

Studying the Eradication of Ebola through the Propagation Modelling and Vaccine Delivery Evaluation

Shuoping Wang^{1*}, Xueyong Yu¹ and Honghao Gao²

¹*School of Computer and Computing Science, Zhejiang University City College, Hangzhou, China*

²*Computing Center, Shanghai University, 200444 Shanghai, P.R. China*

**wangsp@zucc.edu.cn*

Abstract

Ebola is a disease of humans and other primates caused by Ebola viruses. This disease has a high risk of death, killing between 25 and 90 percent of those infected, with an average of about 50 percent. Ebola has become one of the most horrible threats to human beings. In this paper, we develop accurate propagation model of Ebola in order to understand its spread dynamics. In the modeling, human beings are of three exclusive states: 'Susceptible', 'Infected' and 'Recovered'. We evaluate the proposed model according to Ebola's data published by WHO. The experiment results suggest that our model can accurately present the Ebola propagation dynamics in Guinea, Liberia and Sierra Leone. We further study the optimal vaccine delivery strategies in order to restrain the outbreaks of Ebola. When human beings are in short of vaccines, the proposed model analyses the delivery destination, the tendency of Ebola's propagation, locations of medical centers and labs, and the conditions of patients. According to Ebola's data from WHO, the model identifies seven cities as the optimal venues to start the vaccine delivery. The work in this paper greatly benefits the eradication of Ebola when it outbreaks in our society.

Keywords: SIR/CA, Knaosack Model, Ebola

1. Introduction

One of the greatest challenges faced by our human beings is Ebola. Ebola virus disease (EVD; also Ebola hemorrhagic fever, or EHF), or simply Ebola, is a disease of humans and other primates caused by Ebola viruses. The virus spreads by direct contact with body fluids, such as blood, of infected human or other animals. Signs and symptoms typically start between two days and three weeks after contracting the virus with a fever, sore throat, muscle pain, and headaches.

As far as we know, Ebola is one of the most horrible viruses to human beings since Ebola virus was first identified in 1976. The 2014 outbreak in West Africa is definitely the largest and most complex Ebola outbreak. In West Africa, there are three main countries which are Guinea, Liberia, Sierra Leone, suffering from the threat of death. The disease is under a high risk of death, killing between 25 and 90 percent of those infected with an average of about 50 percent [1]. This is usually due to the low blood pressure from fluid loss, and typically follows six to sixteen days after symptoms appear. As of now, more than 8000 people died because of Ebola [2]. The dead include lots of virus infection and numerous health care workers. The number of cases in the current outbreak now exceeds the number from all previous outbreaks combined. Up to now, the most helpful method to stop the spread of virus is to isolate the networks into several parts. It is

*Corresponding Author

time to take other efficient measures to reduce the death rate.

The World medical association has announced that their new medication could stop Ebola and cure patients whose disease is not advanced [1]. In this paper, we build two models to solve this problem. The first model we build is an SIR propagation model that is based on cellular automata (SIR/CA). In the model, we can write program in MATLAB to calculate the estimate number of infective. We could test the effect of our model by comparing the estimated number of patients to the actual number of infected human beings. We can then predict the number of patients and the demand for vaccines in the future. In consideration of the infective number, demand and other factors, the second model we build is the delivery system based on the knapsack model(DS/KM). Afterwards, we will make the proper number of vaccines and send them to the countries where people are urgent to use the vaccines. The model we build is to decrease the rate of death.

The paper will be organized as follows: we describe the problem that the paper will address in Section 2. Section 3, is about the details of the modeling. We then discuss the delivery process in Section 4. We conclude the work of this paper and discuss the future work in Section 5.

2. Problem Statement

Under the circumstance of the new medication could stop Ebola and cure patients whose disease is not advanced, we are required to build a realistic, sensible and useful model to optimal the eradication of Ebola and write a non-technical letter for the world medical association to announce. And the consideration of the model can be listed as followed:

- The spread of the disease;
- The quantity of the medicine needed;
- Possible feasible delivery systems (sending the medicine to where it is needed);
- Locations of delivery (geographical);
- Speed of manufacturing of the vaccine or drug;
- Other critical factors.

We build the SIR spread model based on cellular automata to simulate the spread of disease. With the predicted data, we can identify the quantity of the medicine needed and the speed of manufacturing of the vaccine. For confirming the locations of delivery, we should search the actual epidemic and gather more static. We also have an obligation to build delivery systems to allocate the vaccine reasonably. Whats more, we can do more meaningful research in some ways.

3. The Development of Models and Solution of the Model

There are many factors that may affect the propagation speed and scale of Ebola. In this paper, we simplify the modeling process by only considering the main factors. We have some assumptions in the modeling. First, we do not consider population factors in the countries such as birth and mortality rate. The population in these countries keep steady. Second, if a patient gets vaccination, this patient will not be infected any more. In addition, the cost of medicine transportation is not taken into consideration.

3.1. SIR Spread Model based on Cellular Automata

Cellular automata (CA) is a dynamic system that is discrete in time and space. Many limited and discrete cells constitute a state set. Cells change state by obeying local rules.

Given an arbitrary time, there will be many transformations of cells through simple interaction. The whole transformation process contributes to the dynamic system, for example, Ebola's propagation dynamics in this paper [3]. According to the definition, cellular space and transformation function consist of CA. We therefore describe CA by mathematical symbols $A = (L_d, S, N, f)$, wherein L_d represents network space, S represents a limited and discrete set, N denotes the set of neighbors of a patient in the network topology, and f denotes the local transformation function. Cells, patients' states, cellular space, patients' neighborhood, local propagation rules and time are the main components of our proposed model [4]. Cells are basic part of CA and distribute on the N-dimensional space. As shown in Figure 1, we introduce a quadrilateral to present a cell, and all cells are organized in a two dimensional space. neighbors of a cell are distributed around the central cell. In our modeling, we adopt Moore neighborhood. As shown in Figure 2, each cell has eight neighbors. The states of each patient are limited. The current state of a cell and the states of its neighbors determine the next state of this cell. CA is itself a dynamic model, and the transformation function provides discrete changes of states during Ebola's propagation [5]. In Figure 2, we add artificial boundary at the periphery of the network, which becomes part of the evaluation process. The artificial boundary does not participate the propagation modeling.

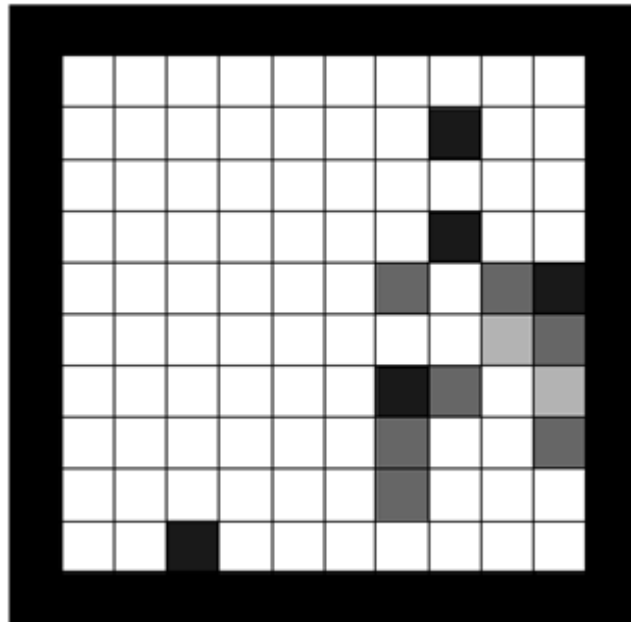


Figure 1. The Location of Human beings: using Quadrilateral to Present a Cell that Denote a Human Being

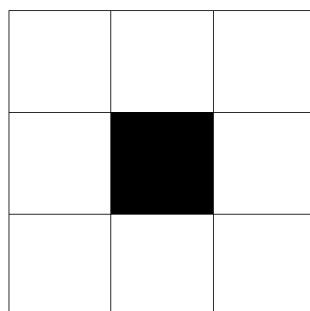


Figure 2. Illustration of Moore Neighbors: each Cell (human being) has Eight Neighbors

3.2. SIR Modeling

As shown in Figure 3, we divide each human being in the Ebola's propagation into three types:

- Susceptible (S): human being is healthy but can be infected;
- Infected (I): human being has been infected;
- Recovered (R): human being gets vaccination and becomes healthy again.



Figure 3. The State Transition Graph of Each Human Being

Susceptible human being will become infected when neighbours becomes contagious and transfer Ebola viruses to this patient [6]. Patient can be recovered through vaccination. We can build up differential equations for our SIR model as follows:

$$\left\{ \begin{array}{l} \frac{di}{dt} = \lambda si - \mu i \quad (1) \\ \frac{ds}{dt} = -\lambda si \quad (2) \\ \frac{dr}{dt} = \mu i \quad (3) \end{array} \right.$$

wherein S(t) denotes the proportion of the susceptible human beings, I(t) denotes the proportion of the infected human beings, and R(t) represents the proportion of the recovered ones. Besides, λ denotes the contact rate of patients every day, and μ represents the recovery rate of patient everyday, t is an arbitrary time in the propagation of Ebola.

3.3. SIR Spread Model Based on CA

Firstly, we describe the details of the structure of SIR/CA. We distribute population that we study in a two dimensional space. The whole space is divided into grid structure. Every quadrilateral represents the place that a human being is located. We use different figure to represent population in quadrilateral. We run the modelling according to the following rules:

- If $S_{\{i,j\}}^t = 1$, then judge $T_a S_{\{i,j\}}^t$
- if $T_a S_{\{i,j\}}^t > T_a$, then $S_{\{i,j\}}^t = 3, T_a S_{\{i,j\}}^t = 0$
- otherwise, $S_{\{i,j\}}^t = 1, T_a S_{\{i,j\}}^t = T_a S_{\{i,j\}}^t + 1$

If the proportion of dead neighbours exceeds three quarter, the human being himself or herself will die for Ebola contagion. We sketch the overall procedure by a flow chart of the modelling. The details are presented in Figure 4.

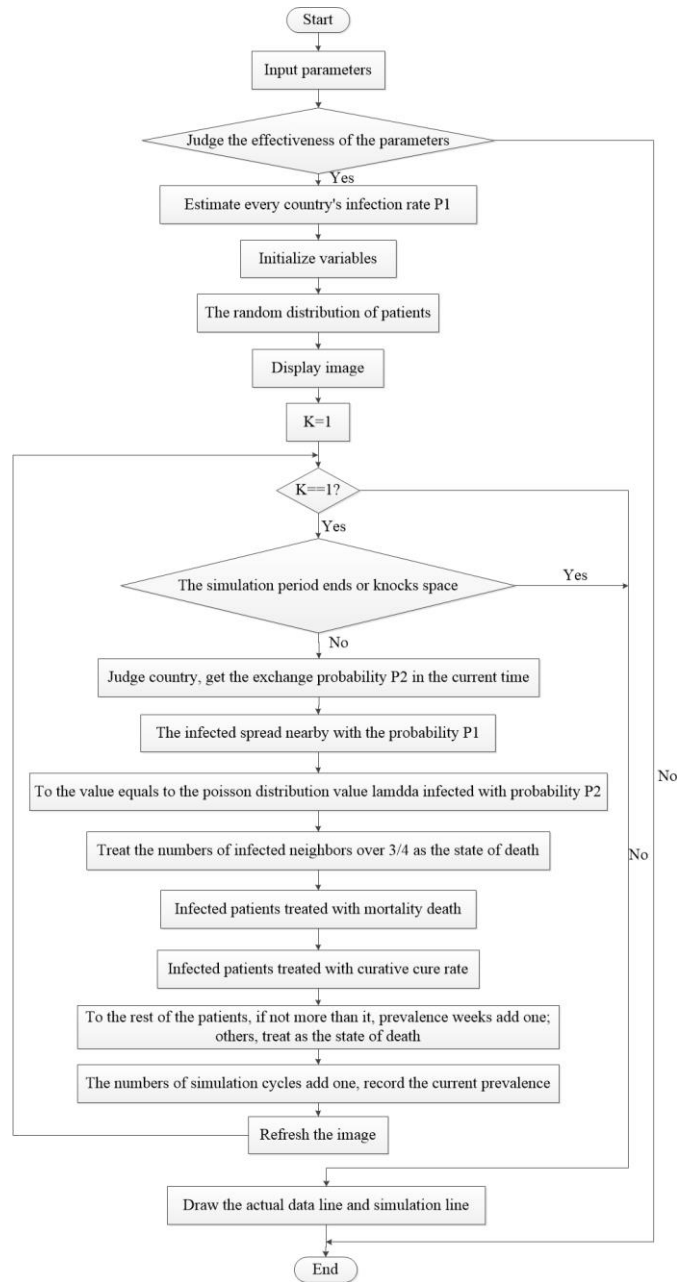


Figure 4. The Flow Chart of the Ebola Propagation in SIR/CA

3.4. Accuracy Evaluation of the Proposed Model

Currently, no previous Ebola outbreaks are as large or persistent as the current epidemic since Ebola virus was first identified in 1976. The 2014 outbreak in West Africa was definitely the largest and most complex Ebola outbreak. In West Africa, there are three main countries suffering from Ebola. They are Guinea, Liberia, Sierra Leone. In this subsection, we evaluate the accuracy of the proposed model. We validate our model by collecting the number of cases, the number of death, and the population of three countries. We compare the modeling results to WHO data from February 24, 2014 to February 1, 2015, during which Ebola viruses got a large-scale outbreak in those three countries [7].

The results in Figure 5, are about the relationship between the propagation time and the number of infected human beings in Guinea. We can obtain from the Figure 5, that the

change of the actual number of patients, the change of the estimated number of patients. It shows that the number of infected human beings increased quickly. Moreover, the speed of Ebola's propagation slowed down at some time during the spreading dynamics. We also have similar results in Figure 6, and Figure 7, for the Liberia and Sierra Leone cases.

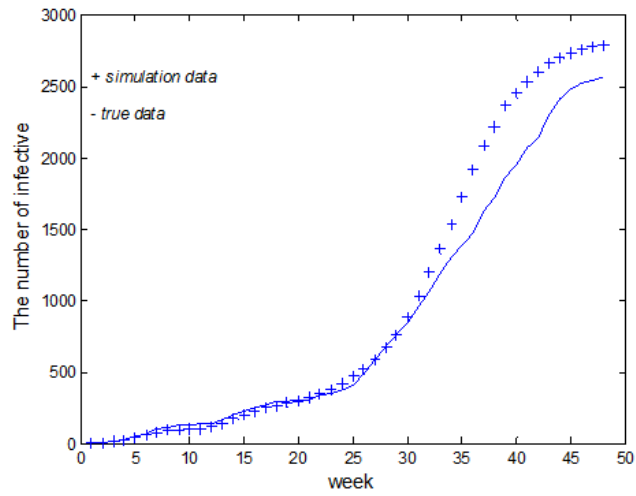


Figure 5. The Relationship between Time and the Number of Infected Human Beings in Guinea

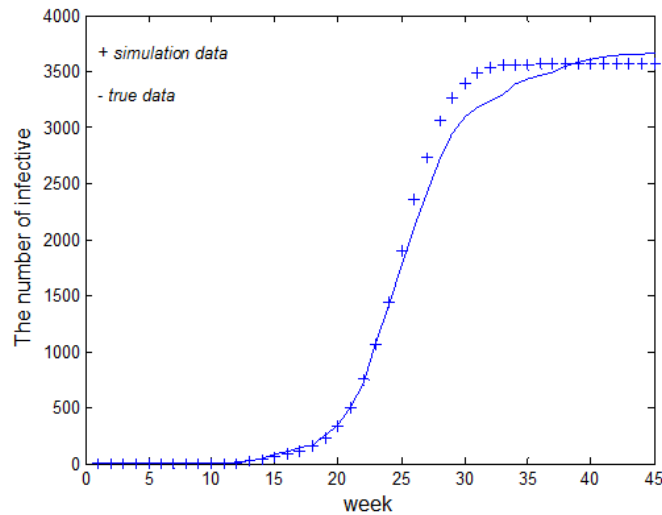


Figure 6. The Relationship between Time and the Number of Infected Human Beings in Liberia

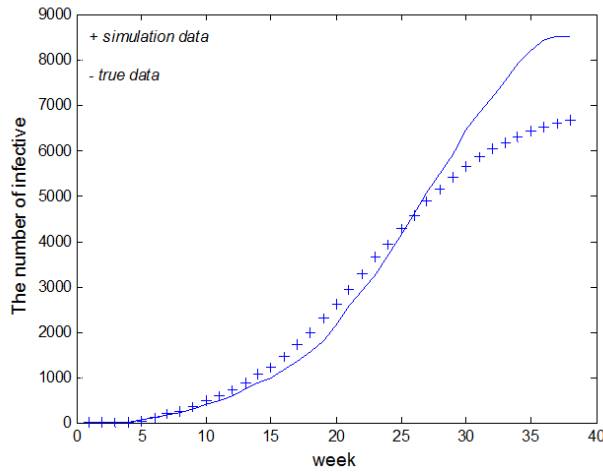


Figure 7. The Relationship between Time and the Number of Infected Human Beings in Sierra Leone

3.5. The Analysis on the Rate of Infection

According to the results of the modeling, we can calculate the infection rate. We show the results in Figure 8, Figure 9, and Figure 10. We can see that the infection rates fluctuate greatly during the propagation of Ebola. However, after Ebola has spread for a period of time, the infection rate becomes steady.

Based on the accurate modeling, we can predict the tendency of Ebola's propagation. The results in Figure 11, show the relationship between time and the estimated number of patients in Guinea. We can therefore predict the number of infective people. According to tendency of the propagation shown in Figure 11, we conduct the demand for new medication. In the next year, the total simulation is 2700, and the number of new patients is 2605. Therefore, the number of required vaccines is about 95. Figure 12, shows the results in Liberia. We will also conduct the medication for Ebola. In the next year, the total number of patients is 3857, and the number of new patients is 188. Therefore, the demand of required vaccines is about 188. Figure 13, shows the prediction results in Sierra Leone later. The total number of patients is 8700, and the number of new patients is 8300. Therefore, the number of required vaccines is about 400. From the experiment results, we can identify the speed of vaccine manufacturing to meet with the maximum demand of vaccination in the countries.

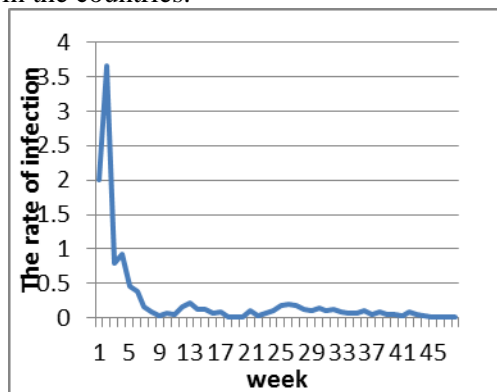


Figure 8. The Infection Rate in Guinea

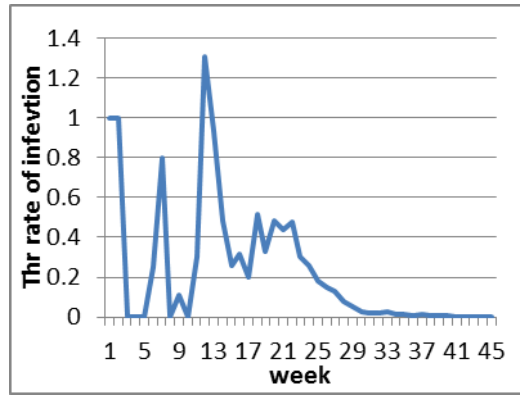


Figure 9. The Infection Rate in Liberia

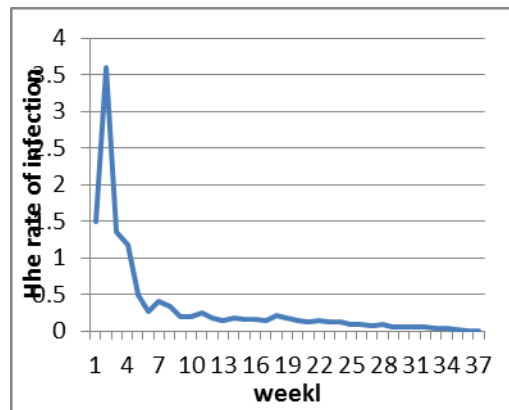


Figure 10. The Infection Rate in Sierra Leone

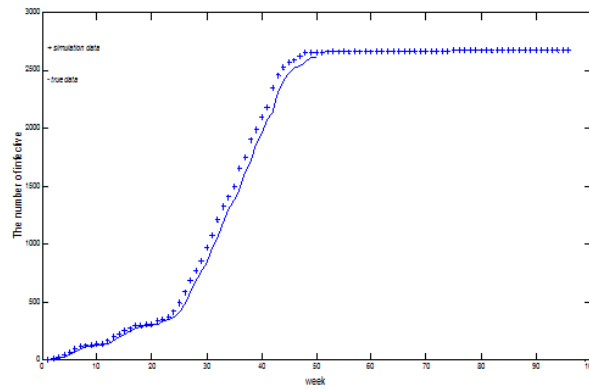


Figure 11. The Prediction of Ebola's Propagation in Guinea

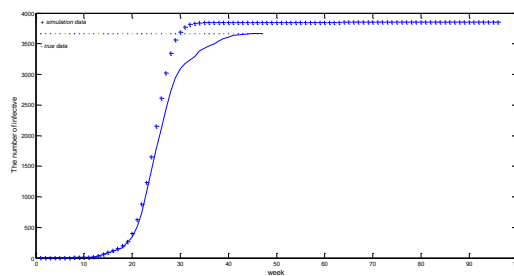


Figure 12. The Prediction of Ebola's Propagation in Liberia

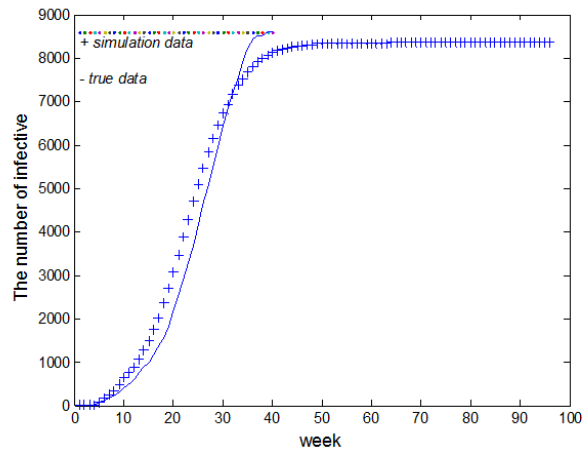


Figure 13. The Prediction of Ebola’s Propagation in Sierra Leone

4. Delivery Analysis

We mainly consider the factors that are the number of Ebolas confirmed cases, the prevalence of trends, the locations of Ebola treatment centers and laboratories, citys economic level to determine the delivery locations in Guinea, Liberia and Sierra Leone. Considering the above five factors, we choose seven cities in the three countries as the delivery locations, which are Macenta, Coyah, Bombali, Port Loko, Kenema, Kailahun and Montserrado.

We filled the delivery locations with black, and concretely analyse the situation in these cities as following:

$$\max \sum_{i=1}^n p_i x_i \tag{4}$$

when

$$\sum_{i=1}^n w_i x_i \leq M \tag{5}$$

wherein $x_i = 0$ or 1 , M denotes the capacity of the package, p_i denotes the price of the item i , and w_i represents the capacity of the item i .

We consider that the vaccine should mainly transport to the areas in serious outbreaks that can directly reduce the sources of infection. We can see from the Figure 14, that the number of confirmed patients in the black area is between 501 and 4000 which are larger than other areas [8]. The size of the circle represents the numbers of cases in the past 21 days which show the prevalence of trends. Therefore, the circles are mainly distributed in the black area, which means the outbreaks of Ebola in these cities are still serious. Considering patients in Ebola treatment centers, sending vaccine to these treatment centers can avoid the waste of transportation time. In Figure 15, we can see most of the black areas are surrounded by the treatment centers, which can provide patients with efficient treatment. The vaccines should be kept safe and scientifically. We consider the vaccines should be sent to laboratories. In Figure 16, the laboratories are distributed near the black area, which meets the requirements of vaccination. From what has been discussed above, we can choose Macenta, Coyah, Bombali, Port Loko, Kenema, Kailahun and Montserrado as optimal delivery locations for eradication of Ebola viruses.

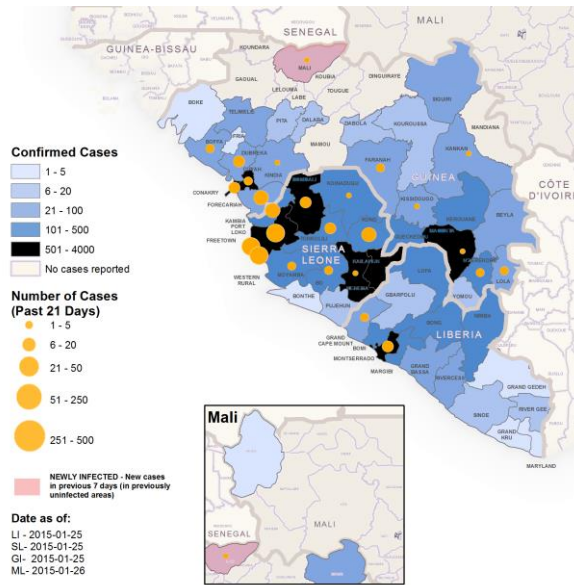


Figure 14. Geographical Distribution Of New And Total Confirmed Data Up To 28 January 2015

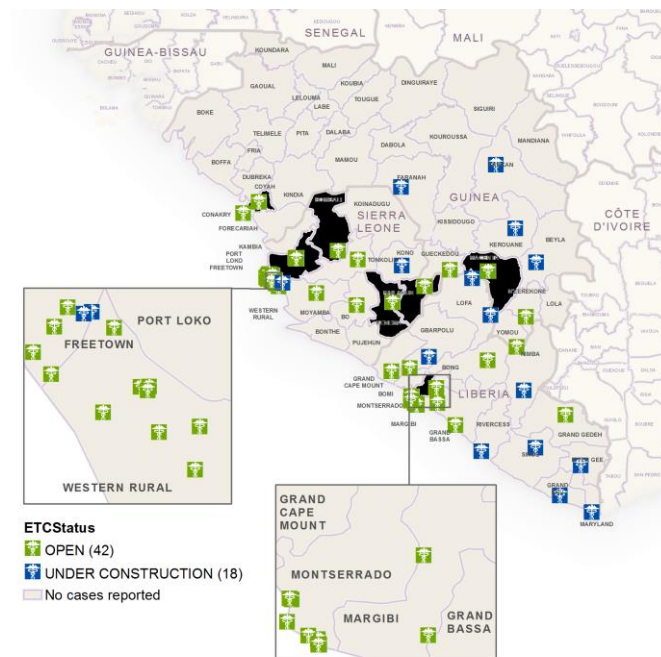


Figure 15. Locations Of Ebola Treatment Centers In Guinea, Liberia And Sierra Leone Data Up To 28 January 2015

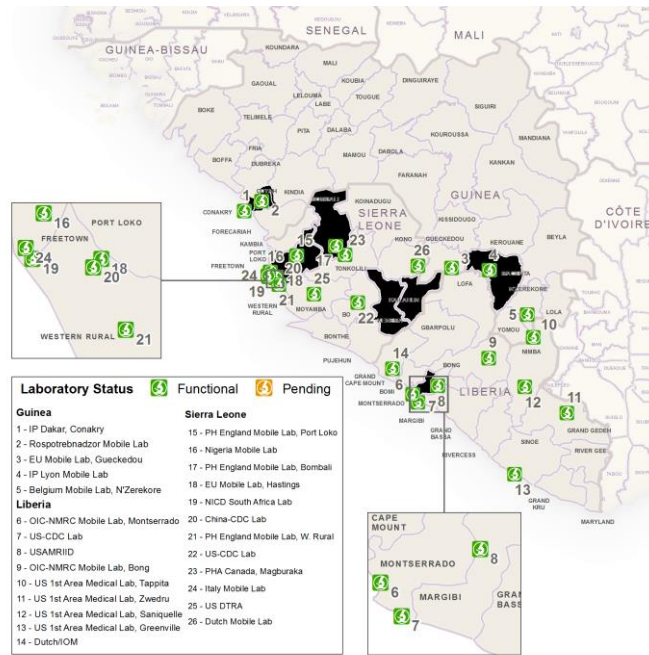


Figure 15. Locations Of Ebola Treatment Centers In Guinea, Liberia And Sierra Leone Data Up To 28 January 2015

Given an outbreak of Ebola, the cost of vaccine transportation is not taken into consideration. The delivery system aims at solving the allocation problem when the vaccines are in short of supply. Therefore, the problem of the vaccine delivery can be converted into the knapsack problem [9-10]. We improved it to conform to the actual vaccine distribution. It changes the objective function into the maximum recovery rate, which equals to the number of recovered patients divided by the number of injections. It also adds a constraint to reflect the shortage: $K \leq D_i$. According to the period of Ebola's propagation, we divided the whole patients into n sections of different disease severity. Every section has its own number of recovered patients. The process can be presented as follows:

$$\max \frac{\sum_{i=1}^n p_i}{\sum_{i=1}^n a_i y_i} \tag{6}$$

when

$$\sum_{i=1}^n a_i y_i \leq k \leq D_i \tag{7}$$

wherein $y_i = 0$ or 1 , K denotes the total number of vaccines, D_i represents the vaccination demand, a_i is the value of the disease severity of an arbitrary patient i , and p_i denotes the number of recovered patients given a disease severity a_i . Through the delivery process, injecting vaccines to those who are in great severity can get the best recovery result. Therefore, in the case of vaccine shortage, we can not only use the vaccines effectively, but also slow down the infection of Ebola.

We also examine the stability and sensitivity of the proposed methods. First for Guinea, we estimated the number of infected patients to be 2750. The actual number

of infected human beings is 2608 (refer to Figure 5). For Liberia, the estimated number of patients is 3502, and the actual simulation number of patients is 3669 (refer to Figure 6). For Sierra Leone, the estimated number of patients is 6805, and the actual number of patients is 8583 (refer to Figure 7). The results of the modeling in all countries are very close to each other.

5. Conclusion

According to the data from WHO, we understand that West Africa is a key region to control the spread of Ebola. Particularly, Guinea, Liberia, Sierra Leone suffered from high risk of death in Ebola's outbreaks. There is no doubt that Ebola is a new challenge. In order to decrease mortality rate, except isolation, we should take other efficient measures.

First is about predicting: prediction plays an important role in eradicating Ebola. Therefore, we need to pay more attention to it. We predict the number of future patients in our modeling. In our analysis, in the next year, the number of patients may grow up to 683. We should produce proper number of vaccines which is more than 683. Second is about the demand of vaccines: with the limitation of produce conditions, the demand of vaccines may be more than production outputs. Therefore, it becomes very important to produce vaccines in advance, which can decrease mortality rate the most. In our research, vaccine quantity should be greater than the death rate. Third is about transportation: given a large outbreak of Ebola, the cost of vaccine transportation is not taken into consideration. We have considered the destination. In our study, we choose seven destinations based on the following factors. We mainly consider the factors including the number of Ebola's confirmed patients, the prevalence of trends, the locations of Ebola treatment centers and laboratories, and city's economic level to determine the delivery locations in Guinea, Liberia and Sierra Leone. Considering the above five indexes, we choose seven cities in three countries as the delivery locations, which are Macenta, Coyah, Bombali, Port Loko, Kenema, Kailahun and Montserrad. Finally, we investigate the medication: the number of medication and the injection time will play a vital role in eradicating Ebola. However, it is difficult to know the effectiveness of vaccines. We should pay more attention to testing vaccine and clinical response.

Acknowledgement

This paper is supported by National Natural Science Foundation of China (NFSC) under Grant No.61502294, Natural Science Foundation of Shanghai under Grant No.15ZR1415200, CERNET IPv6 Innovation Project under Grant No.NGII20150609, 2015 Film Summit Science Foundation of Shanghai University, and Foundation of Science and Technology Commission of Shanghai Municipality under Grant No.14590500500.

References

- [1] Ebola situation report April 2015. URL <http://apps.who.int/ebola/en/ebola-situation-report/situation-reports/>
- [2] Y. Ai-Li and P. Yan, "Swine influenza model based on cellular automata", College of Mathematics and Systems Science in Xinjiang University, vol. 1, (2010), pp. 112–116.
- [3] Shulin C. Sir spread model, vol. 2, (2003), pp. 20–24.
- [4] B. Kreuels, D. Wichmann, P. Emmerich, J. Schmidt-Chanasit, G. de Heer, S. Kluge, A. Sow, T. Renn'e, S. Günther and A. W. Lohse, "A case of severe ebola virus infection complicated by gram-negative septicemia", New england journal of medicine, vol. 371, no. 25, (2014), pp. 2394–2401.
- [5] Y. Lei, "Epidemic spread model based on cellular automata", Computer Engineering and Applications (2007), pp. 67–71.
- [6] L. M. Kasman, A. Kasman, C. Westwater, J. Dolan, M. G. Schmidt, J. S. Norris, "Overcoming the phage replication threshold: a mathematical model with implications for phage therapy", Journal of virology, vol. 76, no. 11, (2002), pp. 5557–5564.
- [7] P. E. Lekone and B. F. Finkenstädt, "Statistical inference in a stochastic epidemic seir model with

- control intervention: Ebola as a case study”, *Biometrics*, vol. 62, no. 4, (2006), pp. 1170–1177.
- [8] W. O. Kermack and A. G. McKendrick, “A contribution to the mathematical theory of epidemics”, *Proceedings of the Royal Society of London A: Mathematical, Physical and Engineering Sciences*, The Royal Society, vol. 115, (1927), pp. 700–721.
- [9] S. You-fa, G. Xu-chong, X. LIANG, L. Cai-yan and Z. Cheng-ke, “Sirs epidemic model under real complex circumstances and its control strategy”, *Journal of System Simulation*, vol. 22, no. 1, (2010).
- [10] J. Y. Wang, “Research on cellular automata consider the propagation delay based on a complex network of virus spread”, *Physics*, vol. 8, (2011), pp. 116–124.

Authors



Shuoping Wang, received her Master degree in Computer Science from Zhejiang University, China in 1996. She is currently an Associate Professor of Zhejiang University City College. Her research interests include Ad Hoc Networks, Software Engineering, Mobile and Internet Applications. She is a member of Zhejiang Scientific and Technical Key Innovation Team of New Generation Mobile Internet Client Software.

