2019 Design for Taxi Driver Making Decisions at Airports

Abstract

The first recorded Ebola outbreak occurred in Nzara, South Sudan in 1967 which infected 284 and killed 151. Since then, Ebola outbreak occurs frequently and there are nearly 20 cases of major or massive outbreaks till now, the most recent of which is the case in Liberia, Guinea and Sierra Leone in 2014. The case fatality rate ranges from 25%(Uganda, 2007) to 90%(Republic of Congo, 2002). Considering its high fatality rate and damage to human society, it is highly valuable to study the property of the spread of Ebola and to find out feasible strategy to fight against the virus.

In this paper, we attempted to untangle the convolution of parameters and variables concerning the spread of Ebola and to give a constructive suggestions regarding what strategy should be taken to deliver limited amount of drug and vaccine. Also, we planned to give an optimized plan to deliver vaccine and drug under a simplified case based on the real case of the recent outbreak in west Africa.

We constructed models based on the biological features of EVD, social features of human society and several reasonable assumptions. Our models consist of two parts: one is considering the the spread of disease within a single city with SIR model and serves as the base of the other; the other takes the people flow among the cities into account, the application of which gave us an optimized plan regarding how should we allocate the resources of medication such as vaccine. In fact, our model is a combination of classic SIR model and graph theory, which is a simple method to solve geography related disease spread problem.

Both of the models were applied to specific cases separately, and the results of computation which were carefully studied justified our model. Through our analysis of the model, we explored and explained the complex relationship among numerous variables and parameters. Then we find the existence of threshold values for those relationship, which indicates a limit condition for outbreak. According to the analysis and literature's instruction, we put forward our own criterion.

The effectiveness of medical treatment (including segregation, vaccination and pharmacotherapy) is verified by our model and the strategy to allocate vaccine and drug is revealed by our investigation. Specifically, the amount of vaccine or drug delivered to each city should be roughly proportional the scale of the city and the amount of vaccine or drug allocated per capita should be larger for the cities in the center of people flow network.

Contents

1 Restatement of the problems

Ebola virus disease (EVD), which is also called Ebola hemorrhagic fever or simply Ebola, is an infectious disease caused by one of the Ebola virus strains, alongside high lethality and rapid epidemicity. EVD was first discovered in 1976 near the Ebola river. Since then, outbreaks have appeared sporadically in Africa. In 2014, the largest outbreak of the disease occurred in West Africa and caused thousands of cases of death.[6] Due to the severity of its outbreak, a feasible method is required to outline its progression and to predict trends, thus being able to form a strategy fighting against infectious diseases like EVD. As is known to all, the spread of EVD is influenced by various factors. Knowing these factors and the role they played can give us a depper understanding of EVD. Therefore, we are eager to figure out factors influencing the spread.

Another problem lies in the delivery system of drug and vaccine. Since *the World Medical Association* has announced a new medication (as is stated in the problem), the quantity and location of medication delivery became a problem of great concern. Considering that pharmaceutical industries may not capable of manufacturing enough drug and vaccine, we need to optimize the delivery plan to suppress the spread of EVD.

In this paper, our purpose is to construct mathematical models that can effectively solve these problems. To meet the goal, we attempt to divide the model into two main parts.

Firstly, we want to construct an initial model discussing the spread of disease in a single city. Some main factors that influence the spread of disease are considered in this model, but the influence and interaction with other cities are not included. This model can describe, at least roughly, the development of EVD in the city after some citizens are infected and measure the importance of different factors, but the spread among cities still cannot be seen. Accordingly, the optimized delivery plan cannot be made with the aim of this single model.

Secondly, we are going to construct a multiple-city model based on the first model. In this model, cities are connected by specific relation, thus allowing pathogen spreads from one city to another. This model can be used to describe the spread of disease in a rather vast geographic regions. With the aim of this model, we use genetic algorithm (GA) to optimize delivery plan.

2 Model Analysis

In this part, we would introduce some natural characters of EVD and historical records of EVD outbreaks. This will help us understand how it spreads and determine appropriate values for the parameters in our models, such as infection rate, recovery rate, etc.

2.1 Analysis of task 1

Many factors related to Ebola influence the spread of EVD or influence the construction of our models. These factors are divided into **Social factors** and **Biological factors** and they are listed as follows.

2.2 Analysis of task 2

In 2014, the largest outbreak of the disease occurred in West Africa, affecting multiple countries mainly including Guinea, Liberia and Sierra Leone.[6]Up to February 4th, there have

been 22,495 reported confirmed, probable, or suspected cases of EVD worldwide, with 8981 reported deaths. Among these reported cases, 99.84% of the cases (22,460) are reported in Guinea, Liberia or Sierra Leone, thus showing a strong regional characteristic and suggesting that we should focus our study mainly within these countries.

2.3 Analysis of task 3

In 2014, the largest outbreak of the disease occurred in West Africa, affecting multiple countries mainly including Guinea, Liberia and Sierra Leone.[6]Up to February 4th, there have been 22,495 reported confirmed, probable, or suspected cases of EVD worldwide, with 8981 reported deaths. Among these reported cases, 99.84% of the cases (22,460) are reported in Guinea, Liberia or Sierra Leone, thus showing a strong regional characteristic and suggesting that we should focus our study mainly within these countries.

2.4 Analysis of task 4

In 2014, the largest outbreak of the disease occurred in West Africa, affecting multiple countries mainly including Guinea, Liberia and Sierra Leone.[6]Up to February 4th, there have been 22,495 reported confirmed, probable, or suspected cases of EVD worldwide, with 8981 reported deaths. Among these reported cases, 99.84% of the cases (22,460) are reported in Guinea, Liberia or Sierra Leone, thus showing a strong regional characteristic and suggesting that we should focus our study mainly within these countries.

3 Model Assumptions

- **Population**
  In general, a large population means high potential of disease's spread. People in a populous area have a greater frequency of contacting the others than those in a sparsely populated area. According to the route of transmission, it is obvious that the probability of getting infected would be larger.

- **Traffic**
  Convinient traffic encourages population mobility, which contributes to the spread of EVD. However, It also encourages freightage, including medicine.

- **Medical Level**
  A society will be less affected by EVD if proper measures are taken efficiently and promptly. These measures include segregating patients and strengthening the sanitary control of public places. The manufacture of drugs and vaccines aiming at EVD is also an important part.

- **Regional Custom**
  Funeral is considered solemn in the African culture. The dead should be cleaned, kissed and touched before buried. This kind of culture facilitates EVD infections.

- **Other Social Factors**
  The spread of diseases is also influenced by factors like social development, health situation, individual's living condition, etc. These factors are not considered to simplify our models.

4 Parameter Table

Symbols that newly appear in this section are listed in table 1. Some of the symbols in table **??** are also used in this section and are not listed here.

Symbol	Defination
$\mathcal{N}_i$	total volume of population in city i
$\mathcal{S}_i$	number of susceptible people in city i
$\mathcal{I}_i$	number of infected but not segregated people in city i
$\mathcal{G}_i$	number of segregated and also infected people in city i
$\mathcal{D}_i$	number of death caused by EVD in city i
$\mathcal{R}_i$	number of recovered people (also immunized) in city i
P_i	Total number of people in city i apart from the people who are dead and segregated
$t_{i,j}$	number of people transmit from city i to city j indeed
α	transmission coefficient
$d_{i,j}$	distance from city i to city j
$vacc_{tot}$	the number of shares of vaccine that can be provided to all the cities every day
$vacc_i$	the number of shares of vaccine that can be provided to city i every day

Table 1: The definition of the symbols.

5 Problem 1: Design for Decision Model

1. **Our model is simple and easy to understand**
   Our model is the simplest model we can conceive to reflect the impact of concerned independent variables (factors regarding medication) and to solve the problem lifted by the question.

   Our single-city model is based on the most elegant model in the field of epidemiology - the SIR model, and we reconstruct the model (mainly add two clusters of people) in order to introduce concerned independent variable into our system.

   Our multi-city model is based on our single-city model and introduce only one 'people flow' to obtain the geographic characteristic of the spread of disease.

2. **Our model is effective and in good agreement with the reality**
   Simple as they are, they are effective in reflecting the complex relationships between numerous variables and parameters, and they not only reveal the intrinsic characteristics of the spread of disease itself but also successfully link factors of medication to the spread of disease.

   Comparing with the data we have find from several resources, the results of our model not only correspond the general trend of the records but also resemble the reality in some critical features.

3. **Good extensibility**
   Flow of people is a critical factor determining the spread of disease. Although our multi-city model only set the volume of people flow as a function of mere geographic distribution and population of cities, the determinants of people flow can be adjusted when other possible factors are considered. Then, the adjusted model can be applied to study the impact of other possible factors relating to epidemiology.

1. **Our model is just a rough model**
   For simplicity, we have neglected many potential parameters, variables or processes, and have made numerous assumptions. Eg. we did not consider the relationship between separate individuals and we did not dig deeper into the properties of social network which is a quite essential part determining the spread of disease. Some important general or specific factors are also neglected by us, a interesting example of which is a folk custom prevalent in the studied region that relatives kiss the death, which plays a significant role in the spread of disease and is categorized into *Super Spread Event*(SSE) academically.

2. **Our model is only a continuous model**
   Numbers of people, number of shares of drug/vaccine, etc. are important quantities in all the process of modeling and computation. For simplicity, we regard the numbers as directly real numbers instead of integers. It is justifiable when the numbers are large, since the decimal part of the number is negligible; when the system scales down, however, the statistics dose not work and the outcome deviates a lot from reality.

6 Problem 2: Verification for the Decision Model

1. **Our model is simple and easy to understand**
   Our model is the simplest model we can conceive to reflect the impact of concerned independent variables (factors regarding medication) and to solve the problem lifted by the question.

   Our single-city model is based on the most elegant model in the field of epidemiology - the SIR model, and we reconstruct the model (mainly add two clusters of people) in order to introduce concerned independent variable into our system.

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7 Problem 3: Design for Schedule Model

1. **Our model is simple and easy to understand**
Our model is the simplest model we can conceive to reflect the impact of concerned independent variables (factors regarding medication) and to solve the problem lifted by the question.

   Our single-city model is based on the most elegant model in the field of epidemiology - the SIR model, and we reconstruct the model (mainly add two clusters of people) in order to introduce concerned independent variable into our system.

   Our multi-city model is based on our single-city model and introduce only one 'people flow' to obtain the geographic characteristic of the spread of disease.

2. **Our model is effective and in good agreement with the reality**
Simple as they are, they are effective in reflecting the complex relationships between numerous variables and parameters, and they not only reveal the intrinsic characteristics of the spread of disease itself but also successfully link factors of medication to the spread of disease.

   Comparing with the data we have find from several resources, the results of our model not only correspond the general trend of the records but also resemble the reality in some critical features.

3. **Good extensibility**
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Numbers of people, number of shares of drug/vaccine, etc. are important quantities in all the process of modeling and computation. For simplicity, we regard the numbers as directly real numbers instead of integers. It is justifiable when the numbers are large, since

the decimal part of the number is negligible; when the system scales down, however, the statistics dose not work and the outcome deviates a lot from reality.

8 Problem 4: Design for Priority Model

1. **Our model is simple and easy to understand**
   Our model is the simplest model we can conceive to reflect the impact of concerned independent variables (factors regarding medication) and to solve the problem lifted by the question.

   Our single-city model is based on the most elegant model in the field of epidemiology - the SIR model, and we reconstruct the model (mainly add two clusters of people) in order to introduce concerned independent variable into our system.

   Our multi-city model is based on our single-city model and introduce only one 'people flow' to obtain the geographic characteristic of the spread of disease.

2. **Our model is effective and in good agreement with the reality**
   Simple as they are, they are effective in reflecting the complex relationships between numerous variables and parameters, and they not only reveal the intrinsic characteristics of the spread of disease itself but also successfully link factors of medication to the spread of disease.

   Comparing with the data we have find from several resources, the results of our model not only correspond the general trend of the records but also resemble the reality in some critical features.

3. **Good extensibility**
   Flow of people is a critical factor determining the spread of disease. Although our multi-city model only set the volume of people flow as a function of mere geographic distribution and population of cities, the determinants of people flow can be adjusted when other possible factors are considered. Then, the adjusted model can be applied to study the impact of other possible factors relating to epidemiology.

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2. **Our model is only a continuous model**
   Numbers of people, number of shares of drug/vaccine, etc. are important quantities in all the process of modeling and computation. For simplicity, we regard the numbers as directly real numbers instead of integers. It is justifiable when the numbers are large, since the decimal part of the number is negligible; when the system scales down, however, the statistics dose not work and the outcome deviates a lot from reality.

9   Model Appraisal

9.1   The strengths of the model

In this paper, we have constructed our models based on the biological features of EVD, social features of human society and several reasonable assumptions. Our models consist of two parts: one is considering the the spread of disease within a single city and serves as the base of the other; the other takes the people flow among the cities into account, the application of which gives an optimized plan regarding how should we allocate the resources of medication such as vaccine.

9.2   The weaknesses of the model

Both of the models are applied to specific cases separately, and the results of computation which are carefully studied justified our model. Through our analysis of the model, we explored and explained the complex relationship among numerous variables and parameters.

9.3   The improvement of the model

The effectiveness of medical treatment (including segregation, vaccination and pharmacotherapy) is verified by our model and the strategy to allocate vaccine and drug is revealed by our investigation.

9.4   The Extension of the model

10   Conclusion

In this paper, we have constructed our models based on the biological features of EVD, social features of human society and several reasonable assumptions. Our models consist of two parts: one is considering the the spread of disease within a single city and serves as the base of the other; the other takes the people flow among the cities into account, the application of which gives an optimized plan regarding how should we allocate the resources of medication such as vaccine.

Both of the models are applied to specific cases separately, and the results of computation which are carefully studied justified our model. Through our analysis of the model, we explored and explained the complex relationship among numerous variables and parameters.

The effectiveness of medical treatment (including segregation, vaccination and pharmacotherapy) is verified by our model and the strategy to allocate vaccine and drug is revealed by our investigation.

References

[1] Kermack W O, McKendrick A G. A Contribution to the Mathematical Theory of Epidemics[J]. Proceedings of the Royal Society of London. Series A, 1927, 115(772):700-721.

[2] W. O. Kermack , A. G. McKendrick Contributions to the mathematical theory of epidemics. Proc Roy Soc,1932:(A138):55-83

[3] Lipsitch I , Cohen T , Cooper B , Transmissions Dynamics and Control of Severe Acute Respiratory Synddrome[J]. Science 10, 1126;1086616(2003 May 23)

[4] Dye C , Gay N . Modeling the SARS epedemic. Science, 2003;300:1884-1885

[5] AsehwandenC.Spatial simulation model for infectious viral diseases with focus on SARS and the common flu. Proceedings of the 37th Hawaii International Conference on System. Science,2004

[6] Website of Centers for Disease Control and Prevention: *http://cdc.gov.com*

Appendices

Appendix A   First appendix

some text...

Here are simulation programmes we used in our model as follow.

Input matlab source:

```matlab
function [t,seat,aisle]=OI6Sim(n,target,seated)
pab=rand(1,n);
for i=1:n
    if pab(i)<0.4
       aisleTime(i)=0;
    else
        aisleTime(i)=trirnd(3.2,7.1,38.7);
    end
end
```

Appendix B   Second appendix

some more text **Input C++ source:**

```cpp
//============================================================================
// Name        : Sudoku.cpp
// Author      : wzlf11
// Version     : a.0
// Copyright   : Your copyright notice
// Description : Sudoku in C++.
//============================================================================

#include <iostream>
#include <cstdlib>
#include <ctime>

using namespace std;

int table[9][9];
```

```cpp
int main() {

    for(int i = 0; i < 9; i++){
        table[0][i] = i + 1;
    }

    srand((unsigned int)time(NULL));

    shuffle((int *)&table[0], 9);

    while(!put_line(1))
    {
        shuffle((int *)&table[0], 9);
    }

    for(int x = 0; x < 9; x++){
        for(int y = 0; y < 9; y++){
            cout << table[x][y] << " ";
        }

        cout << endl;
    }

    return 0;
}
```