For office use only		Team Control Number	For office use only	
T1		**32107**	F1	
T2			F2	
T3		Problem Chosen	F3	
T4		**A**	F4	

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

Abstract

Ebola, with death rate of 50%-90%, is a deadly infectious disease of humans and other species. However, original epidemic model (SIR) is incapable of providing vivid picture of disease prevalence. To solve this problem and to improve effectiveness of disease control, a new method named CASEIQR is proposed, which is mainly composed of two models, namely, optimized epidemic model and cellular automaton model.

Conventional epidemic model SEIR covering four sub populations: susceptible, exposed, infected and recovered individuals, which neglects the influence of human interference. Thus it is inadequate to reflect a whole picture of the actual situation. Therefore, we construct the SEIQR model with the addition of isolation measures and medication treatment. A system of ordinary differential equations is derived from SEIQR. By analyzing the existence and stability of the disease-free equilibrium, a basic-reproductive number R_0 is obtained. This study is aimed to minimize R_0 value by regulating such parameters as cure rate, infection rate, medicine demand, etc.

To clearly clarify the influences of these factors on the control of epidemic prevalence, we utilize cellular automaton to simulate the epidemic distribution in the West Africa. The map of epidemic distribution of the West Africa is divided into 100×100 cells, with each cell endowed with one of the six values: "susceptible","exposed","infected","quarantine","recovered", and"assistance station". Moreover, we formulate a rule of transformation between different status values. The results of our modeling are in accordance with the actual epidemic development.

Several critical factors in the established model are further discussed. We first modify rules mentioned above. Subsequently, we compare the variation tendencies of epidemic derived from pre- and post- modification rules, respectively in order to identify the critical factors of the model. The results show that the construction of assistance stations, the supply of drug, and the research and development of vaccine play important roles in the prevention and control of Ebola. In addition, stepwise regression is employed to analyze the sensitivity of cellular automaton.

Eradicating Ebola

February 10, 2015

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Keywords: Cellular Automaton; SEIQR Model; Epidemic Model;

1 Introduction

Ebola, with a death rate of 50%-90%, is a deadly infectious disease of humans and other primates. Its major causes of death are stroke, myocardial infarction, hypovolemic shock and multiple organ failure. During the incubation period of 2 to 21days, patients are of no infectiousness. But once reaching an advanced stage, patients would suffer angiorrhexis of micro vessel, bleeding both internally and externally. However, due to the typical symptoms in early stage such as fever, sore throat, muscle pain and headaches, Ebola is often neglected and mixed up with other common diseases, thus increasing the risk of transmission. As of 2013, 24 outbreaks of Ebola have been reported by WHO, killing thousands of people. It is reported that the largest outbreak is ongoing in 2015, having already resulted in 8,981 deaths by February 1,2015.

In reality, due to the limitation of regions or environment, the amount of contact an infected person implemented in a given time is finite. Furthermore, human beings have probability to recover naturally. Hence, saturating incidence and recovery rate need introducing into the model. Xueyong Zhou, et al.(2011) presented saturating incidence $\frac{\beta SI}{b+I}$ and saturating recovery rate $\frac{cI}{b+I}$ (4438-4450). Combining this with compartment model, a dynamical model of infectious diseases with saturating incidence and recovery rate is established.

Besides, in addition to the impact of natural environment itself, the development of Ebola is also closely related to the interference of human beings. The spread of Ebola could be effectively controlled with correct isolation measure and treatment method. Therefore, in our model, the outbreak period is divided into two phases, before and after taking actions (i.e. $1 < t < t_1, t_1 < t < t_2$). We employ SEIR and SEIQR model to analyze them respectively. With the application of dynamical model theory, the threshold value that could stop the disease or control it into an endemic disease is obtained. It contributes to providing theoretical basis and prevention strategy to control and prevent Ebola (Yang Xu, 2008).

2 Concepts

Dynamical Model of Infectious Diseases

It is generally accepted that infectious diseases are transmitted through mutual contact among people. The amount of contact between infected individuals and others is called *the contact rate*. It is associated with the population in community, the latter generally denoted by N . Assuming that S denotes the susceptible individuals, then S/N denotes their proportion in population. β denotes the probability of infection once contacting with an infected individual. Thus the quantity of new infection per unit time at time t , namely *the morbidity* is as follows(Kun Chang, 2013).

$$\beta N(t)\frac{S(t)}{N(t)}I(t) = \beta S(t)I(t) \tag{2.1}$$

Table 1: Model parameters.

Parameter	Meaning
N	Total population
β	The probability of infection
$S(t)$	The susceptible population at time t
$E(t)$	The exposed population at time t
$I(t)$	The infectious population at time t
$Q(t)$	The quarantined population at time t
$R(t)$	The recovered population at time t
I	The number of the infected individuals
I_0	Maximal cure capacity
r	The cure rate
μ	Natural mortality rate
ρ	Inoculate rate
α_1	Death rate of infectious population
α_2	Death rate of quarantined population
Λ	The number of immigration
ϵ	Transfer ratio from susceptible to exposed
γ_1	Transfer ratio from exposed to infectious
γ_2	Transfer ratio from infectious to quarantined
γ_3	Transfer ratio from quarantined to recovered
δ	Transfer ratio from infectious to recovered
P_0	The malicious object-free equilibrium
R_0	Basic reproduction rate

3 Assumptions

- In addition to Ebola virus, other death causes, for instance natural hazard, is neglected to simplify the model establishment and analysis.
- The natural mortality rate of every individual is assumed to be the same, including the infected and healthy individuals.
- Assuming that the transformation rates mentioned in this paper are all nonnegative real numbers.
- A region would present in one of the four states: the infected, susceptible, quarantine, recovered state.
- The establishment of station will not be impeded by human factors such as religious believes.
- Given that no recovered patients are reported to be infected again, we assume that people once recovered from Ebola will never get infected.
- We assume that adjacent domains exert no mutual impacts on each other.

4 The SEIR Model

Traditional SEIR model analyzes disease transmission on the conditions of no human disturbance. Therefore, only net flow under natural conditions, natural mortality rate and diseased death rate need considering. The population in the affected districts are divided into four sub populations: susceptible($S(t)$), exposed($E(t)$), infectious($I(t)$), and recovered($R(t)$) individuals. $N(t)$ denotes the population at time t. Thus,

$$N(t) = S(t) + E(t) + I(t) + R(t) \tag{4.1}$$

The schematic flow diagram of a susceptible individual from infection to recovery is provided as **Figure 1**.

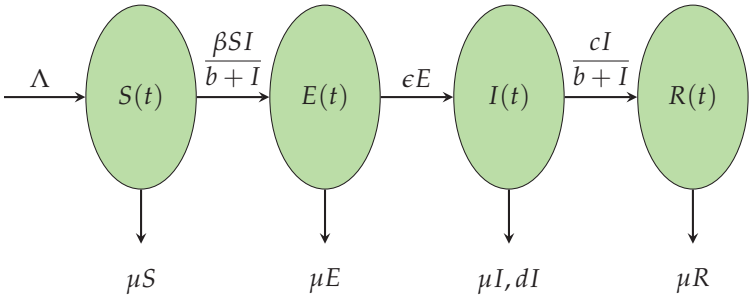


Figure 1: **Schematic Flow Diagram for the SEIR Model in Before Control Phase.**

where $S(t)$, $E(t)$, $I(t)$ and $R(t)$ respectively denote the susceptible, exposed, infectious and recovered individuals. Λ represents the net flow rate of population and β denotes the infectious rate of Ebola. ϵ signifies the proportion of transformation from asymptomatic to symptomatic individuals. Natural death rate is represented by μ, while diseased death rate is represented by d.

A system of ordinary differential equations is provided as (4.2) to describe the epidemic situation before taking actions.

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \mu s - \frac{\beta SI}{b+I} \\
\frac{dE}{dt} &= \frac{\beta SI}{b+I} - (\mu + \epsilon)E \\
\frac{dI}{dt} &= \epsilon E - (\mu + d)I - \frac{cI}{b+I} \\
\frac{dR}{dt} &= \frac{cI}{b+I} - \mu R
\end{aligned} \tag{4.2}$$

5 The SEIQR Model

Without the consideration of human factors, SEIR model could not reflect the entire reality of the condition. In order to improve the SEIR model, necessary human control means need to be added. Therefore, two control means discussed are as follows.

- **Isolation Measure:** The establishment of isolation regions to stop the spread of Ebola virus.

- **Treatment Method:** The employment of latest treatment method to cure the infected and the prevention with the greatest efforts.

5.1 Quarantine Measure

High death rate and easy spread are the characteristics of Ebola virus. It results in that the best way to stop Ebola at present is still the Quarantine measure. Thus, quarantine individuals $Q(t)$ should be added into SEIR model. A proportion of the infected individuals will be quarantine. Meanwhile, quarantine individuals have the probability of spontaneous recovery into recovered ones. The extended model is demonstrated as **Figure 2**.

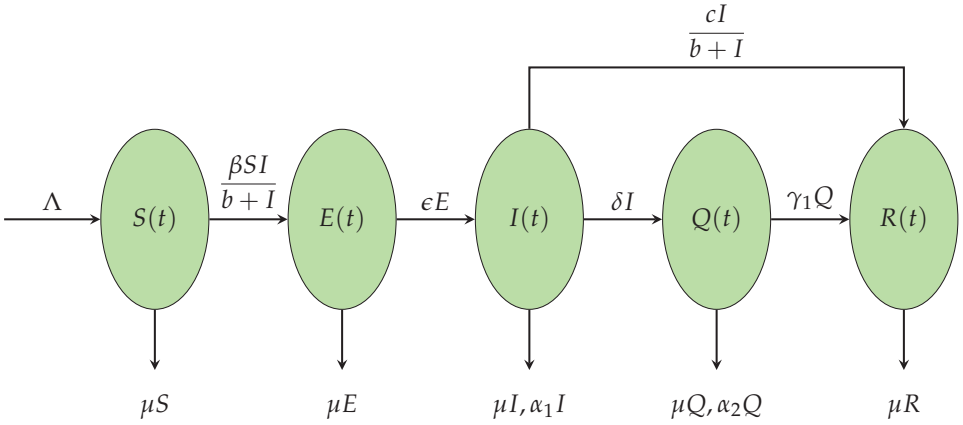


Figure 2: **SEIQR Model with Quarantine Measure.**

where $Q(t)$ denotes the quarantine individuals. δ represents the proportion of infectious individuals having changed into quarantine ones. γ_1 represents the proportion of quarantine individuals having changed into recovered ones.

A system of ordinary differential equations is provided as (5.1) to illutrate the circumstances since the addition of Quarantine measure.

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \mu S - \frac{\beta SI}{b+I} \\
\frac{dE}{dt} &= \frac{\beta SI}{b+I} - (\mu + \lambda_E + \epsilon) \cdot E \\
\frac{dQ}{dt} &= \lambda_E \cdot E - (\mu + \lambda_Q) \cdot Q \\
\frac{dJ}{dt} &= \lambda_Q \cdot Q - (\mu + d + \lambda_J) \cdot J + \lambda_I \cdot I \\
\frac{dI}{dt} &= SE - (\mu + d + \lambda_I) \cdot I - \frac{cI}{b+I} \\
\frac{dR}{dt} &= \frac{cI}{b+I} - \mu R + \lambda_J \cdot J
\end{aligned} \tag{5.1}$$

5.2 Treatment Method

Treatment method exerts significant influence on diminishing the spread of infectious diseases. In classical epidemic models, the treatment rate is assumed to be proportional to the number of infected individuals. This is unsatisfactory because the resources for treatment should be quite large. In fact, every community should have a suitable capacity for treatment. If it is too large, the community will pay for unnecessary cost. If it is too small, the community may have to confront with an outbreak of the disease. Thus, it is critical to determine a suitable capacity for the treatment of Ebola.

Based on W. Wang, et al. (2004), a constant treatment is adopted in our paper, which simulates a limited capacity for treatment. Note that a constant treatment is suitable when the number of infected individuals is large. The treatment is modified into

$$T(I) = \begin{cases} rI, & if 0 \leq I \leq I_0, \\ k, & if I > I_0, \end{cases} \tag{5.2}$$

where $k = rI_0$. r denotes the recovery rate through treatment method. It signifies that when the capacity of treatment is not reached, the treatment rate is proportional to the number of the infected; otherwise, we will take the maximal capacity. It renders for the situation where patients have to be hospitalized: the number of hospital beds is limited. It is also true for the case where medicines are not sufficient. Evidently, this improves the classical proportional treatment and the constant treatment (Wendi Wang. 2006: 58-71).

Considering that there are plenty of factors. For instance, the quantity of the medicine needed, possible feasible delivery systems, locations of delivery, speed of manufacturing of the vaccine or drug. They will be discussed separately and simulated for test in the following. The schematic flow diagram is demonstrated as **Figure 3**.

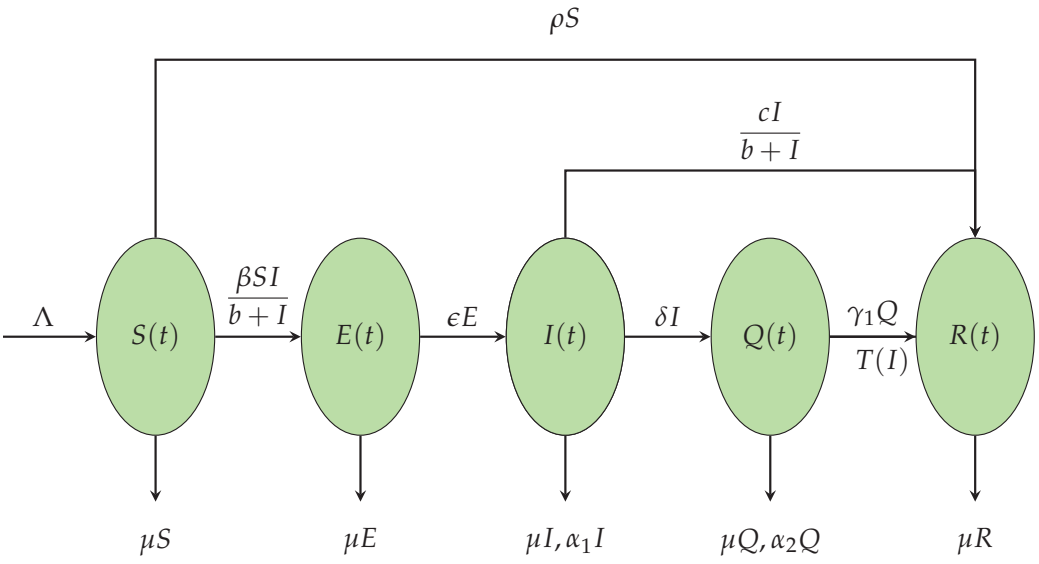


Figure 3: **SEIQR Model with Treatment Method.**

where ρ denotes the proportion of susceptible individuals having recovered from

Ebola.The recovered individuals after treatment is denoted by $T(I)$. Thus, the model can be described by a system of ordinary differential equations as shown in (5.3).

Let

$$\frac{\beta SI}{b+I} \to \gamma_2 \cdot \beta SI, \frac{cI}{b+I} \to \gamma_3 \cdot I,$$

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - (\mu + \rho + \gamma_2 \cdot \beta I) \cdot S \\
\frac{dE}{dt} &= \gamma_2 \cdot \beta SI - (\mu + \epsilon) \cdot E \\
\frac{dI}{dt} &= \epsilon E - (\mu + \alpha_1 + \delta + \gamma_3) \cdot I \\
\frac{dQ}{dt} &= \delta \cdot I - (\mu + \alpha_2 + \gamma_1) \cdot Q - T(I) \\
\frac{dR}{dt} &= \rho S + T(I) + \gamma_1 \cdot Q + \gamma_3 \cdot I - \mu R.
\end{aligned} \tag{5.3}$$

It is assumed that all the parameters are positive constants. Clearly, R is positively invariant for system (5.3). Since the first two equations in system (5.3) are independent of the variable R, it suffices to consider the following reduced model:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - (\mu + \rho + \gamma_2 \cdot \beta I) \cdot S \\
\frac{dE}{dt} &= \gamma_2 \cdot \beta SI - (\mu + \epsilon) \cdot E \\
\frac{dI}{dt} &= \epsilon E - (\mu + \alpha_1 + \delta + \gamma_3) \cdot I \\
\frac{dQ}{dt} &= \delta \cdot I - (\mu + \alpha_2 + \gamma_1) \cdot Q - T(I)
\end{aligned} \tag{5.4}$$

For this epidemic model, the main problem is to obtain the expression of a threshold value by which we could judge whether the disease is prevalent or not. At the same time, the stability of the equilibrium position, the existence and stability of cycle and the sustainability of the system are also critical. We will discuss the existence and stability of equilibrium point in the following.

5.3 Analysis of Threshold

The total population size $N(t)$ satisfies the equation:

$$\frac{dN}{dt} = \Lambda - \mu N - \alpha_1 I - \alpha_2 Q \tag{5.5}$$

When $t \to \infty$, from the above equation we could derive $N \to \Lambda/d$. The solution regions are defined by:

$$A = \{(S, E, I, Q, R) | S \geq 0; E \geq 0; I \geq 0; Q \geq 0; R \geq 0; S + E + I + Q + R \leq \Lambda/\mu\}. \tag{5.6}$$

The system (5.4) always has the malicious object-free equilibrium. An endemic equi-

librium of (5.4) satisfies

$$\begin{cases} \Lambda - (\mu + \rho + \gamma_2 \cdot \beta I) \cdot S = 0 \\ \gamma_2 \cdot \beta SI - (\mu + \epsilon) \cdot E = 0 \\ \epsilon E - (\mu + \alpha_1 + \delta + \gamma_3) \cdot I = 0 \\ \delta \cdot I - (\mu + \alpha_2 + \gamma_1) \cdot Q - T(I) = 0. \end{cases} \tag{5.7}$$

When $0 \leq I \leq I_0$, system (5.5) becomes

$$\begin{cases} \Lambda - (\mu + \rho + \gamma_2 \cdot \beta I) \cdot S = 0 \\ \gamma_2 \cdot \beta SI - (\mu + \epsilon) \cdot E = 0 \\ \epsilon E - (\mu + \alpha_1 + \delta + \gamma_3) \cdot I = 0 \\ \delta \cdot I - (\mu + \alpha_2 + \gamma_1) \cdot Q - rI = 0. \end{cases} \tag{5.8}$$

When $I > I_0$, system (5.5) becomes

$$\begin{cases} \Lambda - (\mu + \rho + \gamma_2 \cdot \beta I) \cdot S = 0 \\ \gamma_2 \cdot \beta SI - (\mu + \epsilon) \cdot E = 0 \\ \epsilon E - (\mu + \alpha_1 + \delta + \gamma_3) \cdot I = 0 \\ \delta \cdot I - (\mu + \alpha_2 + \gamma_1) \cdot Q - k = 0. \end{cases} \tag{5.9}$$

Let

$$R_0 = \frac{\beta(\Lambda/\mu)}{(\epsilon + \mu)(\mu + \alpha_1 + \delta + \gamma_3 + r)}. \tag{5.10}$$

Then R_0 is the basic reproduction number of (5.4).

Theorem 5.1. *If $R_0 > 1$, then A also contains a unique, positive and endemic equilibrium $P^* = (S^*, E^*, I^*, Q^*, R^*)$. Now from (5.3), on simplification, we have(Bimal Kumar Mishra, et al.,2012)*

$$\begin{aligned} S^* &= \frac{\Lambda/\mu}{\gamma_2 R_0} \\ I^* &= (R_0\gamma_3 - 1)\frac{\mu}{\beta} \\ E^* &= \frac{\Lambda(R_0\gamma_2 - 1)}{\gamma_2(\gamma_2 + \mu)R_0} \\ R^* &= \frac{1}{\mu}\{\frac{\epsilon\delta(\gamma_3 R_0 - 1)\mu}{\beta(\mu + \alpha_2 + \epsilon)} + \frac{\delta\mu(\gamma_3 R_0 - 1)}{\beta}\} \\ Q^* &= \frac{(\gamma_1 R_0 - 1)\mu\delta}{\beta(\mu + \alpha_2 + \epsilon)}. \end{aligned} \tag{5.11}$$

Theorem 5.2. *Consider the system (5.3). If $R_0 < 1$, then solution set system (5.6) is locally asymptotically stable. If $R_0 > 1$, then the regions $A - \{(S, E, I, Q, R)|I = 0\}$, is an asymptotically stable regions for the endemic equilibrium P^*.*

Thus, all solutions in the set $I = 0$ go to the disease-free equilibrium P_0 . By **Theorem 5.2**, the system is globally asymptotically stable, when $R_0 < 1$. The similarly, solving for R by using the fifth equation in (5.3), we obtain:

$$\lim_{t\to\infty} R(t) = \lim_{t\to\infty} \frac{\epsilon Q(t) + \sigma I(t)}{\mu} \longrightarrow R^* = \frac{\delta I^* + \epsilon Q^*}{\mu}. \tag{5.12}$$

An application of **Theorem 5.1** shows that endemic equilibrium P^* of model (5.3) is globally asymptotically stable in the regions $A - \{(S, E, I, Q, R)|I = 0\}$.(Bimal Kumar Mishra, et al.,2012)

5.4 Analysis of Control Srategy Based on SEIQR Model

Based on model analysis above, basic reproductive rate can be derived as ((5.3)). If $R_0 > 1$, the infectious disease will evolve into endemic disease and exist permanently within the population. Otherwise it will be controlled and gradually disappeared. In combination with the expression of R_0, specific strategies of prevention and control are presented below. Through regulation of parameters in R_0, the value of $\beta(\Lambda/\mu)$ is controlled to be as small as possible, while that of $(\epsilon + \mu)(\mu + \alpha_1 + \delta + \gamma_3 + r)$ as large as possible.

- Strengthen the precautionary measure ρ to protect susceptible individuals S and newborns. Its enhancement of validity will reduce the final proportion of infected individuals.
- Increase the mortality rate α_1 through concentrate killing of infected birds and beasts.
- Reduce the immigration rate Λ of infected regions.

Furthermore, the most pressing issue for now is to improve the cure rate r. Since the boost of cure rate could prevent and even eradicate Ebola virus in a period of time. However, the cure rate is influenced by various factors demonstrated in the tree diagram **Figure 4**.

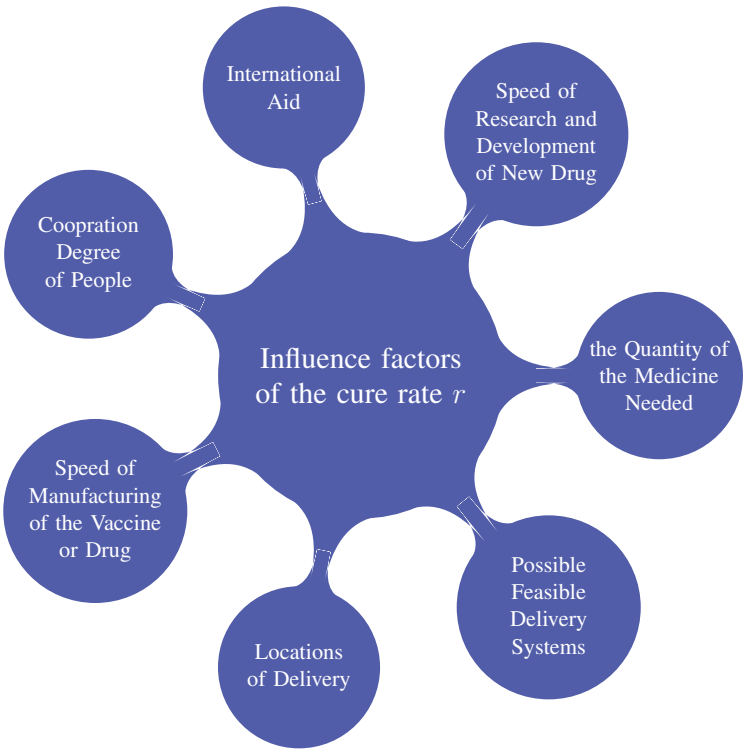


Figure 4: **Influence Factors of Cure Rate.**

6 CASEIQR Method

6.1 Simulation Rules

6.1.1 Abstraction and Simplification of Ebola Situation

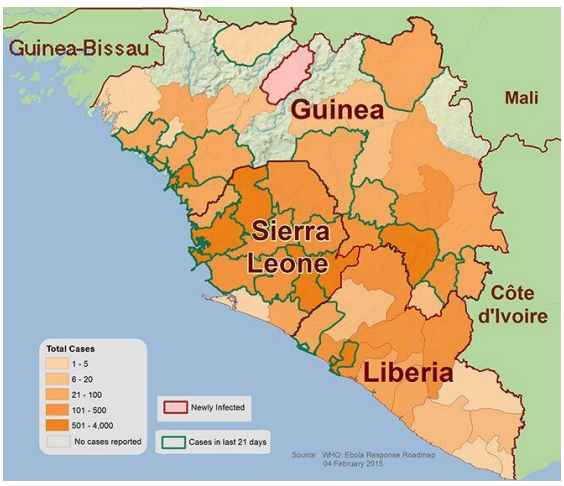
In order to make well simulation of the infectious situation and control strategies, we abstracted and simplified the distribution of Ebola. On the basis of SEIQR model, our cellular automaton is composed of 100×100 cells, each in one of the five states: **susceptible, exposed, infected, quarantine** and **recovered**. In addition, a state of **station** is introduced in our model as needed. West Africa is selected as our object of study. The realistic situation of West Africa and its simulation is provided as **Figure 5**.

6.1.2 Susceptible and Recovered Individuals

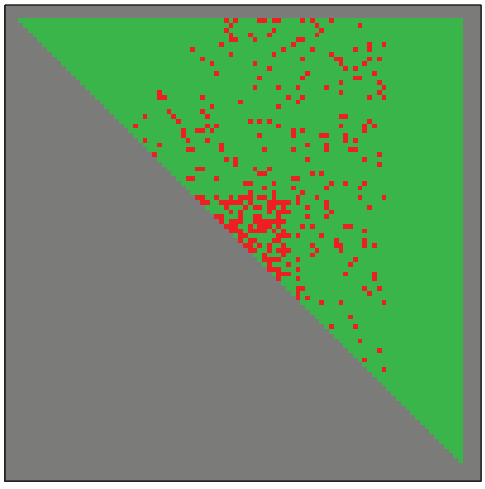
Due to the high infectivity of Ebola to various age group and race, the entire population is initially considered as susceptible individuals. Given that no recovered patients are reported to be infected again, we assume that people once recovered from Ebola will never get infected.

6.1.3 Determination and Function of station

Limited by the quantity of medical staff, the number of stations might be insufficient. Therefore, based on the condition of various regions, a threshold needs setting up to describe the regional severity of Ebola. When the situation of a regions is beyond the threshold value, a station is required to be built to control the local condition.



(a) **Ebola Outbreak in West Africa - Outbreak Distribution Map.** Source:Centers for Disease Control and Prevention



(b) **The Simulation**

Figure 5: **Contrast between Realistic Situation and Simulation**

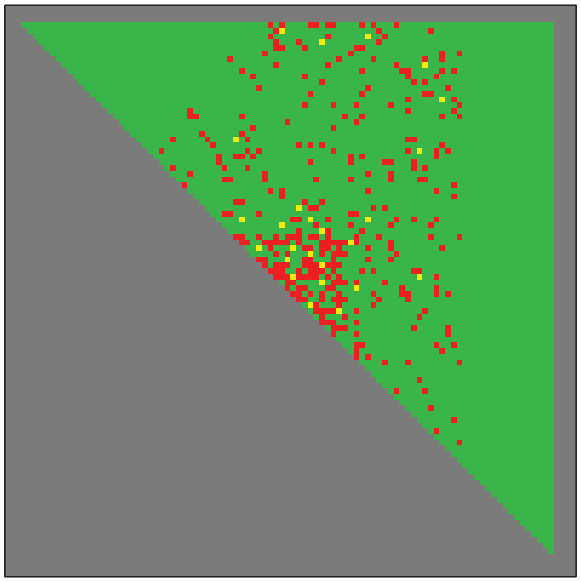
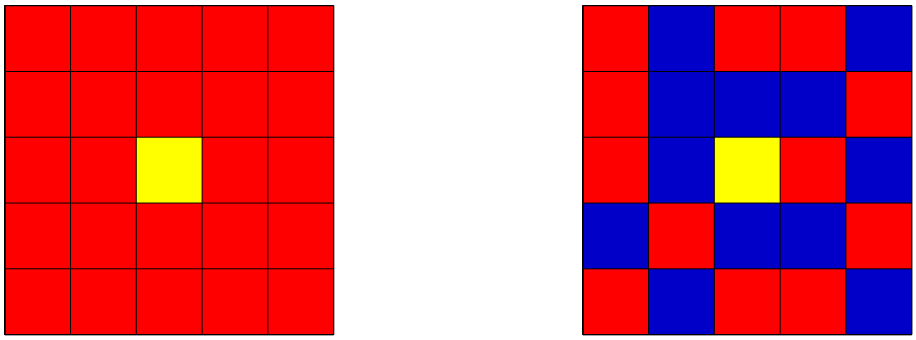


Figure 6: **Station Distribution.**

Due to the continuous variation of the situation, the number of stations can not satisfy the current requirement every once in a while. Thus, the distribution of station needs regulation in accordance with the development of Ebola and the establishment of quarantine every month.

Once a station is built in a district, effective quarantine of the surroundings will be implemented to stop further spread. Meanwhile, stations are able to treat and cure the quarantine individuals. Take transportation problem into consideration. The shorter distance to stations is, the better treatment effects are.



(a) **Before Treatment** (b) **After Treatment**

Figure 7: **Before and After Treatment**

6.1.4 Die of Illness and Natural Recovery

Considering the extremely high mortality rate of Ebola, the case fatality rate is introduced in our model. It denotes the proportion of death because of infection in communi-

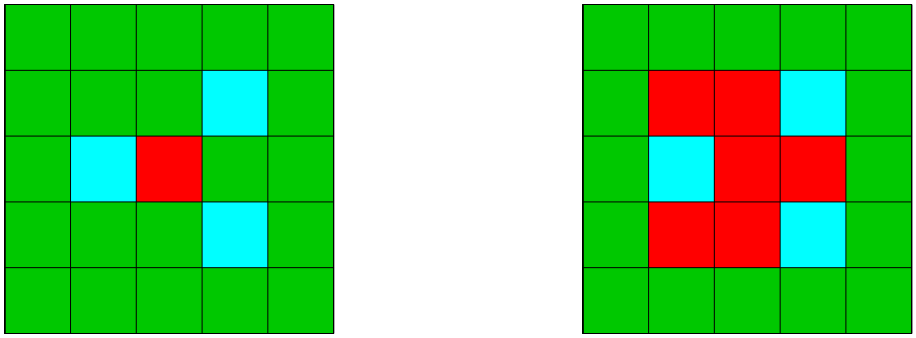
ty. The case fatality rate in quarantine regions is higher than that in non-quarantine one; the case fatality rate of severe epidemic area is higher than that of the normal one.

Given that with strong habitus and mild infection, possibility exists in natural recovery of certain people without treatment. So there is a rate of natural healing. Thus, we introduce the rate of natural recovery. Assuming that the rate of natural recovery in quarantine area is higher than that in the non-quarantine one.

6.1.5 Spread of Ebola

Ebola virus has great infectivity. Once an outbreak occurs in an area, the surroundings will be affected and have a risk of breaking out viral infection.

Take the transportation development in Africa into account. We assume that adjacent domains exert no mutual impacts on each other. As for the quarantine areas, they are considered to have no ability of spreading virus. For the recovered areas, we assume that they will not be infected again.



(a) **Quarantine Before Spread** (b) **Quarantine After Spread**

Figure 8: **Quarantine Before and After Spread**

6.1.6 Speed of Manufacturing and Allocation of Drug

The manufacturing speed of drug in unit interval is denoted by M_t. The larger M_t is, the faster the manufacturing speed will be. The principle of average allocation is adopted in vaccine or drug allocation. It not only embodies the equity, but takes the situation of various districts into account; successfully prevent the possibility of a great outbreak of Ebola.

6.2 Simulated Flow Diagram

The simulated flow diagram is shown as **Figure 9**.

$S = 1, 2, 3, 4$ denotes the state of "quarantine", "infected", "susceptible", "recovered". D represents the distance to assistance station. W denotes the largest sphere of assis-

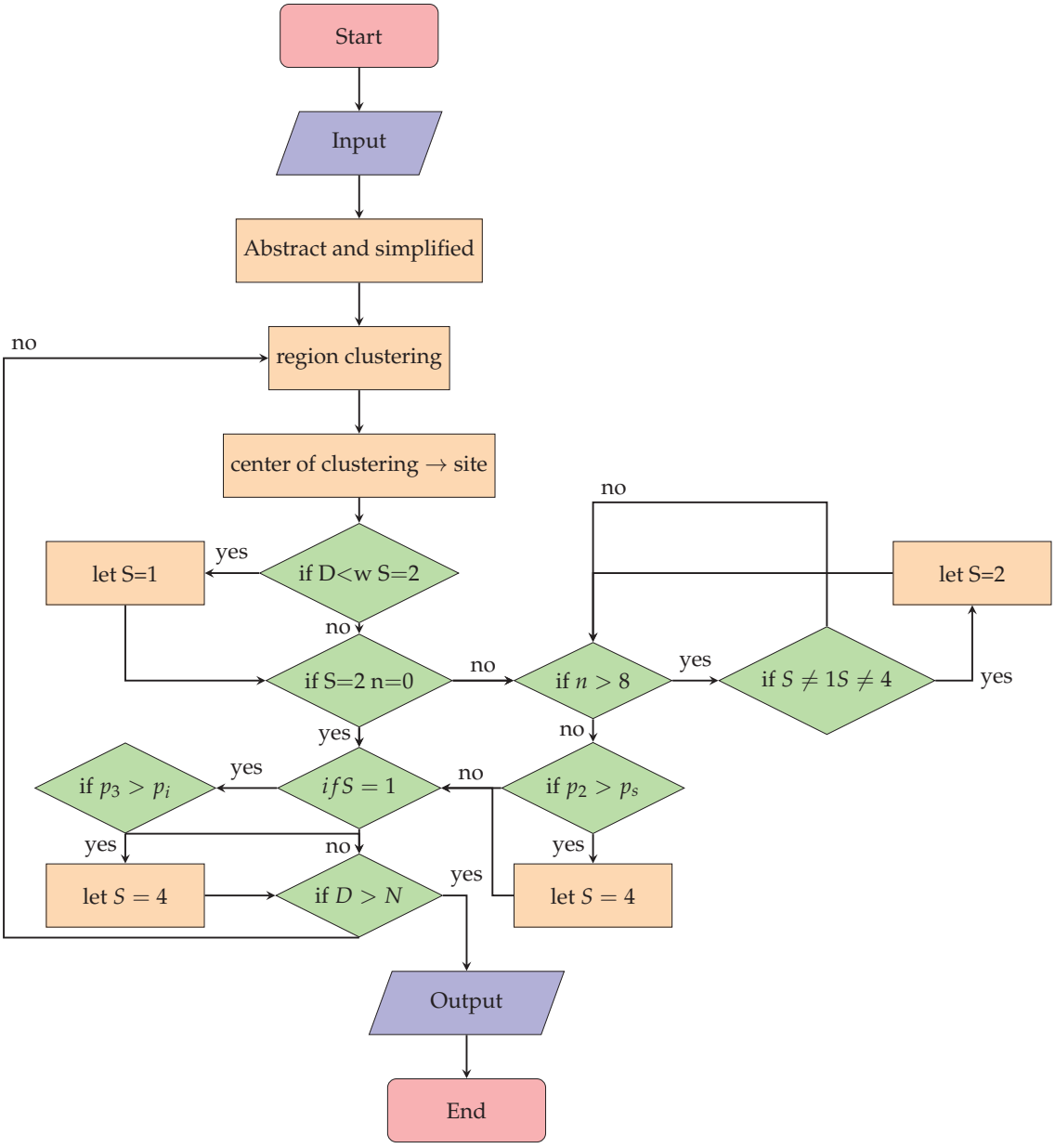


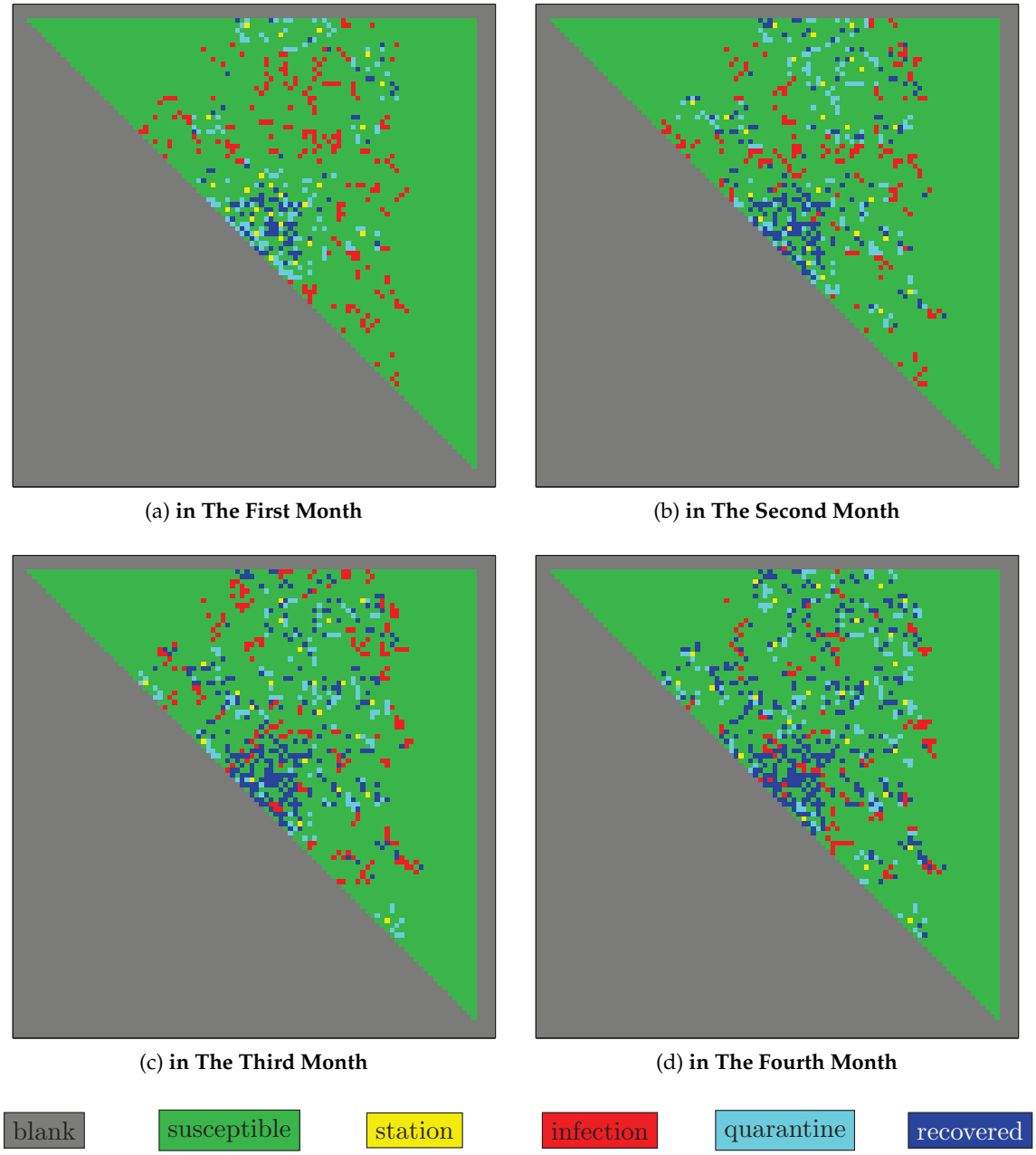
Figure 9: **Simulated Flow Diagram.**

tance station. P_r, P_s, P_i represent the possibility of transtorming into infected state, infected individuals → natural recovery, quarantine state → recovered one. N denotes the maximum time of simulation.

6.3 Analysis of Results

The deadline in simulation program is set as four months. The distribution of infection at the end of each month is shown as **Figure 10**.

It is evident that compared with the original state, the quantity of infected regions has already diminished intensely at the end of the first month. The effect is especially



(a) **in The First Month**

(b) **in The Second Month**

(c) **in The Third Month**

(d) **in The Fourth Month**

(e) **Legend**

Figure 10: **Distribution of Infection at The End of Each Month**

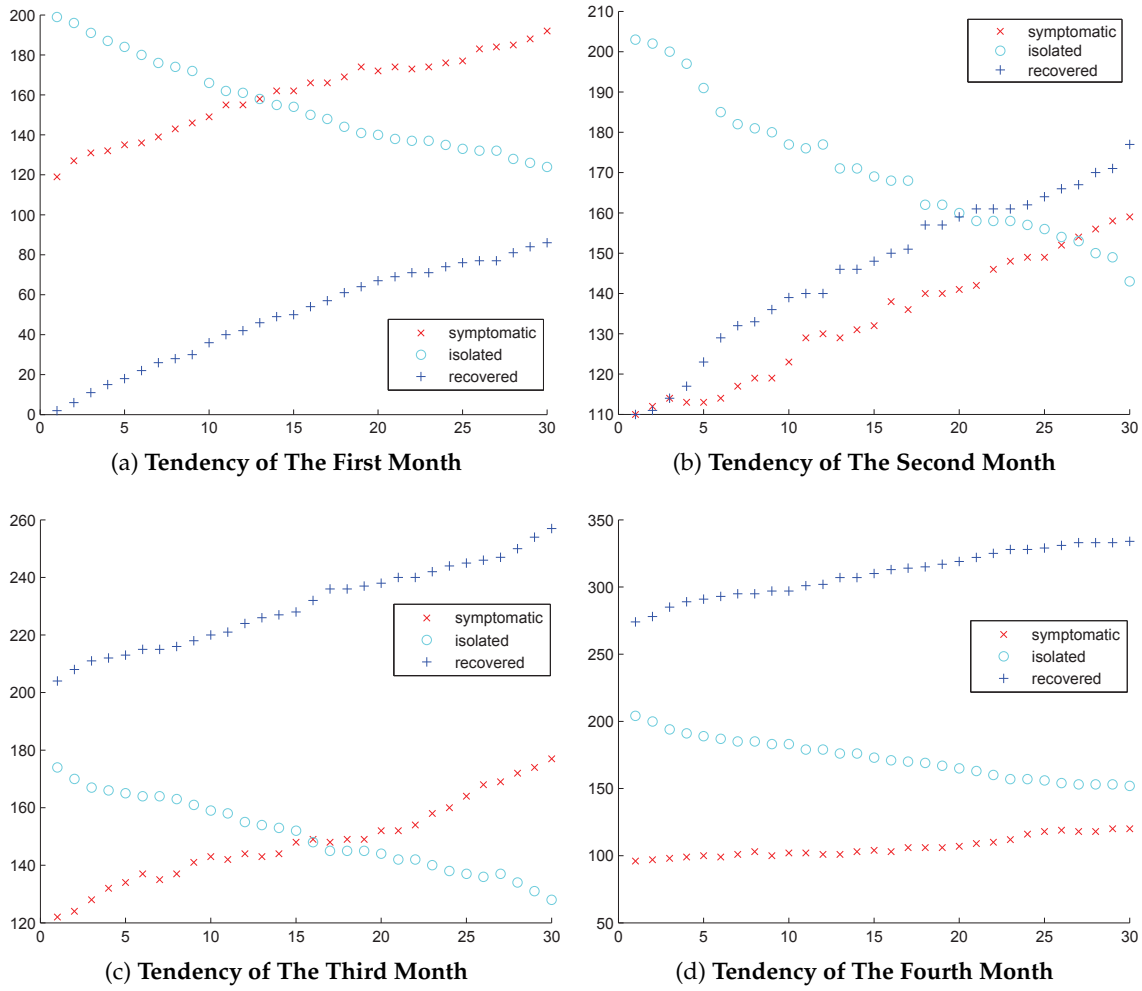
notable for the severe infection regions in the middle part of our model. Ascribing to the central role of station in the middle, most of infected regions has transformed into quarantine and recovered regions. However, due to the small distribution of station in north and east, infected regions are not noticeably controlled. A small proportion of infected regions even have a spread tendency.

At the end of the second month, a great deal of recovered region augmented apparently. It benefits from the quarantine region generated in the first month. Most important of all, due to the reasonable reallocation of stations, the situation was better controlled.

The infected region dropped obviously.

Both the third and the fourth month have been witnessed remarkable progress in disease control. At the end of the fourth month, the situation has basically been controlled within acceptable region. There is little possibility to develop a large-scale of outbreak in the future.

The variation trend of the infected, quarantine and recovered regions is provided as **Figure 11**.



(a) **Tendency of The First Month**

(b) **Tendency of The Second Month**

(c) **Tendency of The Third Month**

(d) **Tendency of The Fourth Month**

Figure 11: **The Variation Trend of The Infected, Quarantine and Recovered regions**

From a comprehensive analysis of the variation tendency in four months, we may derive that quarantine regions always present a negative growth. It is for the reason that a proportion of quarantine regions last month would transform into recovered ones in this month. Hence it is logically acceptable. During the first three month, the recovered and infected regions often share identical amplification. However, the initial point of recovered regions rises gradually, while that of infected ones drops rapidly. It reveals that Ebola is within control gradually. When it comes to the fourth month, the quantity of infected regions remains unchanged basically, meaning that Ebola has been under control.

From what has been analyzed above, Ebola can be better controlled with the employment of planning method in simulation. Moreover, the planning method is capable of allocating and utilizing resource reasonably, achieving the desired effects.

7 Sensitivity

Input: Precision of District, Interval Days of Station Transformation, Cycle Index, Sphere of Influence of Station, a Threshold Value.

Output: Treatment Effect = Recovery/(Rescovery+Quarantine)

Considering that under high precision, the process of simulation would be slow. Therefore, the precision of district will not make great adjustment, limited in the range of 50%. Interval days of station transfer and cycle index are associated with capital consumption. Transfer stations too frequently would bring about a waste of capital. Let alone there is no sufficient capital for the consumption in the long run. Besides, at present the capital mainly consists of the donation from various organizations and countries. Thus, the variation range of interval days of station transfer and cycle index are inappropriate to be too large. The larger the influence sphere of station is, the more surrounding districts can be controlled. But it is restrained by the transportation situation in Africa. The threshold value exerts impacts on the quantity of station. Due to the limitation of staff, the threshold value should not be too small.

Table 2: Sensitivity Test

Precision	T	T_0	Range	Threshold	Effect
50	30	3	2	6	2.6923
50	30	6	2	4	2.1250
150	10	7	3	6	0.6683
150	20	7	1	6	1.3708
120	30	3	3	5	0.7375
100	20	5	3	6	1.3474
50	20	7	1	3	2.7925

With the employment of stepwise regression, the expression below is derived.

$$Effect = 0.002 \cdot precision + 0.117 \cdot Range \tag{7.1}$$

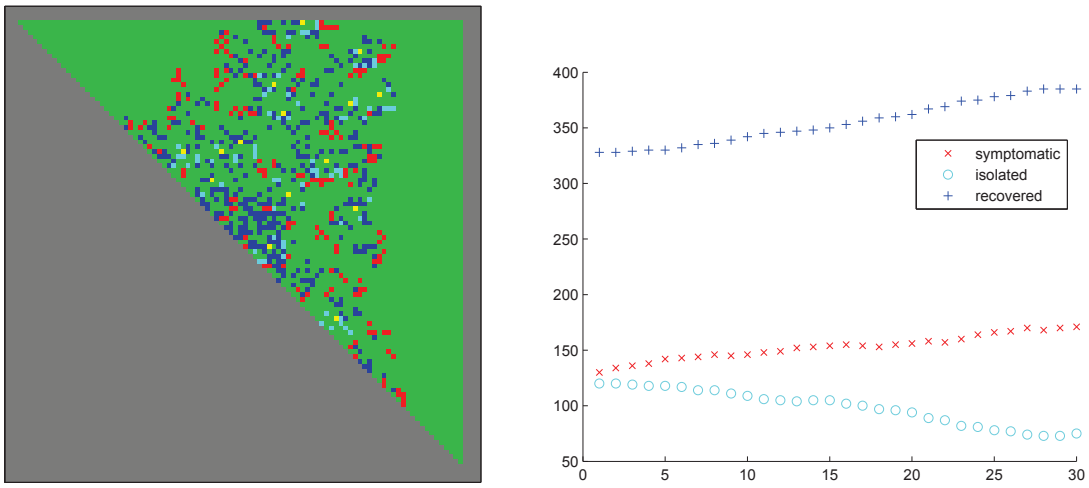
From the expression above, the precision of district division and the influenced sphere of station exert profound impacts on treatment effects, while the transformation of factors, for instance, interval days of station transfer, cycle index, influence sphere of station and a threshold value, has unapparent influence on treatment effects. Essentially, the larger proportion of affected regions in infected ones is, the better treatment effects are. It coincides with realistic situation. With the variation of these variables, treatment effects vary within rational range. It indicates that the simulation model is of great robustness.

8 Discussion

We have derived an overall control measures. But it is not clear to determine which one or group of factors decisively influence the control of epidemic prevalence. Therefore, the model needs further discussion and analysis. First, only the simulation scheme of specific factors is changed, while the state of other factors remain unchanged. Then, by analyzing the results of resimulation, we can know which one or group of factors is of the greatest importance.

8.1 Drug Delivery

In the original simulation system, the transportation capacity of drug limits the isolation efficiency of infected areas which are far away from the assistance stations. Now we erase this limitation. That is to say, every infected area within the affecting scope of assistance stations shares the same probability of being isolated. A part of the results from simulating again is shown as **Figure 12**:



(a) **Distribution** (b) **Tendency1**

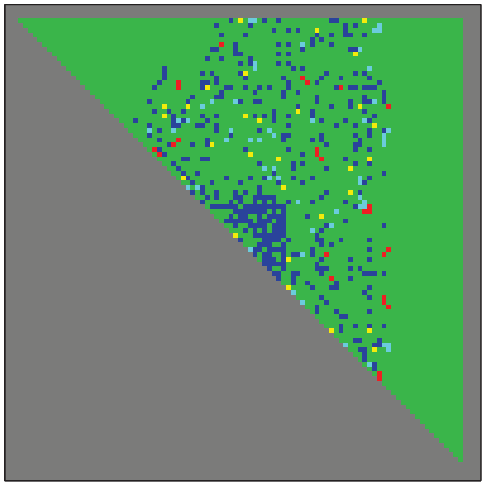
Figure 12: **Contrast in Drug Delivery**

After eliminating the restrictions of transportation, the quantity of recovered areas increased significantly. But the effect of control of epidemic prevalence shows less significant improvement.

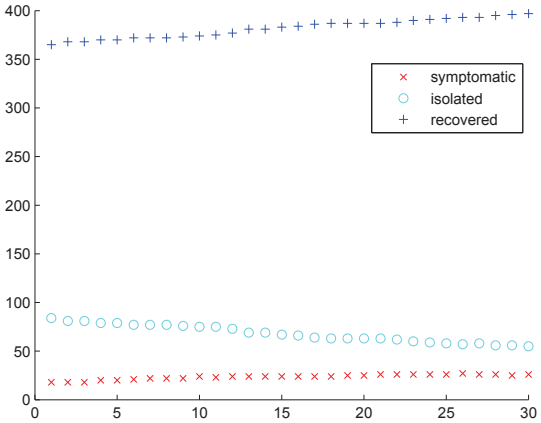
8.2 Establishment of Station and Drug supply

By increasing the quantity of assistance stations and available drug within a reasonable scope, namely, strengthening the construction of station and attempting to satisfy the minimum demand of drug, we obtain a part of results as **Figure 13**:

By the result, Ebola is close to be eradicated. It is reasonable result of simulation.



(a) **Distribution2**

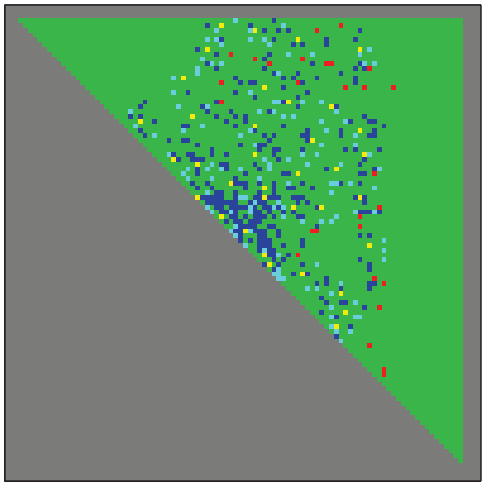


(b) **Tendency2**

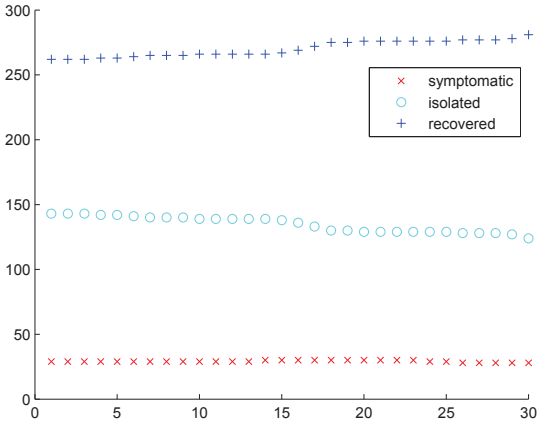
Figure 13: **Contrast in Establishment of Station and Drug supply**

8.3 Preparation of vaccine

Accelerate the preparation of vaccine and clinical trials. After vaccination, a "susceptible" individual can be considered transferring into "recovered". A part of results is shown as **Figure 14**:



(a) **Distribution3**



(b) **Tendency3**

Figure 14: **Contrast in Preparation of vaccine**

From the result, the effect of control of epidemic prevalence is rather evident. The infected area is almost eliminated. The possibility of virus outbreak again is really low.

In conclusion, the function of the drug transportation in the control of epidemic prevalence is relatively limited. The construction of the assistance station, the supply of drug, and the preparation of vaccine make obvious contributions in eradicating Ebola.

9 Strengths and Weaknesses

9.1 Strengths

- **Employ the model with quarantine**
  With the application of quarantine, the complicated internal variation is neglected. The entire variation is reflected in a simple and compendious way, providing great convenience for model establishment and analysis.

- **Improve the traditional SEIR model**
  On the basis of SEIR model, SEIQR model is closer to realistic situation. The addition of quarantine contributes to provide analysis of better pertinence and effectiveness.

- **Simulate the spread of Ebola**
  Computer simulation is more intuitive in analysis the correctiveness of models, and capable of optimizing the scheme available through rational modification of parameters.

9.2 Weaknesses

- **Simplify model**
  The simplified model causes lost of critical details. It might exert intense influence on the final results.

- **Lack of accuracy**
  SEIR model lack of spatial attributes in analysis procedure and the prediction function of spread regions. For some diseases, SEIR model is unable to recognize and judge risk factors.

10 Nontechnical Letter

It is universally acknowledged that Ebola has caused incalculable death in West Africa. The huge loss in politics and economy, the extreme infectivity and fatality rate of Ebola have left profound darkness among people.

The critical job for scientists is to exploit an effective drug. Luckily, the progress of scientific technology has brought us prospect. For now, we have developed two type of drugs for treatments. However, the productivity of these drugs is finite and expensive. We can not guarantee that every patient is provided with this drug since the quantity of the drugs is insufficient. But we would try our best to ensure that our drugs are allocated equally to infected region. And the medical staff in every assistance station will try their best to save lives.

Patients urgently need the support from the entire society. It is also inevitable for them to derive sufficient funding and medical workers. Assistance stations are constructed according to the realistic situation. The epidemic situation of Ebola is controlled by transferring assistance stations at regular intervals. If drugs of better effects and less cost are produced, there is no denying that they will exert extraordinary impacts. Moreover, the positive cooperation of local people will make the rescue operation easier. Besides, only rational usage of drugs can reflect their best effects. The figure of cobweb model is provided as **Figure 15** below.

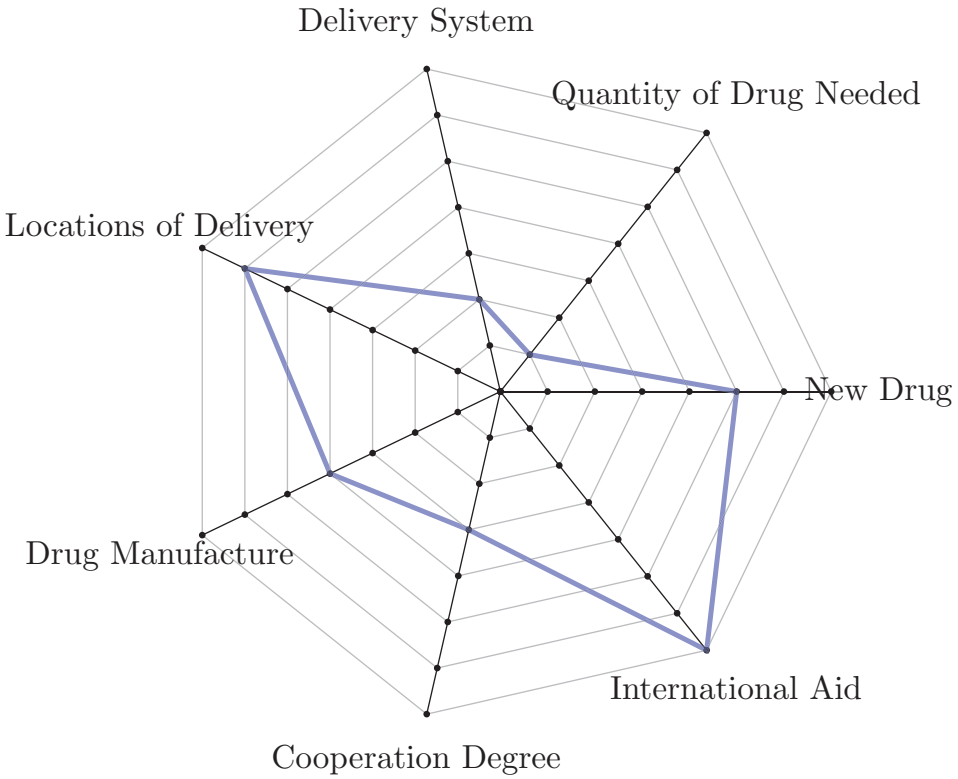


Figure 15: **Cobweb Model.**

Beating Ebola needs global collaboration. Correct program and deployment, and scientific methods are required in prevention and treatment. Through profound research on the characteristics and the origins of Ebola, the core measure of prevention is provided

below.

- **Diagnose timely and isolate strictly**
  The government needs to conduct active case finding and strict isolation in time.
- **Enhance the infection control in hospitals**
  Doctors and nurses should strengthen the infection control in hospitals.
- **Strengthen precautionary measures**
  To protect susceptible individuals and newborns, the precautionary measures need to be strengthened.
- **Increase mortality**
  The mortality rate can be increased through concentrate killing of infected birds and beasts.
- **Reduce immigration**
  Diminish the immigration rate of infected regions.

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`http://dx.doi.org/10.1155/2012/407064`

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Xueyong Zhou, Jingan Cui. Analysis of stability and bifurcation for an SEIR epidemic model with saturated recovery rate. In the *Common Nonlinear Sci Numer Simulat*2011(3) 4438-4450.

Yang Xu. 2008. Dynamical Model and Stimulation of Infectious Diseases Transmission.

Appendices

Here are the simulation programmes we employed in our model.
Input matlab source:

Appendix A

```
function [area, drug] = BuildStation(area, total_drug, range, thre)
%build station to cure patients
[L, W] = size(area);
data = area;
threshold = ((range * 2 + 1)^2 - 1) / thre;
sum = zeros(L, W);
NumOfSta = 0;
for i = range + 1 : L - range
    for j = range + 1 : W - range
        sum(i, j) = SumofNei(data, i, j, 3, range);
        if  sum(i, j) >= threshold
            data = Clear_dis(data, i, j, 3, range);
            area(i, j) = 2;
            NumOfSta = NumOfSta + 1;
            RedOfSta(NumOfSta) = sum (i, j);
        end
    end
end
drug = total_drug / NumOfSta;
data_s = Statistics(area);
disp('After building station:');
Display(data_s);
disp('The disease area of each station:');
disp(RedOfSta);
disp('The number of drug:');
disp(drug);
disp('-----------------------------------------------------');
end
```

Appendix B

```
function result = Change_1(area, i, j, range)
% Change of state 1
result = 1;
epsilon = 0.005; %the probability of E to I
eta = 0.01; %the probability of Q to R
sum3 = SumofNei (area, i, j, 3, 1);
sum2 = SumofNei (area, i, j, 2, range);
if sum3 == 0
    result = 1;
elseif sum2 == 0
    r = rand;
    if r < epsilon
        result = 3;
    end
else
```

```
    dis_2 = Nearest(area, i, j, 2, range);
    r = rand;
    if r < epsilon - eta / dis_2
        result = 3;
    end
end

end
```

Appendix C

```
function area = Change_2(area, i, j, range, drug)
% Change of state 2
eta = 0.025; %the probability of Q to R
death = 0.001; %the probability of I/Q to death
for x = i - range : i + range
    for y = j - range : j + range
        if area(x, y) == 3
            area(x, y) = 4;
        elseif area(x, y) == 4
            r = rand;
            dist = Distance(i, j, x, y);
            if drug >= 1
                if r < (eta + death) / dist
                    area(x, y) = 5;
                end
            else
                if r < drug * (eta + death) / dist
                    area(x, y) = 5;
                end
            end
        end
    end
end

end
```

Appendix D

```
function result = Change_3(area, i, j, range)
% Change of state 3
death = 0.001; %the probability of I/Q to death
result = 3;
gamma1 = 0.0005; %the probability of I to R (nature)
r = rand;
if r < gamma1
    result = 5;
else
    death = death * SumofNei(area, i, j, 3, range);
    if r > gamma1 && r < gamma1 + death
        result = 1;
    end
end
end
```

Appendix E

```
function result = Change_4()
% Change of state 4
result = 4;
gamma2 = 0.001; %the probability of Q to R (nature)
r = rand;
if r < gamma2
    result = 5;
end
end
```

Appendix F

```
function area = Change_area(area, drug)
%Change_area
%%%%%%%%%%%%%%%%%%%%%%% explanation %%%%%%%%%%%%%%%%%%%%%%%
% 0 : black
% 1 : normal
% 2 : station
% 3 : disease
% 4 : isolated
% 5 : recover
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
[L, W] = size(area);
range = 3;
for i = range + 1 : L - range
    for j = range + 1 : W - range
        if area(i, j) == 2
            area(i, j) = 2;
            area = Change_2(area, i, j, range, drug);
        end
    end
end
for i = range + 1 : L - range
    for j = range + 1 : W - range
        if area(i, j) == 1
            area(i, j) = Change_1(area, i, j, range);
        elseif area(i, j) == 3
            area(i, j) = Change_3(area, i, j, range);
        elseif area(i, j) == 4
            area(i, j) = Change_4();
        end
    end
end
end
```

Appendix G

```
function [area, drug] = Change_Renew(area, total_drug, range, thre)
%change the position of stations
[L, W] = size(area);
data = area;
```

```
threshold = ((range * 2 + 1)^2 - 1) / thre;
sum = zeros(L, W);
NumOfSta = 0;
for i = range + 1 : L - range
    for j = range + 1 : W - range
        if data(i, j) == 2
            area(i, j) = 5;
            data(i, j) = 5;
        end
        if data(i, j) == 4
            area(i, j) = 3;
            data(i, j) = 3;
        end
        sum(i, j) = SumofNei(data, i, j, 3, range) + SumofNei(data, i, j, 4, range);
        if  sum(i, j) >= threshold
            data = Clear_dis(data, i, j, 3, range);
            data = Clear_dis(data, i, j, 4, range);
            area(i, j) = 2;
            NumOfSta = NumOfSta + 1;
            RedOfSta(NumOfSta) = sum (i, j);
        end
    end
end
drug = total_drug / NumOfSta;
data_s = Statistics(area);
disp('After Change_Renew:');
Display(data_s);
disp('The disease area of each station:');
disp(RedOfSta);
disp('The number of drug:');
disp(drug);
disp('-----------------------------------------------------');
end
```

Appendix H

```
function area = Clear_dis(area, i, j, n, range)
%change 3 to 1
for x = i - range : i + range
    for y = j -range : j + range
        if area(x, y) == n
            area(x, y) = 1;
        end
    end
end
end
```

Appendix I

```
function area = Create( length )
%UNTITLED3 create an area
area = zeros(length);
for i = 1: length
    for j = 1: length
```

```
        if i > j
            area(i, j) = 0;
        elseif i < 4 || j > length - 4
            area(i, j) = 0;
        elseif j > round(0.8*length) || j <= round(length/4)
            area(i, j) = 1;
        elseif j > round(length/4) && j < round(length/2) && i < round(length/2)-j
            area(i, j) = 1;
        else
            s = rand;
            if i > round(0.4*length) && i < round(0.6*length) && j > ...
                   round(0.4*length) && j <round(0.6*length)
                if s < 0.5
                    area(i, j) = 1;
                else
                    area(i, j) = 3;
                end
            else
                if s < 0.9
                    area(i, j) = 1;
                else
                    area(i, j) = 3;
                end
            end
        end
    end
end
data = Statistics(area);
disp('In the beginning:');
Display(data);
end
```

Appendix J

```
function Display(data)
% 1 : normal
% 2 : station
% 3 : disease
% 4 : isolated
% 5 : recover
str = {'normal','station','disease','isolated','recover'};
for i = 1 : 5
    disp([char(str(i)),char(':'),num2str(data(i))]);
end
disp('--------------------------------------------------');
end
```

Appendix K

```
function distance = Distance(x1, y1, x2, y2)
%distance of the points
dis1 = abs(x1 - x2);
dis2 = abs(y1 - y2);
if dis1 > dis2
```

```
    distance = dis1;
else
    distance = dis2;
end

end
```

Appendix L

```
function Draw_area(area)
%display the area's situation
[L, W] = size(area);
temp = area;

Area(:,:,1) = area;
Area(:,:,2) = area;
Area(:,:,3) = temp;

for i=1:L
    for j=1:W
        if area(i,j)==0
            Area(i,j,:)=[123 123 123];
        end
        if area(i,j)==1
            Area(i,j,:)=[0 200 0];
        end
        if area(i,j)==2
            Area(i,j,:)=[255 255 0];
        end
        if area(i,j)==3
            Area(i,j,:)=[255 0 0];
        end
        if area(i,j)==4
            Area(i,j,:)=[0 255 255];
        end
        if area(i,j)==5
            Area(i,j,:)=[0 0 200];
        end
    end
end
Area = uint8(Area);
   p = imagesc(Area);
   hold on;
%    plot([(0:W)',(0:W)']+0.5,[0,L]+0.5,'k');
%    plot([0,W]+0.5,[(0:L)',(0:L)']+0.5,'k');
   axis image;
   set(gca,'xtick',[]);
   set(gca,'ytick',[]);
%    str = {'grey','green','yellow','red','cyanine','blue'};
% [str(1),str(2),str(3),str(4),str(5),str(6)],
% 'black','susceptible','station','symptomatic','isolated','recovered'
%    legend(p,3);
end
```

Appendix M

```
%%%%%%%%%%%%% cellular automaton %%%%%%%%%%%%%%
clear
clc
close all;
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
total_drug = 20;
length = 100;
T = 30;
Ti = 3;
range = 3;
thre = 6;
% epsilon %the probability of E to I
% gamma1  %the probability of I to R (nature)
% gamma2  %the probability of Q to R (nature)
% rho  %the probability of S to R
% delta  %the probability of I to Q
% eta  %the probability of Q to R
% death  %the probability of I/Q to death
% 0 : black
% 1 : normal
% 2 : station
% 3 : disease
% 4 : isolated
% 5 : recover
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
area = Create(length);
Draw_area(area);
figure;
[area, drug] = BuildStation(area, total_drug, range, thre);
Draw_area(area);
figure;
data = zeros(5,T);
for i = 1 : T
    area = Change_area(area, drug);
    Draw_area(area);
    drawnow;
    data(:, i) = Statistics(area);
end
% data = Statistics(area);
% Display(data);
Plot_data(data, T);
for j = 1 : Ti
    area = Change_Renew(area, total_drug, range, thre);
    figure;
    Draw_area(area);
    for i = 1 : T
        area = Change_area(area, drug);
        Draw_area(area);
        drawnow;
        data(:,i) = Statistics(area);
    end
%     data = Statistics(area);
%     Display(data);
    Plot_data(data, T);
end
% data(5,T) / (data(3,T) + data(4,T))
```

Appendix N

```
function distance = Nearest(area, i, j, n, range)
distance = Inf;
dis = range + 1;
for x = i - range : i + range
    for y = j -range : j + range
        if area(x, y) == n
            if x > y
                dis = x;
            else
                dis = y;
            end
            if dis < distance
                distance = dis;
            end
        end
    end
end

end
```

Appendix O

```
function Plot_data(data, T)
%plot a graph
x = 1 : T;
figure;
hold on;
y3 = plot (x, data(3, :), 'rx');
y4 = plot (x, data(4, :), 'co');
y5 = plot (x, data(5, :), 'b+');
legend([y3 y4 y5],'symptomatic','isolated','recovered');
end
```

Appendix P

```
function data = Statistics(area)
% 1 : normal
% 2 : station
% 3 : disease
% 4 : isolated
% 5 : recover
[L, W] = size (area);
data = zeros(5, 1);
for i = 1 : L
    for j = 1 : W
        if area(i, j) == 1
            data(1) = data(1) + 1;
        elseif area(i, j) == 2
            data(2) = data(2) + 1;
        elseif area(i, j) == 3
            data(3) = data(3) + 1;
```

```
        elseif area(i, j) == 4
            data(4) = data(4) + 1;
        elseif area(i, j) == 5
            data(5) = data(5) + 1;
        end
    end
end
end
```

Appendix Q

```
function sum = SumofNei (area, i, j, n, range)
%the sum of neighbors
sum = 0;
for x = i - range : i + range
    for y = j -range : j + range
        if area(x, y) == n
            sum = sum + 1;
        end
    end
end
end
```