

Study on the Spread model of Ebola

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Keywords: The closed system; the negative feedback system; the open system.

Abstract. In this paper, we will set a negative feedback system to realize automatic adjustment through the feedback coefficient. This system reflects the relationship between actual situation and control strength. We can take timely control measures to make the illness spread decrease rapidly in order to achieve the goal of eradicating Ebola.

1. Introduction

Ebola virus disease is a disease of humans and other primates caused by Ebola viruses. After contracting the virus, signs and symptoms typically start between two days and three weeks. Prevention includes limiting the spread of disease from infected animals to humans. It includes wearing proper protective clothing and washing hands when around a person with the disease [1].

Although a mass of potential treatments are being studied, there is as yet no known effective medication or vaccine. This includes oral rehydration therapy or intravenous infusion therapy as well as treating symptoms. Our model is based on the negative feedback system to analysed the spread of the Ebola.

2. Assumptions

In order to streamline our model, we have made several key assumptions:

We do not take into account birth rate and mortality in related areas.

We neglect the influence of natural disaster.

Only the healthy people can go to the other countries.

The selected data is valid.

3. Symbols

Table 1. Model parameters

Symbol	Definition	Units
X_i	Input signal	unitless
A	Open loop gain	unitless
F	Sensitivity tradeoff of regulatory element	unitless
A_f	Closed loop gain	unitless
K_f	Feedback coefficient	unitless
X_0	Output signal	unitless

4. Model

We divide the propagation process into two categories: short distance transmission and long distance transmission. The short distance transmission corresponds to infected individuals propagate disease to nearest individuals on the circle. The long distance transmission corresponds to infected individuals propagate disease to any one of randomly selected individuals in the network.

4.1 The Closed System

We use SEIR mechanism to develop infectious disease model. In the initial phase, the dynamic characteristic of our model is each infected individual in the period of Δt infects three species of people:

Adjacent individuals in susceptible state with the probability of P_s

Individuals in susceptible state randomly with the probability of P_j

Individuals be removed, no longer infectious and cannot infect other individuals with the probability of P_r

We describe the spread process between adjacent individuals of Ebola in Fig. 1. There is only one vertex infected when $t=0$. Then the infected person propagates disease to adjacent individuals. We regard the adjacent individuals as people in incubation period when $t=1$. Next, people in incubation period turn into infectious and begin to infect their adjacent people when $t=3$. Repeat the process steadily until it remains in numerical simulation process.

$F(t)$ describes the number of a pair of vertices. One is infectious and the other adjacent to it is in susceptible state. The number of pairs of vertices, which can make short distance transmission along the fixed edge. We treat it as the amount of enclosed area. Consequently, the short distance transmission can be thought of as the increase of infectious people with the speed of P_s in enclosed area.

So we can derive the equations (1)-(3) intuitively.

$$\frac{dN'}{dt} = P_s F(t) \tag{1}$$

$$\frac{dE}{dt} = P_s F(t) - \beta E(t) \tag{2}$$

$$\frac{dI}{dt} = \beta E(t) - P_r I(t) \tag{3}$$

Now we consider dynamic characteristics of enclosed areas. Enclosed areas can be produced by long jump. Each jump produces two barriers. When the spread domains of two barriers mix together through collision, the domain produced by infectious people is damaged. It is just like the infectious people have been removed before their adjacent people infected. This long jump is due to the probability that infectious people successfully infect randomly selected people in susceptible state.

The probability is $\frac{N - N'(t)}{N}$.

4.2 The Open System

Open system is an expansion of closed system. In consideration of globalization tendency, it is necessary to think about population flow between different counties.

The first phase is spread along the inerratic network structure. It infects its adjacent individuals, namely the short distance communication. The second phase is the infection to any one of randomly selected individuals in the network, which means random long distance transmission. The third phase is the spread to randomly selected individuals in other circle. Considering of population flow increases the complexity of our model and makes it more comprehensive.

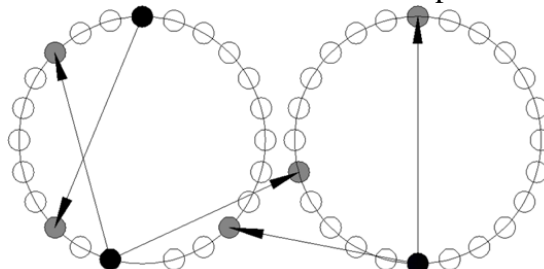


Fig. 1 Dynamic spread of Ebola in open system

We obtain dynamic spread in open system to explain the full spread process of Ebola. In terms of the factor we have discussed, we can correct (4) to get new formulas below.

$$\begin{cases} \frac{dS}{dt} = -kI(t)S(t) + \sum_{\substack{i=1 \\ i \neq j}}^n \alpha_{ij} \tau_{ij} A_i - \sum_{\substack{j=1 \\ j \neq i}}^n \alpha_{ij} \tau_{ij} A_i \\ \frac{dE}{dt} = kI(t)S(t) - \beta E(t) + \sum_{\substack{i=1 \\ i \neq j}}^n (1 - \alpha_{ij}) \tau_{ij} A_i - \sum_{\substack{j=1 \\ j \neq i}}^n (1 - \alpha_{ij}) \tau_{ij} A_i \\ \frac{dI}{dt} = \beta E(t) - P_s I(t) \\ \frac{dR}{dt} = P_s I(t) \end{cases} \quad (4)$$

It is obvious to get the initial conditions $S(0) = S_0, I(0) = I_0, E(0) = E_0$

4.3 Results

According to the above model, we can get the number of Ebola infection. In the conclusion, we take three worst-affected countries for instance, which are Guinea, Liberia, Sierra Leone. And the conclusion is as follows.

Table 2. Results of infections

Country	The cumulative infections	The number of new infections
Guinea	3144	169
Liberia	8861	116
Sierra Leone	11209	469
Total	23214	754

Meanwhile, we choose Guinea to analyse how we get the above results.

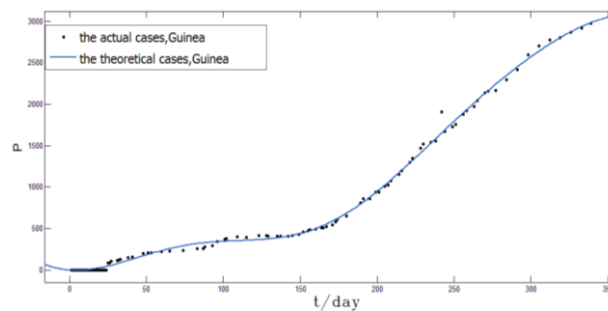


Figure 2 The relationship between cases and time in Guinea

5. Summary

Our model is based on small world network and contact network. It means the long distance contact between individuals appears because the average distance of network edge is very short. The long distance contact can be regarded as unfrequent contact or random contact. This network has an inerratic basic structure, which can explain regular contacts between people in a team.

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