent transmission i.e. $g(S, I, A) = kS(I + A)$ in which we only introduce a **proportionality constant** $k > 0$. There is also the option of considering a frequency dependent transmission i.e. $g(S, I, A) = \frac{kS(I+A)}{S+I+A}$. However, in view of Ebola's spreading abilities we first consider a saturation transition rate $g(S, I, A) = f(I, A)S$, where $f(I, A)$ tends to a saturation level as I and A gets large. Consider,

$$g(S, I, A) = f(I, A)S = \frac{k(I + A)}{1 + \alpha(I + A)} \cdot S.$$

Here, $k(I+A)$ measures the infectious force of the disease whereas $\frac{1}{1+\alpha(I+A)}$, $\alpha > 0$, measures the inhibitory effect from the behavioral change of the susceptible individuals or from the crowding out effects of the individuals. Qualitatively,

1. α defines the magnitude of the inhibitory effect

2. k defines the magnitude of the infection force of the Ebola virus.

Because many of the regions where Ebola is prevalent are underdeveloped areas of the world, it is appropriate to consider $k > \alpha$, since they have less opportunity to change their behavior in order to better protect themselves from Ebola. It is more appropriate to consider $g(S, I, A)$ as nonlinear simply because we do not expect transmission of Ebola to follow a linear pattern. With its ability to be transmitted through bodily fluids and direct contact, it is appropriate to consider the infectious force as $k(I + A)^l$ for some $l > 0$. Furthermore, because we are considering regions where Ebola is known to be prevalent that is in underdeveloped areas of the world, we can expect the inhibitory effect to be fairly linear. For all these reasons, we have further improved our transmission rate for Ebola to be:

$$g(S, I, A) = \frac{k(I + A)^l}{1 + \alpha(I + A)} \cdot S.$$

We continue to develop our transmission rate by incorporating a ratio-dependency factor. It is more than likely, that the transmission rate is dependent on the ratio of the number of infected individuals to the number of individuals that are susceptible. To account for this, we allow the input of our saturation function to be $\frac{I+A}{S}$ which gives us:

$$g(S, I, A) = f\left(\frac{I + A}{S}\right) \cdot S = \frac{Sk\left(\frac{I+A}{S}\right)^l}{1 + \alpha\left(\frac{I+A}{S}\right)}.$$

Qualitatively, this says that in the beginning of the epidemic when $\frac{I+A}{S}$ is small we should expect transmission to be fairly small; however as the Ebola virus continues to spread and $I + A$ increases, it is without a doubt clear that $g(S, I, A)$ will increase as well. Incorporating

the newly defined $g(S, I, A)$ function, we see that our SIA model is:

$$\begin{aligned}\frac{\partial S}{\partial t} &= -\frac{Sk\left(\frac{I+A}{S}\right)^l}{1+\alpha\left(\frac{I+A}{S}\right)}\\ \frac{\partial I}{\partial t} &= \frac{Sk\left(\frac{I+A}{S}\right)^l}{1+\alpha\left(\frac{I+A}{S}\right)} - rI\\ \frac{\partial A}{\partial t} &= rI - dA\end{aligned}$$

4.2 Setting Up an Initial Value Problem

Given the SIA Model, we must define several initial values in order to numerically solve for $S(t), I(t)$ and $A(t)$ at different values of t. In doing so, we will lay the general framework for an initial value problem for a system of ordinary differential equations. Consider the values of $S(0), I(0)$ and $A(0)$:

1. $S(0)$: The number of susceptible individuals at time $t = 0$.
2. $I(0)$: The number of individuals who can be cured of Ebola with proper medication at $t = 0$.
3. $A(0)$: The number of individuals in advanced stages (i.e. incurable even with proper medication) of Ebola at $t = 0$.

We do this in order to see the population dynamics of a given region at time $t = 0$ i.e. the population dynamics exhibited as soon as we begin to examine the region. Given the initial conditions to our SIA model, we can numerically solve an initial value problem and hence the system of ordinary differential equations in order find values of $S(t), I(t)$ and $A(t)$ at different times, t.

4.3 Forward Euler Method

In order to numerically solve the SIA model in MATLAB, we utilized the Forward Euler Method to approximate the solution of the initial value problem. In the most general case, suppose that we want to approximate the solution to:

$$\frac{\partial y}{\partial t} = f(t, y(t)), \qquad y(t_0) = y_0.$$

To do this, we first discretize our time interval. Suppose t_n is the maximum time we are willing to consider for our system and $t_0 = 0$ is our initial time. Then, $h = \frac{t_n - t_0}{n} = \frac{t_n}{n}$, for some n large enough so that our solutions to the initial value problem are stable (i.e. smooth), defines our time step. The Forward Euler Method claims that for $i \in \{1, \ldots, n\}$

$$\begin{aligned}t_{n+1} &= t_n + h\\ y_{n+1} &= y_n + hf(t_n, y_n)\end{aligned}$$

where the value of y_n is an approximation of the solution of the ODE at t_n.

4.4 Algorithms

Here, we apply the Forward Euler Method to our SIA Model. The Forward Euler method states that $y_{n+1} = y_n + hf(t_n, y_n)$ where $\frac{\partial y}{\partial t} = f(t, y(t))$ and $y(t_0) = y_0$. This implies for a given time step h that:

$$S_{n+1} = S_n + h\frac{\partial S}{\partial t}(t_n, y_n)$$
$$I_{n+1} = I_n + h\frac{\partial I}{\partial t}(t_n, y_n)$$
$$A_{n+1} = A_n + h\frac{\partial A}{\partial t}(t_n, y_n).$$

Below is our pseudo code for numerically solving the SIA Model where the values of $\frac{\partial S}{\partial t}$, $\frac{\partial I}{\partial t}$ and $\frac{\partial A}{\partial t}$ are substituted for their respective equations in the SIA model.

Algorithm Solving SIA Model with Forward Euler Method

Define initial condition for S, I, A.
Set n and $time_{step}$.
Define parameters: r, d, α, l.
Define the function $g(S, I, A)$.
Create vectors to store values for t, S, I, A.
for $i = 1 : n$ **do**
  $t(i+1) = t(i) + time_{step}$
  $S(i+1) = S(i) + time_{step} \cdot (-g(S(i), I(i), A(u)))$
  $I(i+1) = I(i) + time_{step} \cdot (g(S(i), I(i), A(u)) - r \cdot I(i))$
  $A(i+1) = r \cdot I(i) - d \cdot A(i)$
end for
Output: $1 \times n$ vector with values of $S(t), I(t), A(t)$ at each time step.

5 Delivery Model

5.1 Introduction to Network Flow

We represent the delivery of medicine to different regions through a network flow graphical model. The general network flow formulation is as follows:

We have a directed graph $G = (V, E)$, where $v_i \in V$ is an node in the vertex set and $e_{ij} \in E$ is an edge in the edge set that joins two vertices v_i and v_j. On each edge we have function $c_h : E \to \mathbb{R}$ that defines the maximum capacity along a particular edge. There is one vertex s defined to be "source" vertex, which indicates the origin of any flow through the network, and one "sink" vertex t which indicates the destination of any flow through the network. However, this can be expanded to multiple sources and sinks by introducing a dummy source vertex s_D that connects to all the source vertices, and a dummy sink vertex t_D where all sink vertices connect to it.

There are several assumptions to the flow network. They are:

- Flow conservation: the sum of flow into vertex j is equal to the sum of the flow out of vertex j, for all vertices except the source and sink vertices, i.e.

$$\sum_{i:(i,j)\in E} f_{ij} - \sum_{k:(j,k)\in E} f_{jk} = 0,\ \forall\, j \in E \setminus T \cup S$$

- Flow capacity: the flow along any edge is less than its maximum capacity, i.e.

$$f_{ij} \leq c_{ij},\ \forall\, (i,j) \in E$$

- Flow nonnegativity, i.e.

$$f_{ij} \geq 0,\ \ \forall\, (i,j) \in E$$

A maximum flow algorithm assigns $f : E \to \mathbb{R}$ that describes the maximum possible flow of medicine along each edge, defined by

$$F = \max \sum_{i:(s_D,i)\in E} f_{s_D i}$$

, which maximizes the objective function subject to the above constraints.

5.2 Theoretical Framework

We use multiple source, multiple sink maximum flow to model the transport of medicine from factories that create medicine to discrete regions affected by Ebola that have a demand for medicine. Each discrete location is represented with a vertex in the vertex set V, and each travel path between two locations v_i and v_j is represented by an edge e_{ij} in edge set E. Some edges may have reciprocal edges to account for the fact that travel can be bidirectional, and thus to encode the assumption that medicine can travel both directions along a route, though usually there is a natural direction that medicine is transported exclusively. There is a set $S \subset V$ of source nodes which correspond to locations that make manufacture medicine at some rate; the rate at which source $s_i \in S$ makes medicine is f_{s_i}. There is also a set $T \subset V$ of termination nodes, which corresponds to regions that require medicine at some rate; the rate at which location $t_i \in T$ consume medicine is f_{t_i}. We will always refer to factories as "source" vertices, and regions afflicted with Ebola as "sink" vertices. To reduce the problem to a single-source, single-sink maximum flow problem, we add artificial dummy nodes s_D and t_D, where there is an edge between s_D and all the $|S|$ source nodes, and an edge between t_D and all the $|T|$ destination nodes. We will always refer to s_D and t_D as "dummy source" and "dummy sink" vertices, respectively.

We assume that the bottleneck (minimum cut) in delivering medicine is in the transport from the factories to the discrete regions, and not in the manufacturing of the medicine itself. We define informally the minimum cut, referred to as the "bottleneck" in our transportation network, as the minimum capacity such that its removal results in no flow from the sources to sinks. Of note is the max-flow min-cut theorem from optimization theory, a special case of linear program duality, which states that the maximum flow is equal to the minimum cut in a flow network.

We assume constant rate of medicine manufacturing and constant rate of medicine consumption when computing maximum flow. Each source will have its own rate of medicine production, and each sink will have its own rate of medicine consumption. For medicine production, this is encoded in the capacity of the edges between s_D and each $s_i \in S$; f_{s_D,s_i} represents the rate at which medicine is produced at factory s_i. Similarly, for medicine consumption, this is encoded in the capacity of the edges between $t_i \in T$ and t_D; f_{t_i,t_D} represents the rate at which medicine is consumed.

We can encode multiple methods of medicine transport and delivery into the capacities along the edges that correspond to travel routes. For example, methods of transport that correspond to a certain edge that can deliver the most medicine would have the greatest edge capacities, and those that deliver the least medicine have the smallest edge capacities.

5.3 Formulation

For the formulation, we consider constant rate of medicine manufacturing and consumption at each source and destination, respectively, i.e.

$$\sum_{i:(s,i)\in E} f_{s,i} = c_s, \ \forall\, s \in S$$

and

$$\sum_{j:(j,t)\in E} f_{j,t} = c_t, \ \forall\, t \in T.$$

We consider two factories that manufacture medicine. There are four routes from each factory to four intermediate locations. From these intermediate locations v_i, they are connected to four destination locations that form a complete graph composed of 5 vertices with the intermediate vertices. Note that this implies an undirected graph structure, so each edge between vertices has reciprocal edges (edges in both directions between two vertices).

We consider three methods of medicine transport: plane, helicopter, and truck. The routes from the factory to four intermediate locations are exclusively plane, route from intermediate locations to discrete regions afflicted by Ebola are traversed by helicopters, and any other edge is traversed exclusively by trucks. This is reasonable because the plane route transports the medicine to larger regions, and other smaller forms of transportation bring medicine to the local regions affected by Ebola. Thus, edge routes deliver medicine to the sink vertices. The rate at which medicine can be delivered by these methods of transport is represented by the edge capacities on the flow network between the appropriate set of vertices.

5.4 Algorithms

Maximum flow is a solution for which highly efficient algorithms exist; two popular algorithms we use for our computations are the Edmunds-Karp and Push-relabel algorithms. While the graphs we test are not very large, applications of our model to larger graphs which represent more regions of interest and since we extend this delivery model to merge with the SIA Model to perform multiple iterations, we need to compute maximum flow efficiently. The

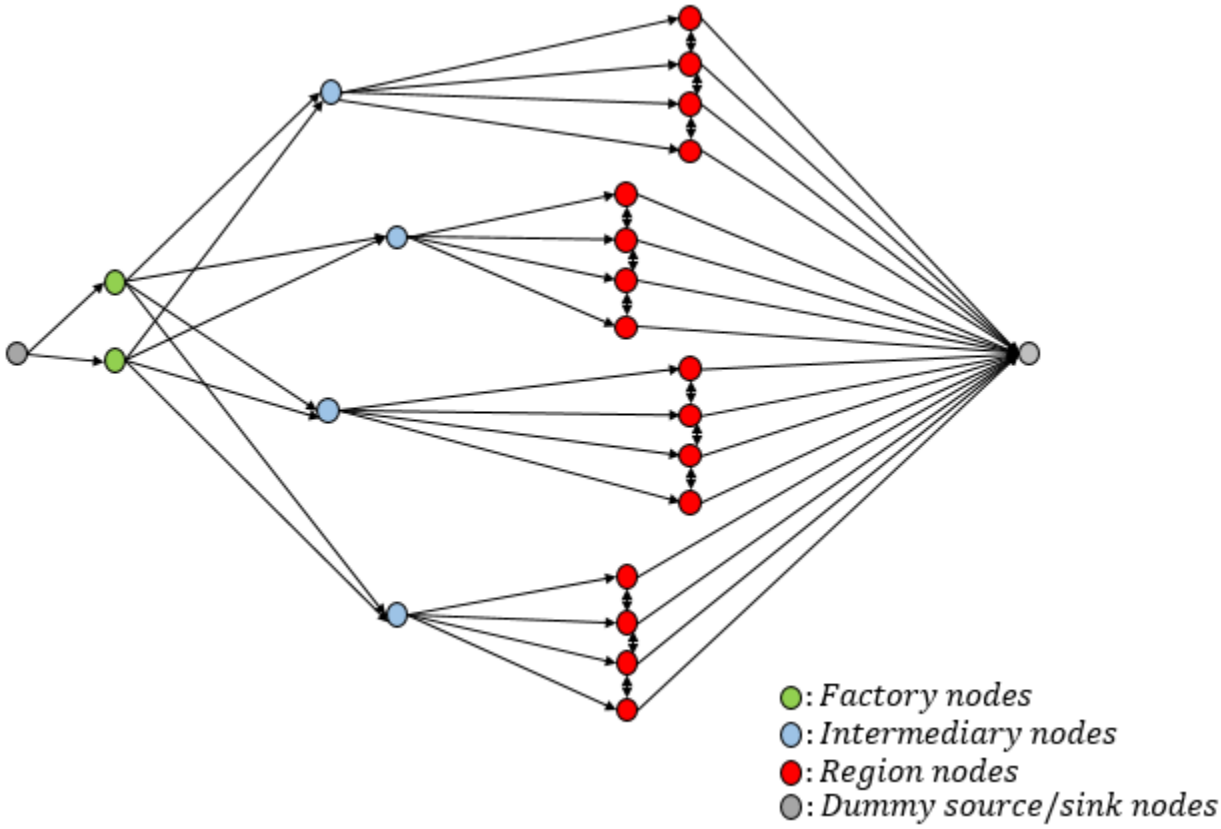

Figure 2: Schematic Diagram of our Network Flow

time complexity of Edmunds-Karp is strongly polynomial: $O(|V|^2|E|)$, while Push-relabel is $O(|V||E|^2)$.

6 Merging the SIA Model and the Delivery Model

6.1 Formulation

To jointly evaluate the delivery of medicine on the epidemiology of Ebola, we merge the SIA model that utilizes a system of ODEs to model disease spread with the Flow Network model that computes maximum flow to model medicine delivery. Again, we call each discrete location that has a demand for medicine a "sink" vertex, and any manufacturing location that supplies medicine at "source" vertex.

For this unified model, we discrete time into "rounds"; in each round, the disease is able to spread without a cure, as modelled by our ODE model. At the same time, medicine flows to each location according to some initial demand specified at the start of each round as modelled by maximum flow. After some time $t \in \mathbb{Z}$, the disease has spread, but so has the medicine. At this point, medicine delivered to each discrete region is instantaneously administered to individuals in that region, and the people who receive medicine are instantaneous not considered as part of the infected population. These numbers are inputted to the ODE

model at the next round.

6.2 Algorithms

The model requires inputs of $S_i(0), I_i(0), A_i(0)$ for each sink vertex i, which correspond to the initial susceptible, infected (curable), and advanced-stage infected (incurable) at discrete geographical location i. Using the ordinary differential equations from the SIA model, we can determine the population sizes at time $t = 1$, $S_i(1), I_i(1), A_i(1)$. However when $t = 1$, new medicine arrives at each discrete location with quantity $f_i(1)$ which computed from maximum flow on the transportation network of the Delivery model. Thus the actual infected population is $\tilde{I}_i(1) = I_i(1) - f_i(1)$. The susceptible population and the population with an advanced form of the disease are unchanged since it is assumed that people who take the drug are instantly cured and gain immunity. We now have new population sizes $S_i(1), \tilde{I}_i(1), A_i(1)$ for each discrete location, which can be inputted to the ODE model for the next round.

Let ODE-SIA be some function that computes the system of ODEs specified by the SIA model given some initial conditions, and outputs how S, I, A changes with respect to time. Let MAXFLOW be some function that computes max flow on graph G. The output is $f : E \to \mathbb{R}$, the flow of medicine along each edge. Let $\tilde{\chi}_i(t+1)$ be the population size of the different disease states initially computed by the ODE model for time $t + 1$. After delivering medicine with max flow, the population sizes will be updated to $chi_i(t+1)$ for the next round.

We thus have the following iterative procedure:

Algorithm 2 Unified Delivery-Epidemiology model

Supply $G = (V, E)$, the flow network with edge capacities $c : E \to \mathbb{R}$.
Supply $\chi_i(0) = \{S_i(0), I_i(0), A_i(0)\}$, the initial conditions of the population.
for $t = 0 : N$ **do**
  Solve ODE system: $\tilde{\chi}_i(t+1) = \text{ODE-SIA}(\chi_i(t))$ for each discrete location i.
  Update sink capacities in G: $c_{t_i} = I_i(t+1)$ for each discrete location i.
  Compute max flow: $f = \text{MAXFLOW}(G)$
  Update size of populations for each discrete location i:
    $S_i(t+1) = \tilde{S}_i(t+1)$
    $I_i(t) = \tilde{I}_i(t+1) - f_i(t+1)$
    $A_i(t+1) = \tilde{A}_i(t+1)$.
end for

7 Cellular Automata Model

In addition to developing our SIA model and utilizing a Maximum Flow algorithm to maximize drug delivery, we also developed a cellular automata in Java to simulate the spread of ebola virus and deployment of vaccines. In doing so, we hope to provide further insight into the strengths and weaknesses of our model.

7.1 Model Assumptions

- The region is divided into a 2D lattice grid of square cells.
- Time progresses in discrete steps and during each time step, cells are updated based upon certain rules.
- Each cell has four possible states: healthy, infected, advanced/death, and vaccinated.
- Only cells that are adjacent to infected cells can become infected.
- Cells that are sick have a certain probability of dying.
- Similar the previous models, vaccines have an instantaneous effect and vaccinated cells can no longer be infected.

7.2 Algorithm

Cellular Automata models involve a series of rules that determine a cell's next state based upon the cell's current state and the states of the cell's neighbors. In our model, the rules are applied to the whole grid simultaneously.

Rule 1 A sick cell will become dead with probability $P(I \to A)$ during every time step.

Rule 2 If a healthy cell is adjacent to a sick cell, then with probability $P(S \to I)$ is will become a sick cell.

Rule 3 m medicine is distributed every t turns. In other words, m sick cells become vaccinated cells every t turns. Our program prioritizes the vaccination of the newly sick since they are more likely to lie on the border of the sick clumps and hence have a higher probability of infecting other cells.

7.3 Program

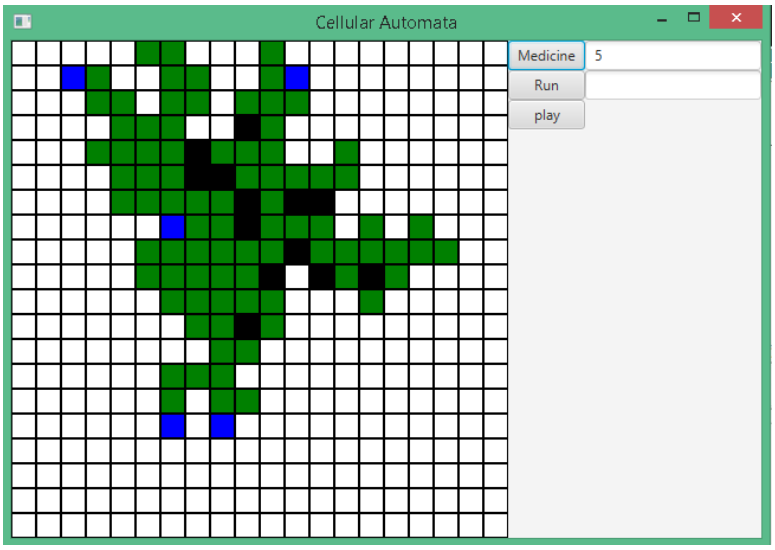

Figure 3: GUI for Cellular Automata program

In Figure 3, the GUI used in our cellular automata program can be seen. White cells represent healthy cells, green cells represent infected cells, blue cells represent vaccinated cells, and black cells represent dead cells. The typical grid size used in our project was 50x50. The medicine text field allows you distribute that many medicine and updates the grid once. Inputting into the run text field allows you to tell the program to run for that many time steps. Play simply runs the program indefinitely on its own. The GUI also enables users to click on any cells, causing them to become considered sick instead.

8 Results

8.1 Network Flow/ODE Model

We run two separate simulations with different parameters. For the first simulation, termed "Simulation 1", we specify parameters that imply weaker transmissibility of disease, and low medicine flow to affected regions. For the second simulation, termed "Simulation 2", we specify parameters that imply a higher transmission rate, and a range of medicine flow to affected regions.

Parameters	Simulation 1	Simulation 2
source to inter. capacities	40	400
inter. to sinks capacities	20	200
sinks to sinks capacities	5	50
ODE r	0.1	0.05
ODE d	0.1	0.00
total initial susceptible	7371158	7371158
total initial infected	2998	2998
total initial advanced-phase	4510	4510

Figure 4: Parameters for Simulations 1 and 2. 'source to inter. capacities' indicate the capacities on edges between source vertices (factories), and intermediate locations of transport (airplane route). 'inter. to sinks' indicate the capacities on edges between the intermediate locations to sink vertices (discrete locations afflicted with Ebola) (helicopter routes). 'sinks to sinks' indicate the capacities on edges between different sink vertices (truck routes).

Figures 5 and 6 highlight the final results of our simulations. We see how the total saved, dead, or sickened changes as the medicine flow increases. For simulation 1, the total dead initially stays the same when the flow is increased from 0 to 20. However, there is a noticeable decrease in total dead at 200 flow. On the other hand, the total people sickened is always decreasing as more medicine is distributed, and the total number of people saved increases significantly. For simulation 2, which has a greater rate of transmission, the control condition without any medicine flow results in a significantly higher number of people sickened. However, by distributing lots of medicine, the number sickened and dead had a significant decline, and the number saved increased significantly.

source capacity	0	20	200
total saved	0	108	660
total dead	688	688	667
total sickened	219	207	197

Figure 5: Simulation 1 overall results

source capacity	0	100	1000
total saved	0	300	3000
total dead	-	1014	713
total sickened	3441	1113	244

Figure 6: Simulation 2 overall results

Figures 7, 8, and 9 illustrate the effects of medicine on the spread of disease in both simulations of our mathematical model. In simulation 1, we see that even without medicine,

the population recovers quickly: the number of susceptible people initially decreases, but stabilizes as the disease kills the originally infected individuals so that they do not have the opportunity to spread the virus to other people. However, by supplying varying amounts of medicine through the transportation flow network, the number of susceptible people falls a smaller amount as the disease runs its course. Likewise, the number of infected but curable people fall quicker when more medicine is applied, which is consistent with the fact that medicine will cure the those individuals and remove them from the infected category.

On the other hand, simulation 2 illustrates the effect of medicine on reversing the spread of disease; whereas no flow of medicine results in a continuous drop in the number of susceptible people (people not sick), flow of a large amount of medicine results in a reversal in the trend of the disease by once again stabilizing the number of infected people. When no medicine is inputted, the number of infected individuals continually increases, but that number falls to zero when we send flow of more medicines. So, in our mathematical model, we were able to find the flow of medicines that reversed and ended the epidemic.

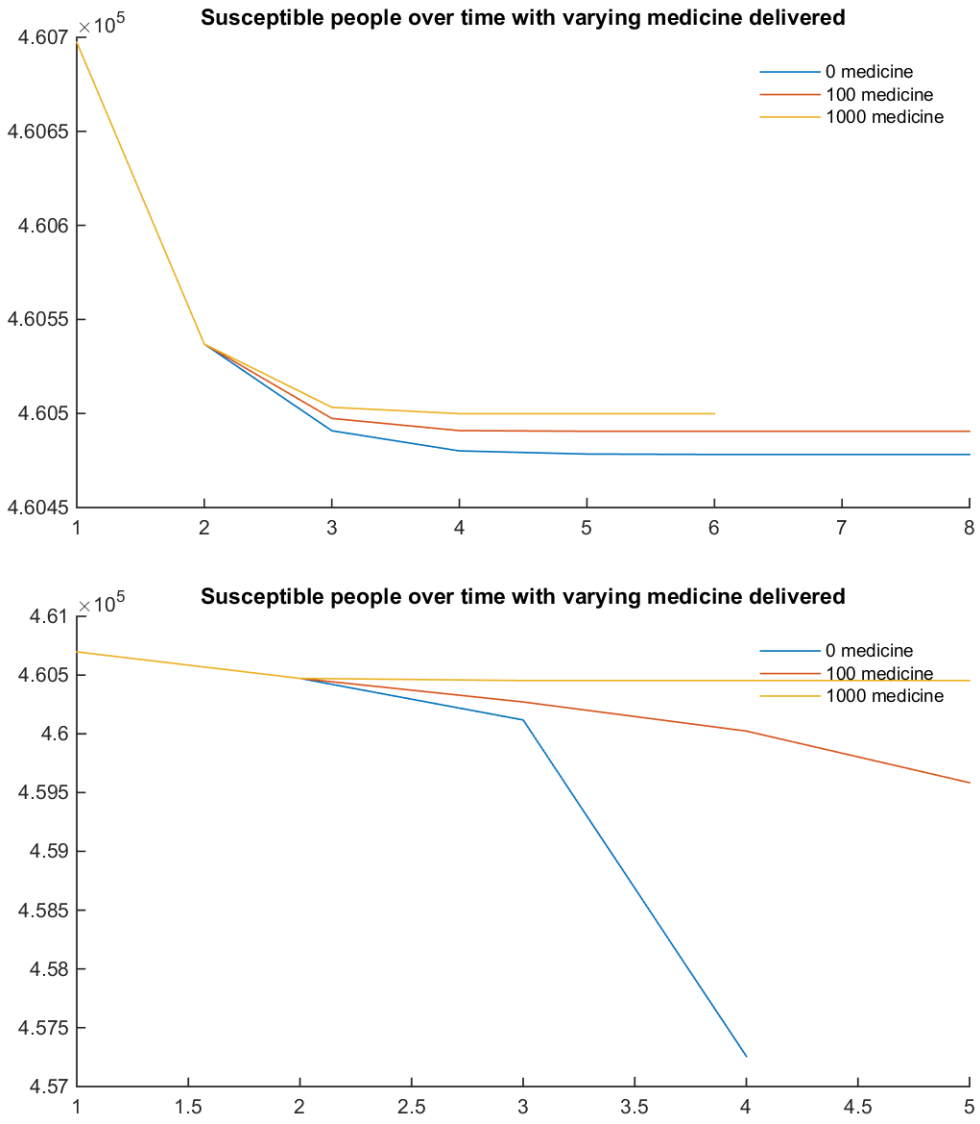

Figure 7: Susceptible people in a discrete region. Simulation 1 on top, Simulation 2 on bottom. All x axis are arbitrary time units, y axis the number of people.

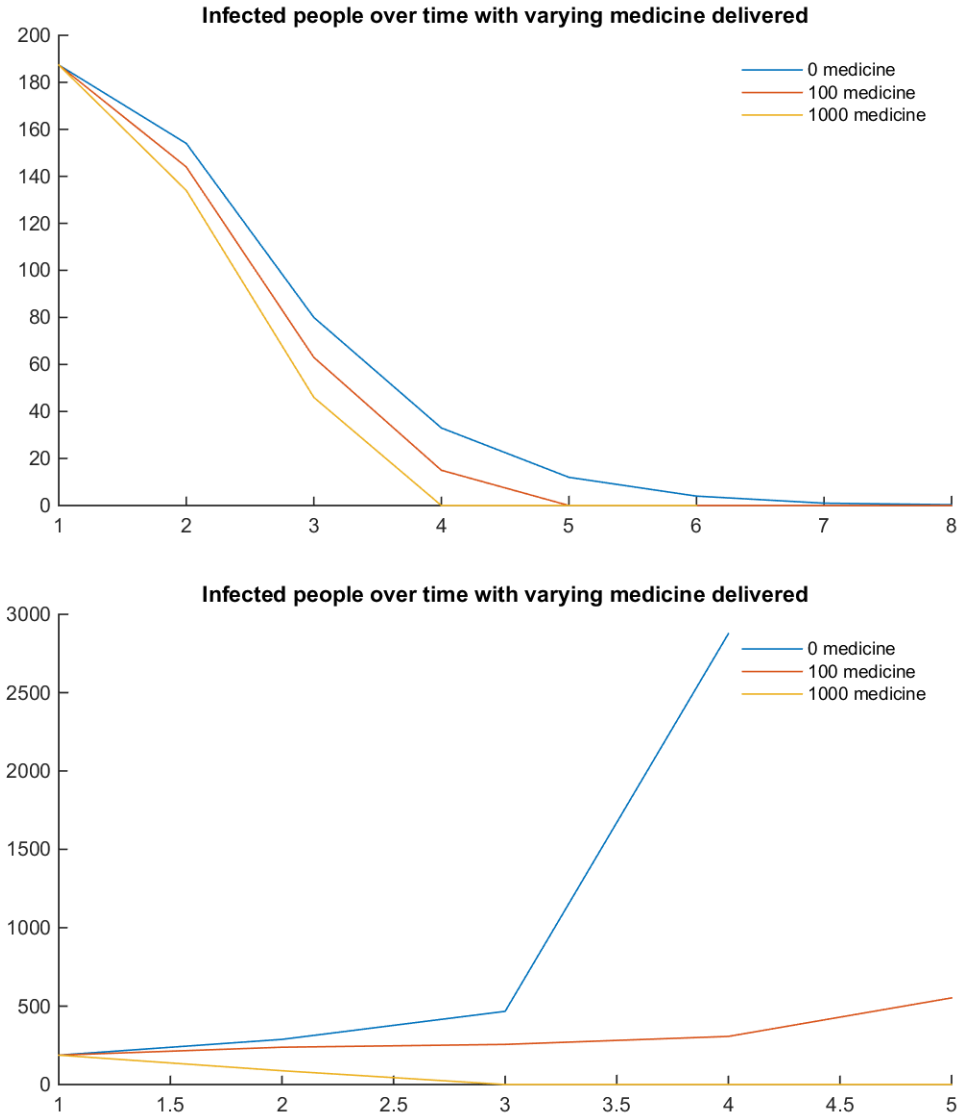

Figure 8: Infected (but curable) people in a discrete region. Simulation 1 on top, Simulation 2 on bottom. All x axis are arbitrary time units, y axis the number of people.

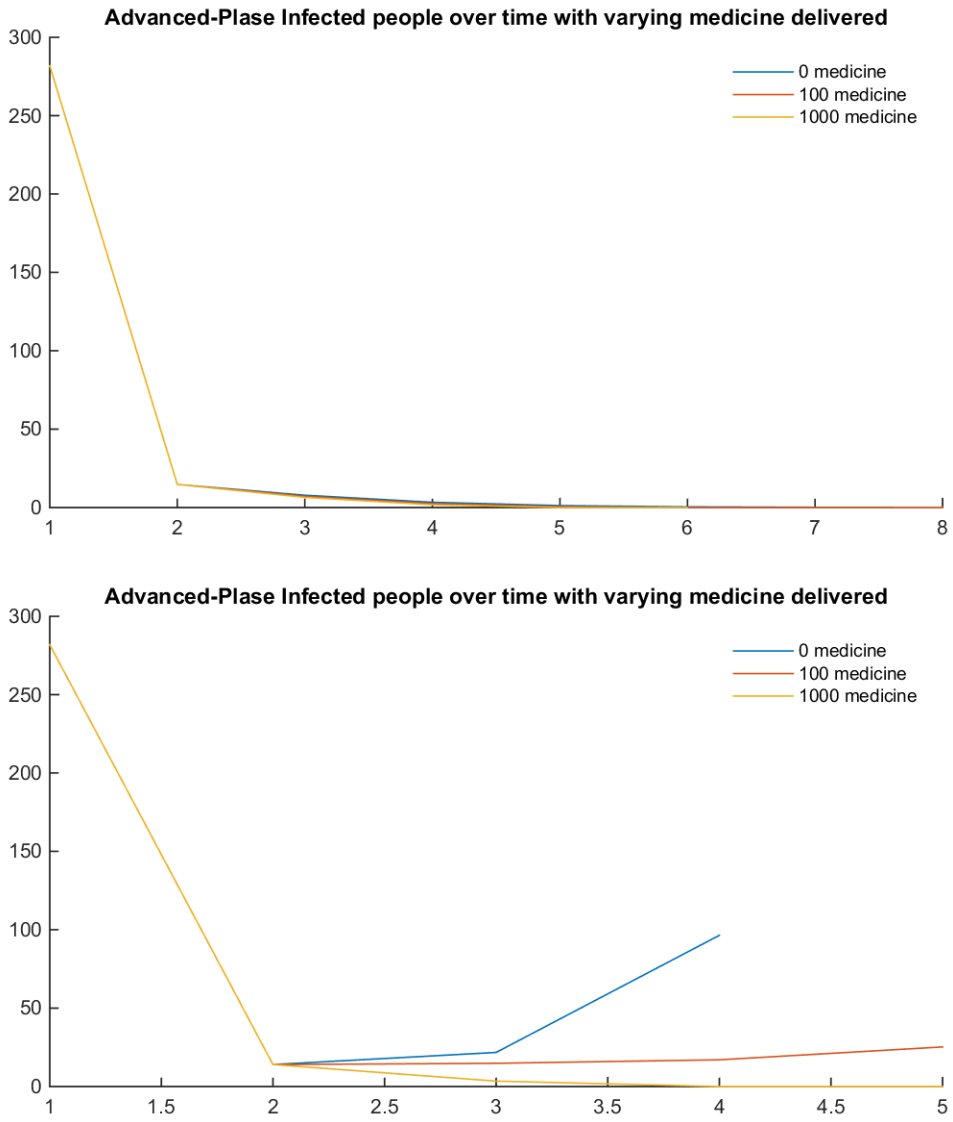

Figure 9: Advanced-stage (incurable) people in a discrete region. Simulation 1 on top, Simulation 2 on bottom. All x axis are arbitrary time units, y axis the number of people.

8.2 Cellular Automata Model

We run our Cellular Automata model based upon a 50x50 grid of square cells. The initial infected population was chosen randomly and apart from each other. $P(S \to I)$ represents the probability that a healthy person next to an infected person becomes infected that time step. $P(I \to A)$ represents the probability that a sick person's virus becomes incurable or a sick person dies during that time step. The rate of medicine is m/n is interpreted as m vaccines are delivered on every n^{th} day.

Typically two scenarios were observed. The first is where the Ebola virus spreads much faster than what the vaccine deliveries can handle and so everyone becomes sick at some time. At this point, it becomes a race between how many vaccines can be delivered and how

many people get the advanced form of the disease or die. The second scenario is the vaccines are delivered at a quick enough rate such that they are able to control the outbreak of the disease. In this second scenario, the majority of people are never infected and the number of people who die is minimal.

Parameters	Simulation 1	Simulation 2	Simulation 3	Simulation 4
Initial infected pop. size	20	20	10	20
$P(S \to I)$	0.1	0.2	0.1	0.1
$P(I \to A)$	0.01	0.01	0.01	0.01
Rate of medicine	100/10	100/10	100/10	50/5
Results				
Vaccinated pop. size	644	1336	80	135
Dead pop.size	73	1162	7	7

Figure 10: Cellular Automata Results

From the results shown above, we see that the results are sensitive to changes in the parameters. What should be noted is that the difference in parameters between Simulation 1 and Simulation 4 is simply the how frequent the medicine is delivered. The average rate of medicine per day is the same yet in Simulation 4 only required approximately 21% of the vaccines needed in Simulation 1 and was able to reduce the the number of sick by 90%.

9 Discussion

9.1 Error Analysis and Stability

Our Network Flow/ODE model outputs relatively stable values when tested with different parameters. For example, with the values tested in our model, number of people saved, sickened, or dead is a monotonically increasing or decreasing function of medicine flow rate. Furthermore, our computation for maximum flow finds the global maximum of our objective function, which is the flow out of the source vertex, i.e. flow of medicine. Thus, in the delivery model we do not run into the problem of finding maximal flows by converging on unstable local maxima. One disadvantage of our flow algorithms is that it requires integral flow, and so our algorithm rounds any input to an integer. However, because of the large numbers as inputs (population sizes), this is not a significant issue. Furthermore, our algorithm for the network flow/ODE model breaks when the number of people becomes close to zero, and so we do not run into convergence problems in terminating.

In both cases, both for our cellular automata model and flow/ODE model, the outputs usually converge to either uncontrolled spread of Ebola or complete eradication. This may be a limitations simply because our models become more inaccurate at each iteration, and so convergence to the two extremes may be expected if we let our models run many iterations.

We also address the condition number of our transmission rate function in the SIA model. Based on our simulations for different inputs for $g(S, I, A)$, it became clear that a small change to S, I or A, where the parameter, k, l and a are held constant, led to a minor

change in output for $g(S, I, A)$. This led us to believe that our system of ordinary differential equations was a well-conditioned problem. In future work, we hope to show that algorithms used to solve the well-conditioned problem are backward stable.

9.2 Cellular Automata vs. Network Flow/ODE Models

Overall, the cellular automata model is very similar to the ODE model.

Advantages of the cellular automata model over the ODE model include that the cellular automata takes into account locations and also that the automata model simulates the spread of the virus. For example, the ODE allows two regions that occur far apart to possibly interact and infect each other while this is unlikely. The ODE model yields no information with respect to how far the virus would have spread but with the automata mode but with the cellular automata model, it is possible to estimate how far the virus would have grown in a given amount of time.

Disadvantages of the automata model lies within the fact that each cell needs to updated and so approximating countries such as Sierra Lone would require large amount of CPU power and memory. In addition, the real world contains more complicated interactions than the simple adjacent interactions included in the automata model. Hence in modeling large populations such as a country, the ODE seems much more practical.

9.3 Strengths and Weaknesses of Model

9.3.1 Strengths

1. **Ability to generate data.** Our computerized model allows us to generate data quickly in real time as we input different parameters. This gives us flexibility to apply our model to different regions regardless of whether or not they are developed or underdeveloped. We can also consider a larger network of nodes and edges with large carrying capacities and a lower value for k (i.e. lower infectious force of the disease) and higher value of α i.e. greater inhibitory effect).

2. **Network Flow/ODE combining delivery with epidemiology** Our unified network flow and ODE model combines considerations about delivery with the transformation of the virus itself. This is realistic in the sense that delivery of medicine is done *in response* to an outbreak of an epidemic and there is a balance between the demand for medicine and the ability for humans to effectively deliver them. So our model naturally captures this dynamic between demand and supply.

3. **Spatial considerations in the Cellular Automata model** One weakness with using ODEs is it does not model the likelihood of spreading disease between individuals based on proximity. The cellular Automata model addresses this issue by only allowing transmission if two individuals are close to each other. This is important for Ebola because it is transmitted through the transfer of bodily fluids.

9.3.2 Weaknesses

1. **Merged model maximizes the rate at which medicine is delivered.** It would be more preferable to minimize the number of people who die instead. However, it would be difficult to predict *a priori* which distribution of medicines optimizes the number of dead people. Indeed, the number of people who need medicine, i.e. amount of medicine that needs to be delivered to each geographical location, is an accessible number and realistically a good parameter to incorporate. Thus, although our model does not explicitly minimize the number of people who die, maximizing the medicine delivery rate should perform quite well.

2. **Heavy reliance on parameters.** Although our model can generate data for different parameters and can be applicable to different regions, one of the things that our group noticed during simulation tests is how improper parameters could lead to odd results. For instance, incorrect parameters led to minor to no change in certain populations whereas other times the choice of parameters led to extreme changes in populations.

9.4 Improvements to our Model

To improve the SIA Model, we hope to do the following:

1. **Incorporate stochastic terms in our system of differential equations:** By incorporating the birth and death process into our SIA model, we could take into account the natural births and deaths per each time step that would inevitably affect population dynamics. Furthermore, incorporating stochastic terms would improve the accuracy of our model in the sense that it would better reflect the spread of Ebola, which may evolve in many different directions. This would reduce our dependence on parameters.

2. **Incorporate a spatial variable:** By incorporating a spatial variable into our SIA model, we would advance our SIA model in a system of partial differential equations. In doing so, utilizing spectral methods would be the alternate to the Forward Euler Method in order to solve the spatially extended system. This would better reflect the spread of Ebola because spatial influence is definitely a variable to consider. For instance, in regions where individuals are much closer together, we should a much larger increase in infected individuals since there would be more interaction and inherently more opportunities to exchange bodily fluids between individuals.

To improve the Network flow delivery model, we hope to do the following:

1. **Incorporate minimum cost flow** to the computation. This considers the effect of cost on the delivery of drugs. Our current model prioritizes each region equally in delivering drugs, but all else being equal, delivering the same amount of drugs as cheaply as possible is a realistic and serious consideration.

2. **Introduce different network topologies** We tested our model on a network with a certain symmetric structure (2 sources, 4 intermediate nodes, 16 sinks), and three

different transportation types. This can be easily extended to other network topologies, with other modes of delivery that may have greater or less flow than the delivery methods we have currently. The different network may be adapted to a specific Ebola outbreak, in which case the regions of interest and the important transportation routes (edges) are case specific.

Any of these additions will naturally fit in to the unified model that incorporates SIA with Network Flows. These additions are interchangeable pieces that may make the unified model more expressive and highlight some interesting behaviors given the introduction of some realistic complexities.

To improve the Cellular Automata model, we hope to do the following:

1. **Considering more complex interactions** The current model involves only simply adjacent interactions between cells. Introducing more complex interactions such as being able to affect cells that are 2 cells apart would better simulate the real world. The current model consists of every cell representing a person. An improved simulation could include the possibility of empty cells which could represent an unhabited region.

10 Conclusion

We present a computational model that relies on initial data provided by our SIA model in order to determine the most efficient method of delivering medication from the factories where the drugs are produced to the regions where they are most needed. With different parameters such as different production capabilities and carrying capacities of certain routes, we are able to generate data that explains which routes of transportation are most efficient given a number of infected regions. Thus, we can provide the world medical association an appropriate, mathematically corroborated strategy to determine where and how they should send their medication.

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11 Non-technical letter

We were recently called upon by the world medical association to determine the most efficient method of delivering their new medication to contain the spread of the Ebola virus. Ebola is generally contained to several regions, in particular it is only really prevalent in Liberia, Guinea and Sierra Leone. As a result, we began our work to determine the number of individuals in a given region who have just contracted the Ebola virus. Since the newly found Ebola medication is shown to be effective only to patients whose disease have not advanced, our group deemed it appropriate to focus on those who have Ebola in its earliest stages evidently being able to be cured. Inherently, this information translates to the demand for medicine in the particular given region assuming that every person who needs it, demands it. The question then becomes what is the most efficient way to deliver the medication that would minimize cost and time, while maximizing the number of patients' lives saved.

Currently, production of all medicine to cure Ebola patients is being held in centers that are considerably far from the regions where we expect to see the most concentrated number of individuals infected with Ebola. In addition, because Ebola is more prevalent in underdeveloped areas of the world, away from major airports, it is unfeasible to assume that planes are the only modes of transportation to deliver these drugs. Considering this geographical factor, we deemed it appropriate to consider utilizing other delivery systems such as trucks and helicopters that could successfully reach these regions. Because of the constraint of accessibility to these regions as a result of lack of proper infrastructure, we also took into consideration the carrying capacity each potential route could offer. For instance, helicopters may be more appropriate vehicles of transportation for regions that are separated from major cities by bodies of water or deserts. However, for regions that are buffered by other areas where there are restrictions on unauthorized aircraft, it is more appropriate to deliver the medicine via roads. With the quantity of medicine demanded by a particular region known, we found a way to determine the best method of transporting the medication from the factories to the infected regions.

With the data that the world medical association has accumulated over the past few decades on Ebola, we hope to use the most accurate criterion to determine where and how we should deliver the medication. It is important to note the effects of optimizing the amount of medicine that we transport on a given route especially when taking into account the transmission rate of Ebola. Like any medical good, improper allocation of the Ebola medication will lead to a scarce supply, which will inevitably lead to more and more cases of Ebola infected patients. We determine routes and drug delivery methods that minimize this misappropriation of medicine. We hope to see the world medical association execute our proposed drug delivery method, to successfully deliver the medication to regions in the most need. We hope to not only contain this lethal virus from spreading, but also eradicate most cases efficiently to promote a rise in global health.