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2015 Mathematical Contest in Modeling (MCM) Summary Sheet
(Attach a copy of this page to each copy of your solution paper.)

Summary

In this paper, we focus on the eradication of Ebola virus disease mainly due to the new medication. We first use some epidemic models to simulate the spread of the disease in and across regions, and then build the models on the medication delivery system. We design experiments to examine the performance of our models. Finally, we also discuss some other factors in preventing the Ebola.

For the epidemic model, we extend the basic and classic SIR model by adding the latent period and quarantine stages. Moreover, we consider the migration of people between epidemic regions in our model. The natural birth and death rate, recovery and mortality rate under the hospitalized situation or not, transfer rate of people from different stages, and so on, are taken into account, which makes it more suitable for real cases.

For drug and vaccine, we regard them as additional parts to our previous model. Drug will help more infected people recover and vaccine can make susceptible people become immune. Based on the current situation, we propose a three-level medication delivery system, and optimize the danger level sensitive transport plan between levels by linear programming. Furthermore, we analyse the need of each region and consider the tradeoff between new delivery locations and transport costs under the case that the need can be met.

We calculate and determine the parameters in our model based on the real data and methods recommended by some research papers. Especially, we use modified gravity model and fuzzy analytic hierarchy process to determine the transfer rate and danger level.

In the three experiments, we run the delivery system and location selection program to evaluate the performance of them and the impact of medication. We give detailed parameter setting and analysis on results for experiments. The results indicate the reality and effectiveness of our model.

In the last of our paper, we discuss other possible factors for eradicating Ebola. The measures, such as quarantining, detection, and safe burial, are useful supplementaries for the medication cure.

Eradicating Ebola: the Medication and Others

February 9, 2015

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Key Words: Epidemic model; medication; delivery system

Contents

1 Introduction

Currently, several countries in West Africa are still suffering from the widespread outbreak of Ebola virus disease. The unprecedented epidemic is marked with the persistent propagation ability, and horrible mortality rate. [3] Although several prevention measures, such as detection and quarantine, are adopted to stop the spread of Ebola, the appearance of specific drug and vaccine is thought to be much more effective. In this paper, we use epidemic models [4] to simulate the spread of disease in an epidemic region, and extend it to a multi-region spread model. And then we consider the influence of drug and vaccine, and adopt a three-level medication delivery system to manufacture and distribute the medication. We utilize linear programming to optimize the transport plan, in order to maximize the efficiency of medication and minimize the population of death. Moreover, the selection of new delivery locations is also included in the paper. Until now, only the spread and interchange between epidemic regions are modelled, so we also simulate the initial phase of Ebola spread in a region previously free of disease in the last model. Finally, we also explain the determination of parameters in detail.

Restatement of the Problem We are required to build a mathematical model to simulate the spread of Ebola virus, and propose a realistic medication delivery system. We need to evaluate the performance of the system under different delivery locations, needs of epidemic regions, and speed of manufacturing (supply of insufficient medication).

2 Model Overview

In this section, we introduce the models used in the paper. The models can be divided into two parts, the epidemic spread and the influence of medication. In Sect. 2.1 and 2.2, we build models on the propagation of disease. From the basic model, SIR model, we extend it into a more realistic and accurate system step by step. Besides the infections between people in a single region, the migration of people between epidemic regions are added in the multi-SEIQR model. The impact of drug and vaccine is handled by adding components to the epidemic spread model. We build a three-level medication delivery system to plan the transport between levels by linear programming. The selection of new storage location can also be done by linear programming. Besides the currently epidemic region, we also model the spread of disease to other places in the world in an adaptive way. Finally, we discuss the determination of parameters in our model.

2.1 The SEIQR Model

2.1.1 The SIR Model

An epidemic model is a simplified method to analyze and predict the spread of epidemics among people in a region. There are many forms of epidemic models, which depend on the stages of people and transition equations. The most basic model among them is the SIR model proposed by W. O. Kermack and A. G. McKendrick in 1927 [5]. In SIR model, three stages of people are considered: S (Susceptible), I (Infected), and R (Removed). S denotes the people who are not infected with the disease, but susceptible to the disease. I is those who have been infected and are able to spread the disease to S. The characteristic of R is that they are recovered from the disease and have the immunity against the disease (or already dead). The transition

flow of SIR model is depicted in Fig. 1. The blocks represent the stage of people, and the arrows between them reflect the transition rate.

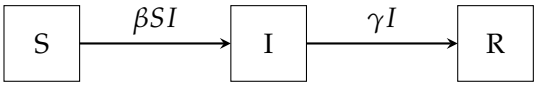

Figure 1: The Flow of SIR Model

We use $S(t)$, $I(t)$, and $R(t)$ to denote the number of people in each category at time t, and $N = S(t)+I(t)+R(t)$ is the total number in the region at any time. Then we have the following equations:

$$\begin{cases} \frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI, \\ \frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - \gamma I, \\ \frac{\mathrm{d}R}{\mathrm{d}t} = \gamma I, \end{cases} \tag{1}$$

where β is the infection rate (infections through contact between S and I per unit time) and γ is the removing rate (recovery or death from disease per unit time).

Furthermore, we can add natural birth and death into consideration. Here, we assume that a region has the same birth rate and the death rate, thus we use μ to describe the natural birth rate and natural death rate, then we get

$$\begin{cases} \frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI + \mu(N - S), \\ \frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - \gamma I - \mu I, \\ \frac{\mathrm{d}R}{\mathrm{d}t} = \gamma I - \mu R. \end{cases} \tag{2}$$

Compared to Eq. (1), only the additional birth and death are added. The birth and death can be also regarded as the migration of people to and from the region. We will see a more precise model later.

Assumptions

- There are only three stages (suspected, infected, and removed) among people. The epidemic region is separated from other regions and the overall population in the pool is fixed in a long time period.
- The contact and infection possibility is the same for every pair of people from S and I categories.
- The number of people leaving from S is equal to the number of those entering I. Also, all those leaving from I comes into R.
- The infection, recovery, birth and death rate remain stable in a long time period.

2.1.2 The Exposed Period and Quarantines

Now, we consider a more complete and realistic model in describing the spread of Ebola. The SEIQR model, which takes E (Exposed) and Q (Quarantined) into account, imports two new stages and several parameters in addition to the SIR model (Fig. 2).

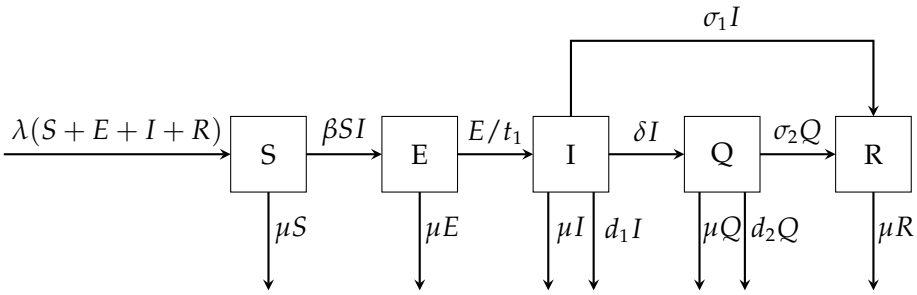

Figure 2: The Flow of SEIQR Model

Exposed Period E

- E is the stage of exposed or latent period at which people are already infected, yet do not show any symptoms or infectivity. In order words, they are treated as S, but will becomes I in a few days. $E(t)$ is the number of people in E at time t.
- t_1 is the average exposed period, which reflects the number of people transiting from E to I (E/t_1).

Quarantines Q

- Q represents the stage of being quarantined and treated, which means the patients in Q are separated from susceptible people, thus are no more infectious and they are more likely to recover due to the medical therapy. Similarly, $Q(t)$ is used to denote the number of people in Q at time t.
- The natural recovery rate (the counterpart of mortality rate) is denoted by σ, which is the ratio from I and Q to R.
- δ is the quarantining rate from I to Q, and also the reciprocal of average time between symptom onset and case isolation.
- σ is divided into σ_1 and σ_2, which represent the recovery rate in I and Q, respectively.
- d_1 and d_2 are the death rate, or the death cases over the population in that category, of I and Q. Typically, d_2 is less than d_1 due to the better medication condition in health center.

Moreover, the natural birth rate and death rate are represented by λ and μ respectively, which is more suitable for the situation in Western Africa ($\lambda > \mu$). Based on Fig. 2 and the defined parameters, the transition equation of each category in SEIQR model is

$$\begin{cases} \frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI + \lambda(S+E+I+R) - \mu S, \\ \frac{\mathrm{d}E}{\mathrm{d}t} = \beta SI - E/t_1 - \mu E, \\ \frac{\mathrm{d}I}{\mathrm{d}t} = E/t_1 - \sigma_1 I - \delta I - d_1 I - \mu I, \\ \frac{\mathrm{d}Q}{\mathrm{d}t} = \delta I - \sigma_2 Q - d_2 Q - \mu Q, \\ \frac{\mathrm{d}R}{\mathrm{d}t} = \sigma Q + \sigma I - \mu R. \end{cases} \tag{3}$$

Assumptions

- There are five stages (suspected, exposed, infected, quarantined, and recovered) among people. The epidemic region is separated from other regions. The natural birth and death rate are considered in the model, and they are not affected by the outbreak of disease.
- All rates referred in the model are the same for all the people in the region.
- The people leaving from one category is sure to enter another category, except that the dead people are removed.
- The infected and quarantined person has a possibility to recover even without treatment.
- The recovered people are assumed to be no longer infectious and also never infected with the disease again, although some of their body fluid may still be infectious due to the reports [10].

2.2 The Multi-SEIQR Model

In the SEIQR model, only one epidemic region is considered. In the real world, however, several relatively separated regions are suffering the outbreak of Ebola. The contact and infection between people **in** each region is the main channel of spread, while there still exist the communication and migration of people in various categories **across** the regions, which increases the complexity of the model.

In the multi-region SEIQR (multi-SEIQR) model, each region is marked with an index i. The transition rate of each category in a region is determined by not only the parameters in Eq. (3), but also the transfer rate between cities. The transfer rate ρ_{ij}, defined by the number of people leaving from region i to region j over the population of i, is influenced by the geographic distance, telephone communication frequency, flights or freights, etc. Additionally, ρ_{Si}, ρ_{Ei}, ρ_{Ii}, and ρ_{Ri} are the fraction of departing people in each category from region i. Obviously, $\rho_{Si} + \rho_{Ei} + \rho_{Ii} + \rho_{Ri} = 1$ for all i. These parameters are set to examine the effect of detection at departure and destination in a travel. Originally, they equals to the portion of people in the overall population (except Q), that is, $\rho_{Xi} = X_i/(S_i + E_i + I_i + R_i)$, $X = S, E, I, R$.

The transition rate for each region after introducing the transfer rate can be represented by

$$\begin{cases} \frac{\mathrm{d}S_i}{\mathrm{d}t} = -\beta_i S_i I_i + \lambda_i(S_i + E_i + I_i + R_i) - \mu_i S_i + \sum_{j\neq i} \rho_{S_j}\rho_{ji} S_j - \rho_{S_i} \sum_{j\neq i} \rho_{ij} S_i \\ \frac{\mathrm{d}E_i}{\mathrm{d}t} = \beta_i S_i I_i - E_i/t_1 - \mu_i E_i + \sum_{j\neq i} \rho_{E_j}\rho_{ji} E_j - \rho_{E_i} \sum_{j\neq i} \rho_{ij} E_i \\ \frac{\mathrm{d}I_i}{\mathrm{d}t} = E_i/t_1 - (\sigma_i + \delta_i + d_1 + \mu_i) I_i + \sum_{j\neq i} \rho_{I_j}\rho_{ji} I_j - \rho_{I_i} \sum_{j\neq i} \rho_{ij} I_i \\ \frac{\mathrm{d}Q_i}{\mathrm{d}t} = \delta_i I_i - (\sigma_i + d_2 + \mu_i) Q_i \\ \frac{\mathrm{d}R_i}{\mathrm{d}t} = \sigma_i(Q_i + I_i) - \mu_i R_i + \sum_{j\neq i} \rho_{R_j}\rho_{ji} R_j - \rho_{R_i} \sum_{j\neq i} \rho_{ij} R_i \end{cases} \tag{4}$$

In this model, all but Q people can transfer between regions. Therefore, the corresponding leaving and arriving people are added in the transition rate.

Assumptions

- Only epidemic regions are considered in the multi-SEIQR model. The outbreak of disease in other areas will be covered in the following sections.

- The transfer rate is a constant in a long time period, regardless of the outbreak of disease.
- The disease detections in departure, on board, and in destination are all reflected in the decrease in transfer rate of infected.
- The travel between cities can be done in one unit time.

2.3 The Delivery System

2.3.1 Drugs and Vaccines

Although it is reported that there is no drugs available for curing Ebola by now, we assume some medicines will come out in a few months. The influence of drugs could be thought as an additional flow from Q to R in the SEIQR model, since only those who are being hospitalized would probably be cured. An average medication taking period of t_2 and drug effective rate of η_D are used in the model. Therefore, a patient needs t_2/η_D time to recover with one unit volume of drug per day. The drugs are transported to the epidemic regions in a pulse-fashion, which means a volume of D_i pulse drugs will be sent to the region i every T_D time period. Thus, we obtain that when $t = kT_D$, $k = 1, 2, \ldots$,

$$\begin{cases} \frac{\mathrm{d}Q_i}{dt} = -\eta_D T_D D_i / t_2, \\ \frac{\mathrm{d}R_i}{dt} = \eta_D T_D D_i / t_2. \end{cases} \tag{5}$$

Vaccines are similar to drugs to some extent. The impact of vaccines is to make susceptible people become immune to Ebola without infected. This process can be regarded as a flow from S to R in the previous model. Assume the pulse vaccines are sent to the region i every T_V time period with a volume of V_i and effective rate of η_V. When $t = kT_V$, $k = 1, 2, \ldots$,

$$\begin{cases} \frac{\mathrm{d}S_i}{dt} = -\frac{S_i}{S_i+E_i}\eta_V T_V V_i, \\ \frac{\mathrm{d}R_i}{dt} = \frac{S_i}{S_i+E_i}\eta_V T_V V_i. \end{cases} \tag{6}$$

The complete transition flow after adding drug and vaccine is shown in Fig. 3. Note that the impact of drug and vaccine is not updated for every unit time, but T_D and T_V.

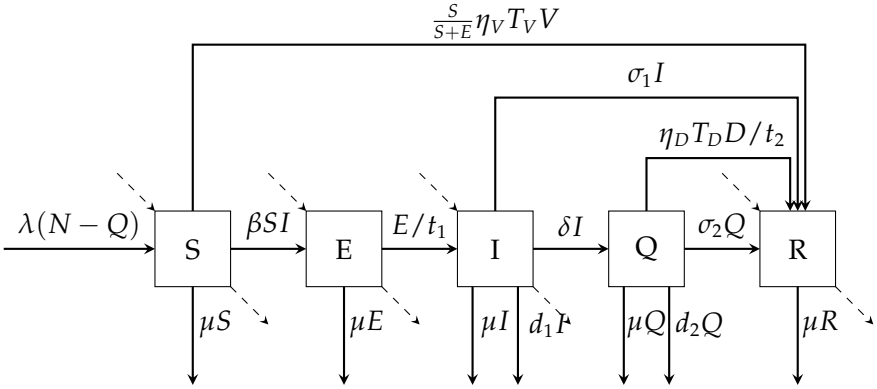

Figure 3: The Flow of Multi-SEIQR Model

Assumptions

- One unit volume of drug is for one person in unit time. One unit volume of vaccine is for one person.
- The consumption of drug will last t_2 time continuously. Assume Q_i is large enough, then $\eta_D T_D D_i/t_2$ of them will recover for every pulse on average.
- Vaccine targets are randomly selected from people in E and S. However, the vaccine injected into E is not effective.

2.3.2 The Three-Level Delivery System

The research and development of medication should be done in a critical environment and under abundant economic supply. The situation of epidemic regions is unlikely to be suitable for manufacturing and storage. Thus, based on the previous research [12, 13] and the current situation, there would be three levels in a reasonable medication delivery system.

- All the resources are manufactured in the supply center (S) level, which is on the top of the system. They may lay in some laboratories or factories in developed countries.
- Then the produced medication would be transported into the lower level, intermediate storage center (T). The medication can be stored in the depots of T temporarily and also distributed to the epidemic regions more quickly. They are typically local health center and each of them has a capacity of cap_{Di} and cap_{Vi} for drug and vaccine.
- The final level in the system is the epidemic region (M). On the case that the medication is enough, they will be delivered to M according to their needs. If not, then the priority of M will be determined by the danger level ω_i, which will be discussed in the following sections.

We use s, t, and m to denote the total number of S, T, and M. The goal of the delivery system is to maximize the people recover from the disease, and we need to optimize the transportation plan between levels. For determining the distribution plan, we have the transportation cost and time between Ss and Ts, and Ts and Ms in four matrices, $\mathbf{C_{ST}}$, $\mathbf{C_{TM}}$, $\mathbf{T_{ST}}$, and $\mathbf{T_{TM}}$. Given the drug and vaccine produced each unit time for each S, or we say speed, $drug_i$ and $vacc_i$, and overall cost C, we can solve the problem by adopting linear programming. For drug, our optimization goal is to find the drug contribution matrix in the first and second level $\mathbf{D_1}$ and $\mathbf{D_2}$, in order to meet the requirement of dangerous places as much as possible:

$$\max_{\mathbf{D_1},\mathbf{D_2}} \sum_{i=1}^{m} \omega_i D_i, \tag{7}$$

subject to:

$$\begin{cases} \sum_{ij} \left(\mathbf{D_1} \circ \mathbf{C_{ST}}\right)(i,j) + \sum_{jk} \left(\mathbf{D_2} \circ \mathbf{C_{TM}}\right)(j,k) \le C, \\ \mathbf{T_{ST}}(i,j) + \mathbf{T_{TM}}(j,k) \le T_D, \forall i,j,k, \text{ where } \mathbf{D_1}(i,j) \ne 0 \text{ and } \mathbf{D_2}(j,k) \ne 0, \\ T_D drug_i \ge \sum_{j=1}^{t} \mathbf{D_1}(i,j), \forall i = 1,2,\cdots,s, \\ cap_{Di} \ge \sum_{j=1}^{s} \mathbf{D_1}(j,i) \ge \sum_{j=1}^{m} \mathbf{D_2}(i,j), \forall i = 1,2,\cdots,t, \\ D_i = \sum_{j=1}^{t} \mathbf{D_2}(j,i), \forall i = 1,2,\cdots,m. \end{cases} \tag{8}$$

The first two equations in Eq. (8) restrict the overall transportation cost and the time (should be less than the pulse period). The next two equations shows that the drug taken from the upper level can not go beyond its maximum volume. Also the capacity limit in T should be preserved. Finally, the received drug in M is equal to the sum of all sent drug to it from T.

Similarly, for vaccine, the optimization goal is to find the vaccine contribution matrix in the first and second level $\mathbf{V_1}$ and $\mathbf{V_2}$, in order to

$$\max_{\mathbf{V_1},\mathbf{V_2}} \sum_{i=1}^{m} \omega_i V_i \tag{9}$$

subject to:

$$\begin{cases} \sum_{ij} \left(\mathbf{V_1} \circ \mathbf{C_{ST}} + \mathbf{V_2} \circ \mathbf{C_{TM}}\right)(i,j) \leq C, \\ \mathbf{T_{ST}}(i,j) + \mathbf{T_{TM}}(j,k) \leq T_V, \forall i,j,k, \text{where } \mathbf{V_1}(i,j) \neq 0 \text{ and } \mathbf{V_2}(j,k) \neq 0, \\ T_V vacc_i \geq \sum_{j=1}^{t} \mathbf{V_1}(i,j), \forall i = 1,2,\cdots,s, \\ \sum_{j=1}^{s} \mathbf{V_1}(j,i) \geq \sum_{j=1}^{m} \mathbf{V_2}(i,j), \forall i = 1,2,\cdots,t, \\ cap_{Vi} \geq \sum_{j=1}^{m} \mathbf{V_2}(i,j), \forall i = 1,2,\cdots,t, \\ V_i = \sum_{j=1}^{t} \mathbf{V_2}(j,i), \forall i = 1,2,\cdots,m. \end{cases} \tag{10}$$

Assumptions

- The medication remains effective despite the distance and time it traveled.
- The volume of transportation do not have a upper boundary, that means whatever needed could be transported in time.
- Fractions in the result of linear programming can be accepted, since they can be omitted compared to the integer part.
- The cost of transport goes linearly as the distance or the volume goes up.

2.4 The Location of Delivery

Now that the resource and storage center seem to be scarce in the epidemic regions, we may construct some new storages in the country. In this model, the problem is selecting among several possible new location candidates to determine the ones that can minimize the cost of delivery, while satisfying the demand of drugs or vaccines claimed by epidemic area. First we need to calculate the volume of medication needed by each region, and then transport and distribute it smartly. For simplicity, we only consider S, I, Q, and R stages in the epidemic model.

2.4.1 The Need of Epidemic Regions

The transition rate in SIQR model for each region is:

$$\begin{cases} \frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI + \mu(I+R), \\ \frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - \sigma I - \delta I - d_1 I - \mu I, \\ \frac{\mathrm{d}Q}{\mathrm{d}t} = \delta I - \sigma Q - d_2 Q - \mu Q, \\ \frac{\mathrm{d}R}{\mathrm{d}t} = \sigma Q + \sigma I - \mu R. \end{cases} \tag{11}$$

Since we mainly focus on the transport cost now, we assume the vaccine (or drug) is enough to make $\frac{dI}{dt} < 0$. Dai and Zhao [2] studied the relationship between the pulse vaccination period and the vaccination rate (the portion of vaccine targets), and determined the minimal vaccination rate [7]

$$p = \min\left\{ \frac{\mathrm{d}T_V\left(\mathrm{e}^{\mathrm{d}T_V}-1\right)(\beta-\delta-\sigma-\mu-d_1)}{\beta\left(\mathrm{e}^{\mathrm{d}T_V}-1\right)-\mathrm{d}T_V(\beta-\delta-\sigma-\mu-d_1)}, \frac{\left(\mathrm{e}^{\mathrm{d}T_V}-1\right)(\beta-\delta-\sigma-d_1)}{\delta+\sigma+d_1} \right\}. \tag{12}$$

In this way, we can compute p_i of each region and select $d_i = p_i S_i N$ people to be the vaccine target in region i.

2.4.2 Location Selection Model

To determine the location of new intermediate storage center (T), we use linear programming again. Assume there are t available Ts, which include those already in use ($\mathbf{cost}(i) = 0$), and those will be constructed ($\mathbf{cost}(i) \neq 0$). The vector $\mathbf{t}$ indicates the existence of them (1=exist, 0=not exist). The overall cost to be minimized is the sum of transport cost and T construction cost:

$$\min_{\mathbf{t},\mathbf{V_1},\mathbf{V_2}} \mathbf{t}^T\mathbf{cost} + \sum\nolimits_{ij} \mathbf{T_{ST}V_1}(i,j) + \sum\nolimits_{jk} \mathbf{T_{TM}V_2}(j,k), \tag{13}$$

subject to:

$$\begin{cases} d_i \leq \sum_{j=1}^{t} \mathbf{V_2}(j,i)\mathbf{t}(j), \forall i = 1,2,\cdots,m \\ \sum_{j=1}^{m} \mathbf{V_2}(i,j) \leq \sum_{j=1}^{s} \mathbf{V_1}(j,i), \forall i = 1,2,\cdots,t \text{ and } \mathbf{t}(i) = 1 \\ \sum_{j=1}^{m} \mathbf{V_2}(i,j) \leq cap_{Vi}, \forall i = 1,2,\cdots,t \text{ and } \mathbf{t}(i) = 1 \\ \mathbf{t}(i) \in \{0,1\} \text{ and for existed locations } \mathbf{t}(i) = 1 \\ \mathbf{T_{ST}}(i,j) \leq T_V, \forall \mathbf{V_1}(i,j) \neq 0 \\ \mathbf{T_{TM}}(i,j) \leq T_V, \forall \mathbf{V_2}(i,j) \neq 0 \end{cases} \tag{14}$$

Assumptions

- The transport speed between S and T is significantly larger than that between T and M, at the same time, the cost is also larger.
- The drug and vaccine available can meet the requirements of regions.

2.5 International Spread

In the previous models, we are mainly concerned with a few epidemic regions, which is an abstract of the real situation - severe outbreak in Guinea, Liberia, and Sierra Leone, while few cases out of them. This method can perform well on the simulation, however, we still need to consider the possibility of spread in other places of the world.

One extremely simple approach is that we can take all cities in the world into consideration. However, the striking problem is that there are too many cities! We need quite large memory to keep track of the S, E, I, Q and R for all the cities. Since almost all the cities on continents other than African will suffer no disease invasion for a long period of time, we know that

$$S_i = N_i \tag{15}$$

will hold for each such city i. Thus, using this method is quite challenging and wasteful!

One another alternative is that we can ignore cities in another continents except for Africa first and add them into our three-level delivery model only when a newly patient is diagnosed as being infected by Ebola. This approach seems practible at first glance, however, this leaves us a tiny problem, which is how to model the migration between Africa cities and non-Africa ones.

Thus, we propose the following method to achieve a tradeoff between these two methods.

Model Sketch For both accuracy and simplicity, we regard every other continents as single regions in our model at first. To be specific, each continent is represented as one set of (S, E, I, Q, R). Using this approach can make our model not only correct but compact as well.

And, as the time goes by, an once Ebola-free continent may encounter some newly Ebola patients. When the number of patients on this continent increases, we may need to keep record of their migration among nations. Then, we adaptively separate this continent into several nations, meaning that we consider each nation as a single node in our model. This will help us model the migration between nations on this continent. Similarly, when a nation finds many new patients, we can further separate it into several cities in this nation.

This dynamically heuristic method is useful to model international spread due to the fact that it guarantees both accuracy and feasibility.

Separation Threshold When to separate a high-level node into several low-level ones? We build a toy model to study an appropriate threshold.

Consider each person as a single node v_i. Each v_i has his or her own set of friends, which is of quite small size relative to the whole population in the continent. Denote F_i to be the friend set of v_i. Each day, v_i may have closely interactions with some of his or her friends u_j's. For each interaction, if u_j is infected with Ebola, then there is a non-zero possibility p that v_i will be infected. Denote the number of friends v_i may interacts as $S_i \subseteq F_i$. We know that the possibility that v_i gets infected is

$$1 - (1 - p)^{|S_i|}. \tag{16}$$

If we assume N to be the total number of people on this continent, then we can notice that

$$\frac{S_i}{N} p = \beta \tag{17}$$

where β is the infection rate in our epidemic diffusion model.

Using this model, we can keep track of number of people who get infected everyday. If this number exceeds some prefix threshold, we should consider separate this continent into several nations.

2.6 Parameters

In the epidemic spread and delivery system model, there are many parameters indicating the situation of regions, the characteristic of medications, the relationship between three-level delivery system, etc (Table 1). If we could calculate the parameters accurately, we are able to simulate the real case of Ebola outbreak. Therefore, the determination of parameter is important in modeling. Some of them can be inferred from census data, but there are still some need to be speculated based on fitting curves or previous researches:

Table 1: Parameters Used in the Model

Parameter	Description
T	unit time
T_D, T_V	period of drug and vaccine delivery
S_i, E_i, I_i, Q_i, R_i	the number of people in each category in region i
λ_i, μ_i	natural birth and death rate in region i
ρ_{ij}	transfer rate from region i to region j
$\rho_{S_i}, \rho_{E_i}, \rho_{I_i}, \rho_{R_i}$	fraction of people departing from region i in each category
β_i	infectious rate in region i
t_1	exposed period
t_2	drug-taking period
η_D, η_V	effective rate of drug and vaccine
d_1	death rate among infected people
d_2	death rate among quarantined people
σ_{1i}	natural recovery rate in region i
σ_{2i}	recovery rate with medical therapy in region i
δ_i	quarantining rate in region i
ω_i	the danger level of region i
$\mathbf{C_{ST}}, \mathbf{C_{TM}}, \mathbf{T_{ST}}, \mathbf{T_{TM}}$	traveling cost and time matrix between regions

- T is the unit time, or the period of iteration, when $t = kT$, $k = 1, 2, \ldots$, we will update the model like Eq. 3. In our experiment, the unit time is set to 1 day.
- T_D, T_V describe the period of drug and vaccine delivery, as well as the time span between two applications of medicine, since the model of pulse vaccine and drug delivery and application is used in our paper. In our experiment, T_D and T_V are both set to be 5 days.
- The initial number of people in each category $S_i(0), E_i(0), I_i(0), Q_i(0), R_i(0)$ are based on the population of region.
- λ_i, μ_i are the natural birth and death rate in region i. The natural birth rate could be directly found in World Data Bank website, while the natural death rate could be described as the inverse of mean life expectancy of one person.
- ρ_{ij} is transfer rate from region i to region j, in other words, it describes the probability of traveling to region j for each person in region i.

Several conditions could promote the traveling between two countries or regions, such as the geographical distance, the economical level, the population, the language, the degree of opening and so on. Since some of the conditions are hard to described by particular number, we choose geographical distance from region i to region j: d_{ij}, the economical level of region i: E_i and the population of region i: P_i as the gist of parameter ρ_{ij}'s assignment.

The gravity model is a classical rules to predict the interaction on migration, information, commerce and so on. There are many modifications on this model, a successful attempt is the gravity model in migration proposed by Michael J. Greenwood.[6] Use the model as a reference, we put a simpler mathematics model forward:

$$M_{ij} = C\frac{P_i^{\beta_1}P_j^{\beta_2}}{d_{ij}^{\alpha}}E_i^{\gamma_1}E_j^{\gamma_2} \tag{18}$$

where M_{ij} represent the degree of prosperity on trade and migration between region i and region j. α,β_1,β_2,γ_1,γ_2 are exponent of the parameters, they change along with the variational importance of the factors. Usually, α is assigned 2 and others are assigned 1.

Here, ρ_{ij} represents the probability of traveling for single person. So we have:

$$\rho_{ij} = \frac{M_{ij}}{P_i} = C\frac{P_j}{d_{ij}^2}E_iE_j \tag{19}$$

The economical level of each countries could be derived from Gross Domestic Product (GDP). GDP, along with the population of each region and the geographical distance between two regions could also be achieved from websites.

- $\rho_{S_i}, \rho_{E_i}, \rho_{I_i}, \rho_{R_i}$ represent the fraction of people departing from region i in each stage. They could all be derived from ρ_{ij} using Bayes' rules. Here we use ρ_{s_i} as an example:

$$\rho_{S_i} = \rho_{ij}\frac{S_i}{S_i + E_i + I_i + R_i} \tag{20}$$

- β_i is infectious rate in region i. Population density Den_i, the economical level E_i, which has been mentioned before, and the average temperature Tem_i are generally considered to be the influence factors. Here we raise a descriptor ϕ_i to compare different regions' condition in order to determine in which region people may have larger probability to be infected.

$$\phi_i = \frac{Tem_i * Den_i}{E_i} \tag{21}$$

According to MOMAT research group's research[1], Guinea, which is the origin infected country, has the infectious speed $Speed_{ref}$ of 0.2095 ($persons{\cdot}day^{-1}$). In our model, we use Guinea as a reference. Other regions' infectious rate could be calculated by:

$$\begin{aligned}\beta_{ref} &= \frac{Speed_{ref}}{P_{ref}}\\ \beta_i &= \beta_{ref}\frac{\phi_i}{\phi_{ref}}\end{aligned} \tag{22}$$

- t_1 is the incubation period of the disease, people who are already infected, yet have not show any symptoms will move to stage I (Infected) in t_1 days on average. The incubation period of Ebola is 10 days on average.

- t_2 is the drug-taking period.
- η_D, η_V are the effective rates of drug and vaccine.

  These three parameters above depend on the characteristic of the newly developed drug and vaccine. Because the existence of the effective medicines is only a consumption, we just select these parameter's value by experience.

- d_1 is the death rate among infected people. Since no medical treatments is received by infectors, the death rate is only determined by the fatality rate of the virus.
- d_2 is the death rate among quarantined people. By receiving the appropriate therapy and taking some medicine which could control disease development, the death rate should be a little bit lower than d_1. Thus, the medical environment of the hospital become the only significant factor which influenced the death rate. We use MHE_i to represent the Mean Health Expenditure per year per person. By reading the reports of the Ebola's treatment conditions, death rates vary from about 25% (Developed countries, such as USA) to about 73% (Underdeveloped areas, such as Guinea).[9] Here we got:

$$d_2(i) = 0.25 * \frac{MHE_i}{MHE_{imax}} + 0.73 * (1 - \frac{MHE_i}{MHE_{imax}}) \tag{23}$$

- σ_{1i} and σ_{2i} are recovery rates in region i. The relationship between them is extremely similar to which between d_1 and d_2. Thus, a analogous method could be applied on the assignment of these parameters.
- δ_i is the quarantining rate in region i. To consider the variation of the parameter's value among regions, we take the same method as d_2's assignment to solve the initialization problem. Since the degree of attention of people to the seriousness of the infectious disease become higher along with the spread of the virus, a coefficient function is added to the initialize value. Assume that $Time_{passi}$ represent the time period since the first infector appeared in region i, we have:

$$\delta_i = \delta_{initiali} * log_a(Time_{passi}) \tag{24}$$

  where a should be assigned appropriately according to the fatality rate of the disease.

- ω_i is the descriptor of the danger level of region i. The higher danger level a particular region has, the more urgently we distribute enough medical resources to that region. A region is considered to be dangerous in disease condition, is usually because the infectious rate is above the average, the increasing speed of the population of infected persons who have already been diagnosed, or the ability of the region to cure the patient. There are several factors which could contribute effect to the danger level in varying degrees. Since the quantization of the importance of these factors is not such simple, Fuzzy Analytic Hierarchy Process (FAHP) [8] could be used in the determination of the factors' weight that could appropriately inflect the significance.

  Fuzzy Judgment Matrix (FJM) is a efficient mathematics tool in FAHP. Assume a_{ij} stands for the element of the matrix. The meaning of its value is shown in Table 2.

  After evaluation of the Fuzzy Judgment Matrix, the weight of each factor could be calculated by:

$$W_i = \frac{\sum_{j=1}^{n} a_{ij} + n/2 - 1}{n(n-1)} \tag{25}$$

Table 2: The value of Fuzzy Judgment Matrix's elements

Value(a_{ij})	**Meaning**
$[0.1, 0.5)$	a_i is less significant than a_j, lower value means larger disparity.
0.5	a_i holds the same significant as a_j. Actually, the elements in diagonal line of FJM must be 0.5.
$(0.5, 0.9]$	a_i is more significant than a_j, higher value means larger disparity.

Table 3: Significant factors in evaluation of particular region's danger level

Factor(f_i)	**Description**
f_1	Infectious rate denoted by β_i.
f_2	The number of people who is in stage Q(Quarantines), denoted by Q_i.
f_3	The recovery rate without therapy denoted by σ_i.
f_4	Recent increase of people in stage Q(Quarantines) during T_D or T_V, denoted by $$dQ_i(t) = \frac{Q_i(t) - Q_i(t - T_{D/V})}{Q_i(t - T_{D/V})} \quad (26)$$

In our model, the four factors we have considered to be able to effect the danger level are shown in Table 3.

According to the qualitative analysis of the four factors, we could give rank to each factor and generate the Fuzzy Judgment Matrix A_{ij} based on Table 2.

$$A_{ij} = \begin{pmatrix} 0.5 & 0.3 & 0.7 & 0.2 \\ 0.7 & 0.5 & 0.8 & 0.4 \\ 0.3 & 0.2 & 0.5 & 0.1 \\ 0.8 & 0.6 & 0.9 & 0.5 \end{pmatrix} \quad (27)$$

Given the Fuzzy Judgment Matrix A_{ij}, it is not complicated to generate the weight vector W use Eq. (25).

$$W = \begin{pmatrix} 0.225 & 0.283 & 0.175 & 0.317 \end{pmatrix} \quad (28)$$

After solving the problem of weight distribution, data normalization will be done in order to make each factor f_i be valued in the same range. Here we use β_i as an example:

$$f_{1i} = \frac{\beta_i - \beta_{min}}{\beta_{max} - \beta_{min}} \quad (29)$$

Eq. (29) maps the range of β_i into (0,1), where β_{min} and β_{max} represent the minimum and maximum value of β_i. Other factors need to be normalized by the same method.

Finally, the danger level is described by:

$$\omega_i = \sum_{j=1}^{n} W_i(j) * f_j \quad (30)$$

- $\mathbf{C_{ST}}, \mathbf{C_{TM}}, \mathbf{T_{ST}}, \mathbf{T_{TM}}$ describe the travelling cost and travelling time between regions. Obviously, travelling cost and travelling time are both derived from the distance d_{ij} between two regions. Here, we firstly raise a method to calculate the distance matrix:

$$d_{ij} = \Phi(1 - r_{ij}) + \lambda \overline{d}_{ij} \tag{31}$$

where $r_{ij} \in$ {0,1} represent the road conditions, 1 stands for the existence of connection, 0 stands for the lack of access between them. Φ is an extremely large number, in order to make the distance large enough when there is no access between two regions. λ is the coefficient of the transition from the Euclidean distance $\overline{d}_{ij}$ to the realistic distance.

Traveling time has a linear correlation to the distance, thus we could simply multiply a coefficient stands for the traveling speed. Consider that the first level of our delivery system usually use faster vehicle, such as planes, while the second level use trucks or trains, we should assign a larger value to the speed of first level.

Traveling cost is more complicated because it is determined by several factors such as the mode of transportation, the distance from starting point to terminal station and even the oil price. Finding all of these realistic data is almost impossible, so in our simulation, a simple coefficient is also used in parameter's assignment, similar to the method above.

3 Result

3.1 The Impact of Drug and Vaccine

Experiment Setting We set $s = 2$, $t = 4$ and $m = 20$, which are the number of supply centers, intermediate storage centers and epidemic regions respectively. The locations for all Ss, Ts and Ms are randomly picked on a 100×100 plane. Refer to Fig. 6 as an example. Some of Ms are selected to be real epidemic regions, where $E_0, I_0, Q_0, R_0 \neq 0$. While in other regions, we initially set $E_0 = I_0 = Q_0 = R_0 = 0$.

Another parameters are set as Table 4 and Fig. 4.

$T = 1$	$\eta_V = \eta_D = 0.9$	$t_1 = 10$	$t_2 = 1.2$	$d_1 = d_2 = 0.02$	$\delta_i = 0.3$
$T_V = 5$	$T_D = 3$	$v_{level1} = 1000$	$v_{level2} = 100$		

Table 4: Parameters

Result and Analysis The impact of drug and vaccine compared to the natural spread of disease is shown in Fig. 7∼12. Given the input Fig. 6 with the locations of S, T and M, we run the delivery system with drug and vaccine transport, only drug transport, and no medication transport (natural spread). From the 20 regions, we select region No. 5 and No. 12 as representatives for illustration.

Region 5 is an epidemic region with initial patients in E, I, and Q. Comparing Fig. 7, 9, and 11, we find the use of drug and vaccine can significantly prevent the spread of the disease and reduce the death population. However, the impact of vaccine alone is not evident, mainly due to the reason that the decreased population of I is too slight.

Region 12 is a region without initial patients. Figure 8, 10, and 12 also show the effectiveness of medication. Note that the natural spread of the disease in the region without any initial patients could also become severe after some days because of the migration of people.

- $S \sim \mathcal{N}(30000, 100)$.
- $E \sim \mathcal{N}(50, 5)$.
- $I \sim \mathcal{N}(30, 3)$.
- $Q \sim \mathcal{N}(10, 1)$.
- $R \sim \mathcal{N}(40, 5)$.
- $\lambda_i \sim \mathcal{N}(0.04/365, 0.005/365)$.
- $\mu_i \sim \mathcal{N}(0.03/365, 0.005/365)$.
- $\sigma_i \sim \mathcal{N}(0.02, 0.005)$.
- $\beta_i \sim \mathcal{N}(1e-6, 1e-7)$.
- d_{ij} follows Eq. 31.
- $C_{ST}(i,j) = d_{ij}\mathcal{N}(0.1, 0.01)$.
- $C_{TM}(i,j) = d_{ij}\mathcal{N}(1, 0.01)$.
- $T_{ST}(i,j) = d_{ij}/v_{level1}$.
- $T_{TM}(i,j) = d_{ij}/v_{level1}$.

Figure 4: First Experiment

- $S \sim \mathcal{N}(30000, 100)$.
- $E \sim \mathcal{N}(100, 10)$.
- $I \sim \mathcal{N}(50, 5)$.
- $Q \sim \mathcal{N}(20, 3)$.
- $R \sim \mathcal{N}(70, 10)$.
- $\lambda_i \sim \mathcal{N}(0.04/365, 0.005/365)$.
- $\mu_i \sim \mathcal{N}(0.03/365, 0.005/365)$.
- $\sigma_i \sim \mathcal{N}(0.02, 0.005)$.
- $\beta_i \sim \mathcal{N}(1e-6, 1e-7)$.
- d_{ij} follows Eq. 31.
- $C_{ST}(i,j) = d_{ij}\mathcal{N}(0.1, 0.01)$.
- $C_{TM}(i,j) = d_{ij}\mathcal{N}(1, 0.01)$.
- $T_{ST}(i,j) = d_{ij}/v_{level1}$.
- $T_{TM}(i,j) = d_{ij}/v_{level1}$.

Figure 5: Second Experiment

3.2 Performance of Delivery System

Experiment Setting We set $s = 2$, $t = 4$ and $m = 20$, which are the number of supply centers, intermediate storage centers and epidemic regions respectively. The locations for all Ss, Ts and Ms are randomly picked on a 100×100 plane. Refer to Fig. 13 as an example. Some of Ms are selected to be real epidemic regions, where $E_0, I_0, Q_0, R_0 \neq 0$. While in other regions, we initially set $E_0 = I_0 = Q_0 = R_0 = 0$.

Another parameters are set as Table 5 and Fig. 5.

$T = 1$	$\eta_V = \eta_D = 0.9$	$t_1 = 10$	$t_2 = 1.2$	$d_1 = d_2 = 0.02$	$\delta_i = 0.3$
$T_V = 5$	$T_D = 3$	$v_{level1} = 200$	$v_{level2} = 10$		

Table 5: Parameters

Result and Analysis We simulate the delivery of medication with the geographic locations shown in Fig. 13. We select the drug and vaccine delivery for several pulses from Fig. 14 to Fig. 20. From the first to the seven pulse of drug, the same Ms were served, however the transport plan is adaptively varying with the change of ω_i. From the fourteen to eighteen pulse of drug, the spread of disease in most Ms is controlled, therefore less and less drug is needed. For vaccine, the distribution is also dependent on the ω_i. Only the need of those Ms with the highest danger level can be met, although almost all Ms are requiring vaccine.

We also take two Ms, No.4 and No.6, as the representatives to illustrate the impact of drug and vaccine. In region No.4 (Fig. 21), there are a portion of people in E, I and Q at the very beginning. After about one month, the disease is controlled to a very low level. Figure 23

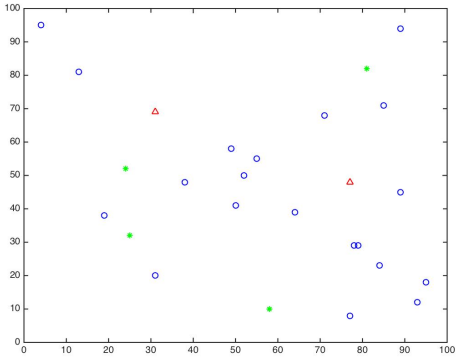

Figure 6: The Input Figure

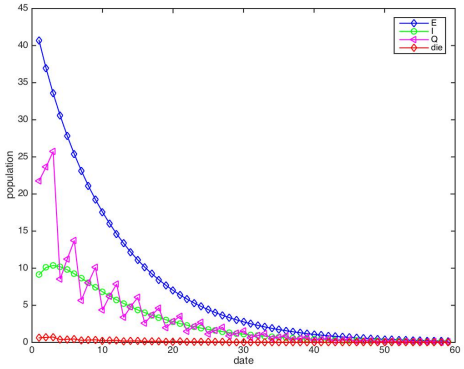

Figure 7: M5 with Drug and Vaccine

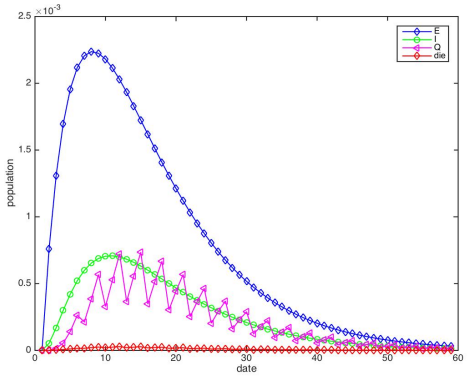

Figure 8: M12 with Drug and Vaccine

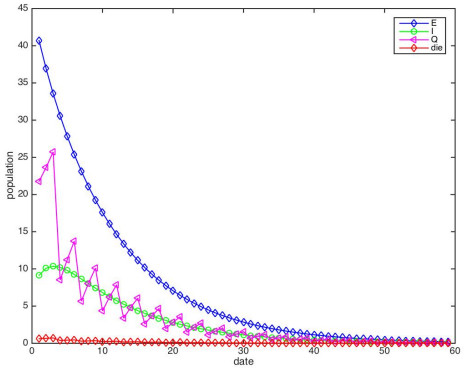

Figure 9: M5 with Only Drug

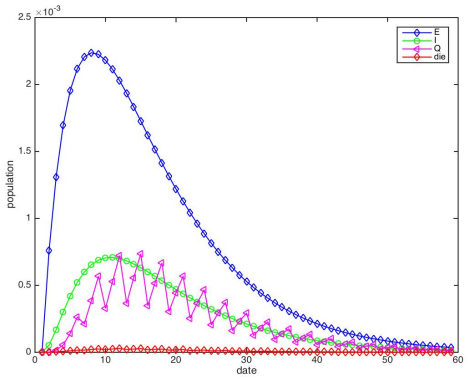

Figure 10: M12 with Only Drug

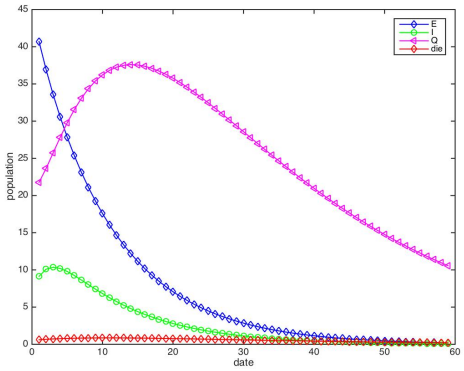

Figure 11: M5 with No Drug or Vaccine

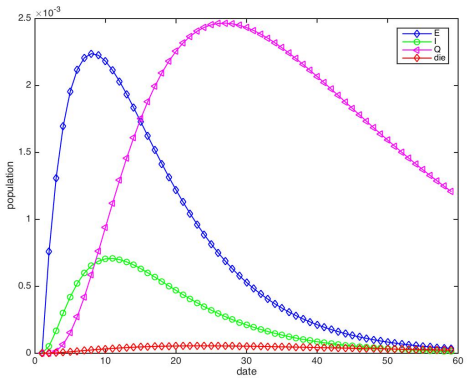

Figure 12: M12 with No Drug or Vaccine

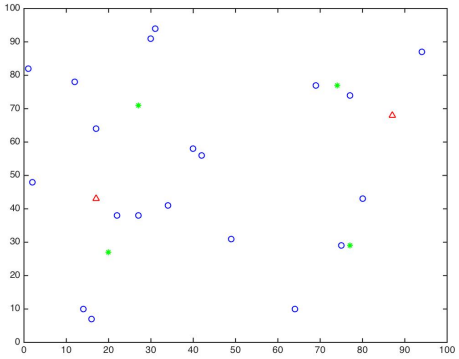

Figure 13: Input Figure

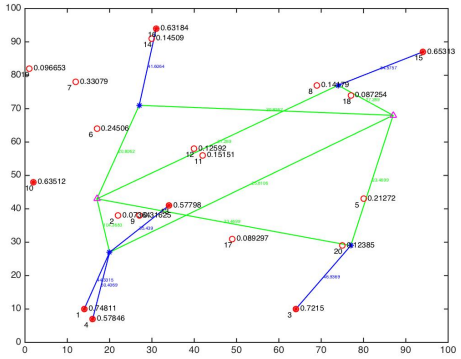

Figure 14: The First Pulse of Drug

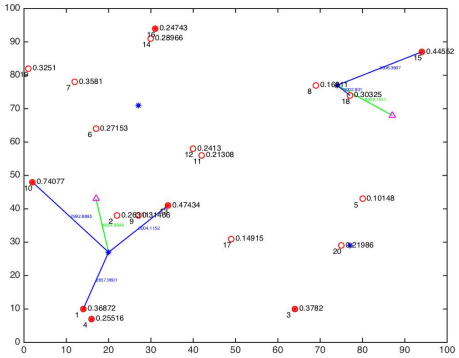

Figure 15: The First Pulse of Vaccine

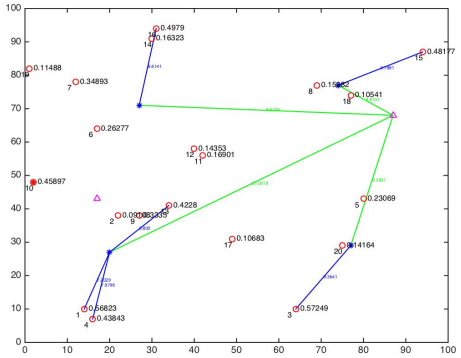

Figure 16: The Seventh Pulse of Drug

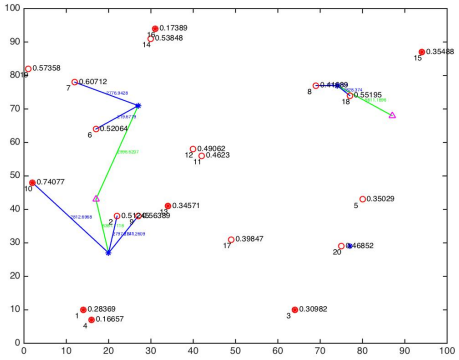

Figure 17: The Third Pulse of Vaccine

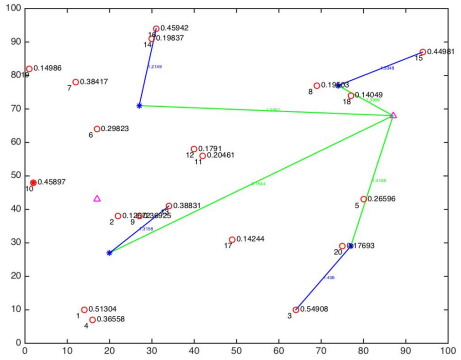

Figure 18: The Fourteenth Pulse of Drug

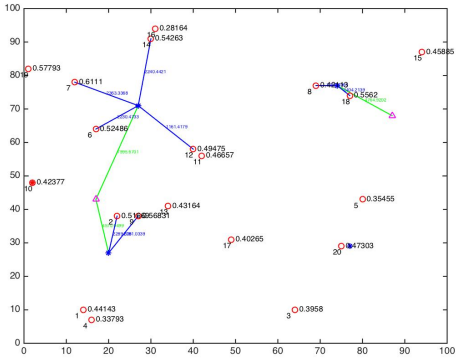

Figure 19: The Eleventh Pulse of Vaccine

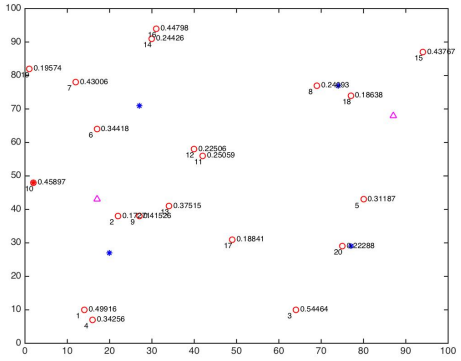

Figure 20: The Eighteenth Pulse of Drug

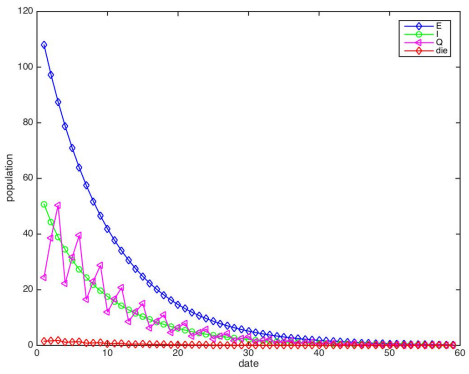

Figure 21: The E, I, Q, and Dead of M4

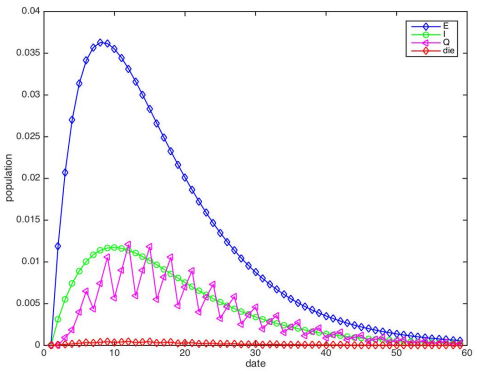

Figure 22: The E, I, Q, and Dead of M6

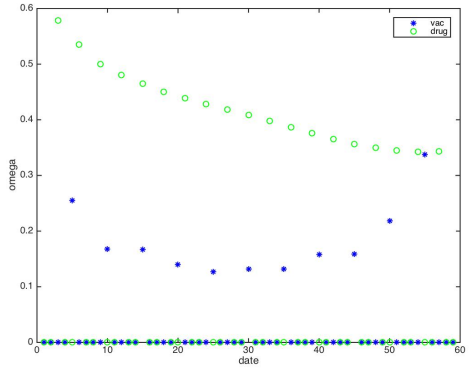

Figure 23: The Danger Level of M4

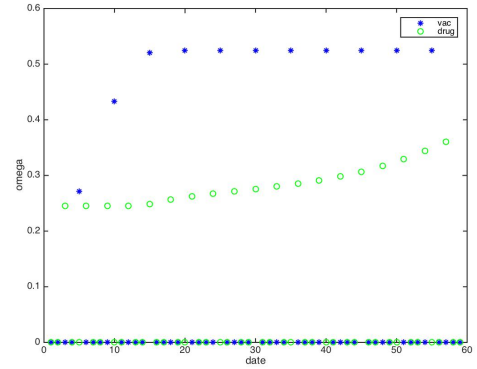

Figure 24: The Danger Level of M6

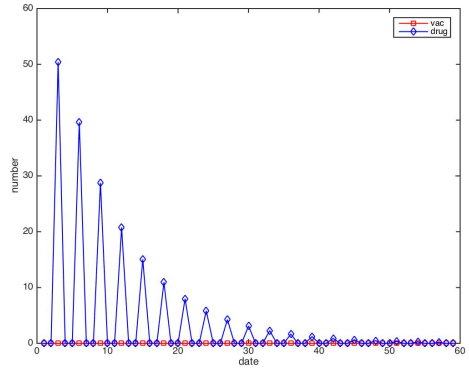

Figure 25: The Delivery to M4

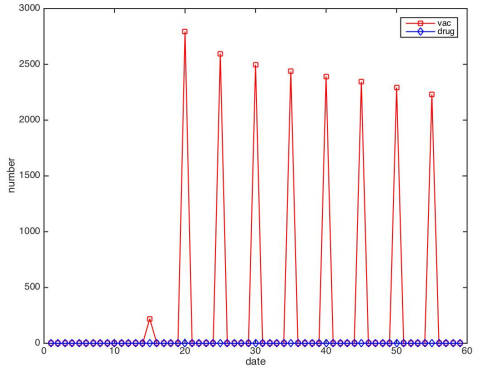

Figure 26: The Delivery to M6

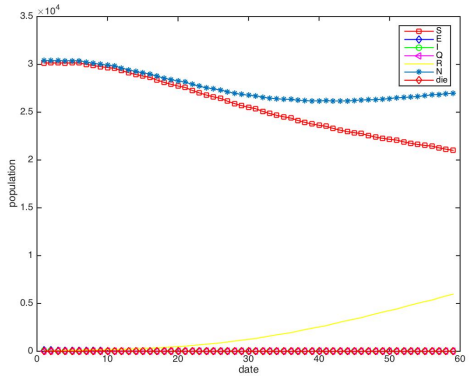

Figure 27: The Population in M4

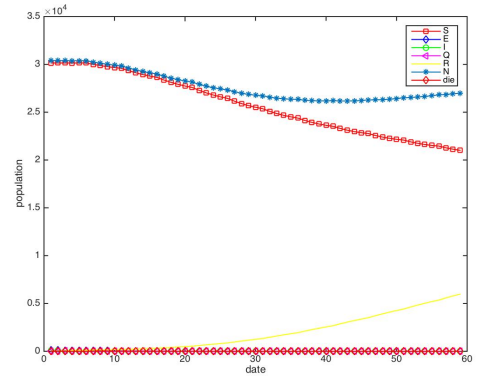

Figure 28: The Population in M6

shows the danger level of the region in every pulse. We find the level generally goes down in these days. Therefore, more drug was transported here in the first several pulses, and then become less and less (Fig. 25), which is the same as the trend of danger level. This can be also seen from Fig. 21, since the sudden drops of Q indicate the arrival of drug.

From Fig. 22 we know, there is no patient here initially. However, as the time goes, migration makes the people in E, I, Q increase. At the same time, the danger level in this region continuously goes up (Fig. 24). Different from region No.4, the danger level of vaccine is higher. Therefore, the vaccine is transported in a large quantity after the 20th day (Fig. 26). Correspondingly, the serrated cure of S and R in Fig. 28 clearly show the impact of vaccine.

3.3 The Selection of Location

Experiment Setting In this experiment, we fix the $s = 3$ and $m = 50$, which are the number of supply centers and epidemic regions respectively. We provide $t = 20$ intermediate storage center candidates, some of which are already built. The locations for all Ss, Ts and Ms are randomly picked on a 100×100 plane. Refer to Fig. 29 as an example. Another parameters are set as follows.

- $d_i \sim \mathcal{N}(200, 10)$.
- $cap_{V_i} \sim \mathcal{N}(10000, 1000)$.
- $dist_{ij}$ follows Eq. 31.
- $T_{ST}(i, j) \sim dist_{ij} \times \mathcal{N}(0.1, 0.01)$.
- $T_{TM}(i, j) \sim dist_{ij} \times \mathcal{N}(1, 0.1)$.
- 15% of t_i's are selected to be permanently 1.

Result and Analysis In the input Fig. 29, there are four kinds of locations, S, T already in use, possible new locations of T, and M. With the different building cost for new T, the location selection and transport plan vary. From Fig. 30 to Fig. 33, the relative building cost decreases from 100,000 to 10,000, 500, and finally to 10. The blue lines are the transportation from the S to the T, and green lines are that from the T to the M. We can see that the number of selected locations increase as the cost decreases.

In Fig. 30, only one additional T location was adopted and the Ts are responsible for a wild range of Ms. However, in Fig. 33 more new locations make it possible for Ts to manage only the local Ms. Figure 34 and 35 shows the trend of total cost and storage under different building cost. Unlike [13], which only optimizes the building cost, our model can optimize the sum of building cost and transport cost. The building cost can be thought as an prediction of future cost and storage.

4 Further Discussion - How to Eradicate Ebola

- **Reduce migration rate between epidemic regions and non-epidemic ones:** By reducing ρ_{ij} where region i is struggling from contagious disease and region j is not, we can effectively reduce the spread of Ebola over the nation, even over the world.

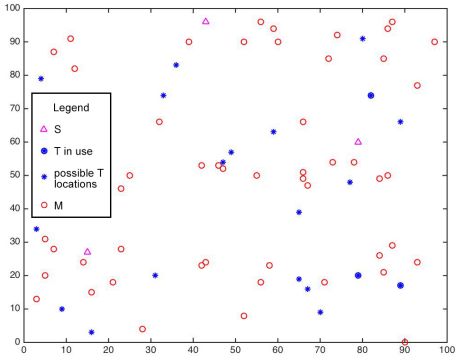

Figure 29: The Input Figure

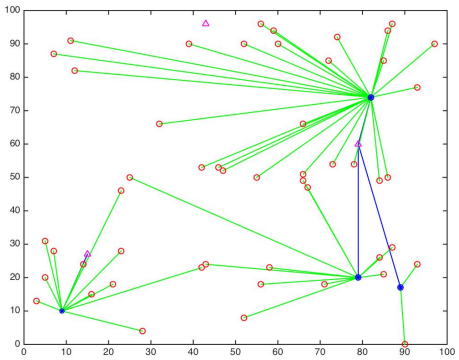

Figure 30: The Selection of Location (cost=100,000)

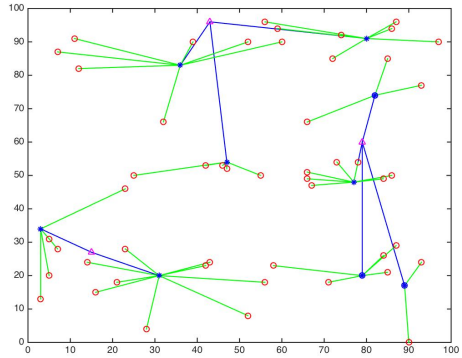

Figure 31: The Selection of Location (cost=10,000)

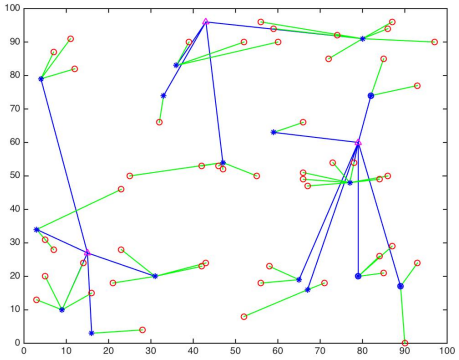

Figure 32: The Selection of Location (cost=500)

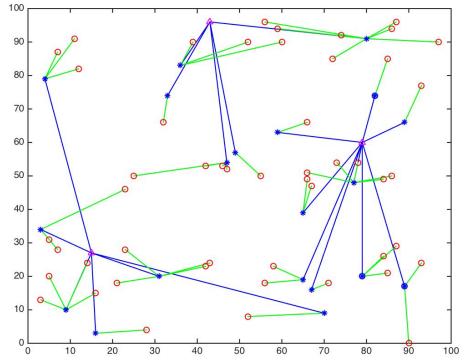

Figure 33: The Selection of Location (cost=10)

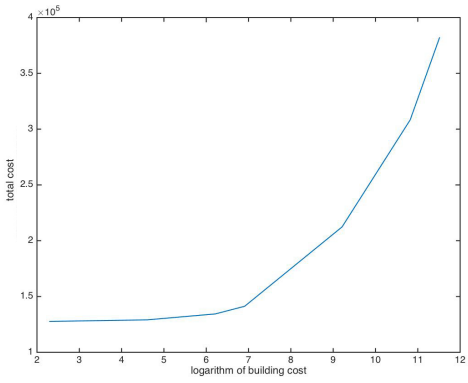

Figure 34: The Total Cost and Building Cost

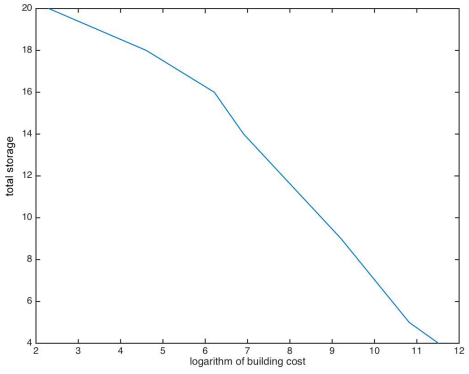

Figure 35: The Total Storage and Building Cost

Actually, this can be achieved automatically in the real world, when people know that infectious disease are rampant, they may be lessly inclined to travel to another place. Or, from the aspect of government's macro-control, traveling to or from extreme epidemic region are little or more restricted.

- **Reduce the fraction of infected migration:** By reducing ρ_I, we can similarly reduce the number of infected people who travels to another regions. Notice that it is the infected people who are both allowable for traveling and capable of infecting others.

  In fact, government can reduce this parameter by actively guard the geographic boundaries around serious epidemic areas. When one person coughs or has a fever, government should bring them to the doctor and let them go before eliminating the possibility that he or she is infected with Ebola.

- **Reduce the infection rate:** By reducing β, we can allow less suscepitable people to be infected with Ebola. Thus, we can fundamentally reduce the number of people of stage E. Since people of stage E will transit to stage I and Q finally, we should allow less people to be infected with Ebola.

  In many west African countries [11], people there have peculiar burial customs that they will wash a death body after one of their friends' death. This will dramatically increase the infection rate in this area, which may contribute to the seriousness of Ebola there.

- **Improve the quality and quantity of drugs and vaccines:** In case of drug or vaccine shortage, scientists should devote more time and attention to increasing the speed of producing drugs or vaccines. While, enhancing the effectiveness of drugs or vaccines(η_D, η_V) will also increase the eradication of Ebola.

- **Increasing the quarantine rate:** By increasing the quarantee rate δ, we can more quickly eliminate infected people(I)'s capability of infection to others. Thus, we can reduce the number of newly infected people due to that

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI \tag{32}$$

  is one equation in Eq. 1.

5 Analysis of Sensitivity

Due to the limitation of time, we only analysize the sensitivity of two parameters: drug and vaccine effective rate(η_D and η_V); quarantine rate(σ).

- **Increase effective rate:** I set $\eta_D = \eta_V = 0.1, 0.5, 0.9$ respectively and draw a histogram of death population related to Ebola(exclude natural death population).

  We find that with the increasing of effective rate η_D and η_V(the quality of drugs and vaccines), our death population is decreasing, which accords to our expectation. Look at Fig. 36.

- **Increase quarantine rate:** I set $\sigma = 0.3, 0.7, 1.0$ respectively and draw a histogram of death population related to Ebola(exclude natural death population).

  We find that with the increasing of quarantine rate σ, our death population is decreasing, which accords to our expectation. Look at Fig. 37.

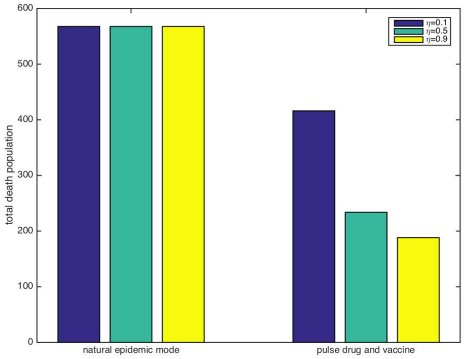

Figure 36: Effective Rate

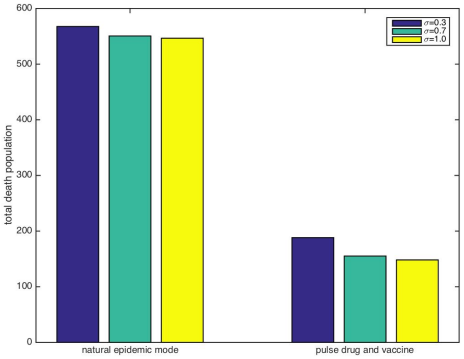

Figure 37: Quarantine Rate

6 Strengths and Weaknesses

6.1 Strengths

- The spread of disease model is complete and complex enough to include most of the main factors. These factors are the contact infection, exposed period, quarantine, natural birth and death rate, as well as multi-region interaction, etc.
- The pulse-fashion medication delivery, and the three-level delivery system, are both realistic and accurate. The linear programming in determining the transport plan and location of delivery can simulate the current situation and find the optimal solution.
- We not only consider the spread of disease in the epidemic regions, but also use an adaptive way to model the possible outbreaks in other areas.
- All of the models derive from the original SIR epidemic model, yet they focus on the different aspects of the main problem, which makes the models become both feasible and precise.

6.2 Weaknesses

- There are a large quantities of parameters involved in the models. Although we spent a lot of efforts to search and calculate the value of them, some parameters are still not easy to determine. Therefore, the parameters used in the experiment may not be accurate.
- Due to the limited time, our experiments are not based on the real geographic and infectious data. However, the result on random data can still prove the soundness of our models. Given appropriate parameters and adjustment, our models are very likely to be used on real case.

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Non-technical Announcement

Recently, the world medical association has developed new medication for preventing the spread of Ebola disease. The medication can be categorized into drug and vaccine. The drug could cure patients whose disease is not advanced, and the injection of vaccine will make ordinary people become immune from Ebola. Research and simulation have been done on the spread of disease and impact of medication. The result turned out that the medication can indeed eradicate Ebola.

The drug could significantly prevent the spread of disease and reduce the death population with a relatively high effective rate. However, the influence of vaccine is not very obvious, since only a small portion of people can receive it.

To distribute the medication effectively, a three-level delivery system is recommended to be used. The medication will be delivered from the supply center, to the intermediate storage center, and finally to the epidemic regions.

Considering the limited speed of manufacturing, the medication may not meet the requirement of all the regions. The supply system tends to send more volume of medication to the most dangerous regions, which is determined by the medical level and the recently diagnosed cases, etc.

Now that the intermediate storage center is scarce, we plan to build some new ones among some possible locations to reduce the transport cost and increase the capacity. An optimizing mechanism is also proposed to minimize the overall cost.

Following the settings above, the computer simulation proved the system to be sound and robust. Results show that the system can adaptively distribute the medication and aid the regions with the most severe situation. A shorter time for eradicating Ebola and lower mortality rate can be reached with the help of medication.

Moreover, other measures should not be omitted despite the existence of medication. Detection in travelling, stopping the contact with bodies, and quarantining after infected are also very useful for both protecting ourselves and eradicating Ebola.