The Ebola virus based on SIR and SEIR model

Ganzhou Wu

School of science, Guangdong University of Petrochemical Technology, Maoming 525000, China.

275385973@qq.com

Abstract

In this paper, we apply a SEIR model to study the Ebola virus. Both time and spatial considerations are conducted. Computational results and analyses are given. Interpretation and connection between real world and model world were carefully done.

Keywords

Ebola virus, SIR model, SEIR model.

1. Introduction

Ebola virus first appeared in 1976, is a human primate can cause severe infectious disease of zoonotic hemorrhagic fever, highly infectious and pathogenic characteristics, and high mortality, disease mainly popular in African countries. Began in March 2014, the spread of the Ebola outbreak in the West African countries, is the largest, infections and deaths on the history of the disease most of the time. Up to now, Liberia, Sierra Leone, Guinea declared a state of emergency, World Health Organization called on States to help countries suffering from Ebola virus outbreak, the multi-national immunization and medical teams has joined to the fight against Ebola epidemic actions [1].

Controlling the spread of the infectious disease is one of the most challenging problems human face [2]-[3]. The wide spread and spread of Ebola virus has brought bad influence to the development of economy, the public's health and life, making people realize the importance of mastering the transmission dynamics of the epidemic and forecasting its severity, so as to provide the reference for people to evaluate the control and intervention measures and optimizing the development of new control measures. Due to the lack of targeted drugs, we can only establish the scientific mathematical model [4] according to the Ebola transmission mechanism and on the basic of survey data, to reveal and predict the growth trend of Ebola patients in the future, and take what interventions [5].

2. The foundation of SIR model

The spread of the Ebola virus is an infectious disease dynamics model. It has been a lot of research on this subject in the field of mathematical modeling. For example, the SIR model is relatively simple and practical mode. It usually adopts the method of isolating the infected to prevent epidemic and infectious diseases, but too high isolation rate will have great influence on people's livelihood and economy, so it must find an optimal rate of isolation. Ebola virus disease is a lethal human and primate disease that currently requires a particular attention from the World Health Organization due to important outbreaks in some Western African countries nations of Guinea, Sierra Leone and Liberia is the largest in history in 2014.

The main purpose of our paper is to establish a feasible and used model about Ebola.

Firstly, based on SIR differential model for the spread of epidemic [6], the Ebola outbreak is simulated. Through threshold analysis in this mathematical model, the isolating treatments of patients with epidemic are presented. Then the future epidemic situation after adopting isolation measure is predicted and some conditions for controlling the infections are propose.

Secondly, considering the complexity of the infectious process and the West African backward medical level and lack of medicines, we set up more perfect SEIR model. Therefore, we predict that the number of infected persons will grow rapidly.

2.1 Assumptions and Notations

The assumptions are as follows.

To simplify our problems, we make the following basic assumptions, each of which is properly justified.

The speed of changing from the infectious to the recovered is proportional to the number of the infected.

Assuming the infectious due to the impact of the infectious diseases， the time-changing rate of the population and the result of multiplying the number of the vulnerable persons with the Infectious one become proportional.

Table 1 The notations in this paper

Numble	notation	implication
1	S(Susceptible)	Individuals who have not yet caught the disease from contact with an infectious individual.
2	I(Infectious)	Individuals who have the disease. They have some probability of infecting susceptible people.
3	R(Recovered)	Individuals who have experienced the full infectious period, and are now non-infectious and immune.
4	ρ	The rate of isolation
5	R_0	The basic reproduction number
6	σ	Removal rate of infected persons
7	δ	The lurker removal rate

2.2 The model of SIR

Susceptible persons and Infectious persons become infectious persons after the effective contact. The growth rate of $R(t)$ with respect to time is proportional to the $S(t)$, and the constant of propotionality is λ ,and the quit rate of infectious is ν. Suppose the number of the susceptible that each infectious will effectively contact. So

$$\frac{dS(t)}{dt} = -\lambda S(t)I(t) \tag{1}$$

In unit time, the changes of leavers is equal to the decrease of the Infectious ,that is to say,

$$\frac{dR(t)}{dt} = \nu I(t) \tag{2}$$

The change of the infectious is equal to the amount of the Susceptible that have been transferred into accounts.

$$\frac{dI(t)}{dt} = \lambda S(t)I(t) - \nu I(t) \tag{3}$$

Recording the proportion of healthy people and the patient in the initial moments are S_0 , R_0 (we may assume $R_0 = 0$).

2.3 Results & Analysis of the Model

Analytic solution can't be figured out by Equations (1), (2), (3) .So we defined a new variable as $\sigma = \lambda / \nu$. Thus we can find out the solution for the equation：

$$\mathrm{I}_{\max} = I_0 + S_0 - \rho + \rho \ln \frac{\rho}{S_0} \tag{4}$$

The analysis of the change of $S(t)$, $I(t)$, $R(t)$ is as follow:

No matter how the initial condition S_0, R_0 ,the patient will eventually disappear, that is $I_\infty = 0$.

Eventually the ratio of healthy people who have not been infected is S_∞ .

As S_0 there will begin to have: $I(t)$ increases firstly, while S_0, $I(t)$ reaches the maximum, then $I(t)$ decreases to 0, $S(t)$ decreases monotonically to S_∞ .

As S_0, then $I(t)$ decreases monotonically to 0, $S(t)$ decreases monotonically to S_∞ .

We use the above model to simulate in appearing infect diseases in three West African countries and regions of the Ebola virus outbreak. The following information is posted online according to WHO data .We regard Liberia in March 2014 data as the initial data. We set $I_0 = 8$, $R_0 = 6$, $S_0 = 4309675$, Using the Principle of Least Squares to ensure the first model's parameters.

Making $\rho = \frac{1}{\sigma}$, $\rho = 1240.98$,substituting this into equation (4) ,we can get $I_\infty = 52863$.

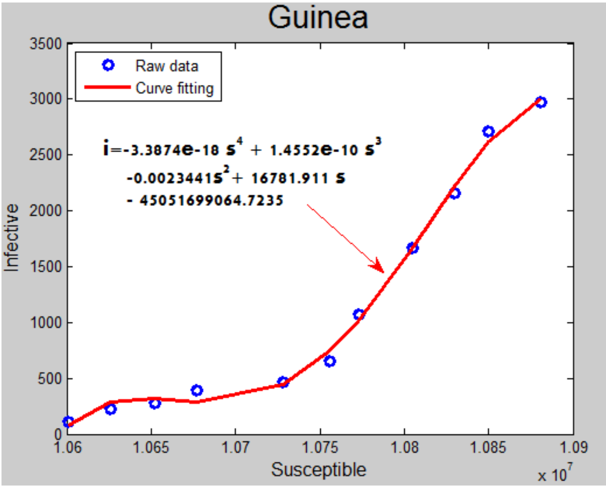

Fig. 1 The relationship between the Infective and Susceptible in Guinea

We can clearly see from the Figure 1, the simulation results are in good agreement with the actual outbreak by curve fitting between infectious disease dynamics model and SIR model.

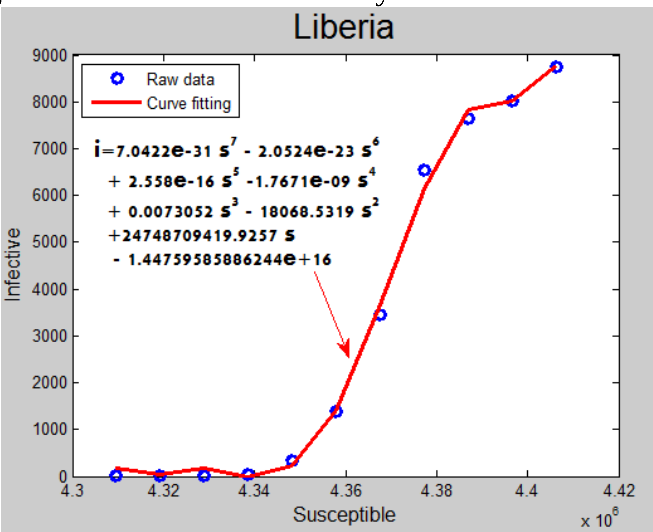

Fig. 2 The relationship between the Infective and Susceptible in Liberia

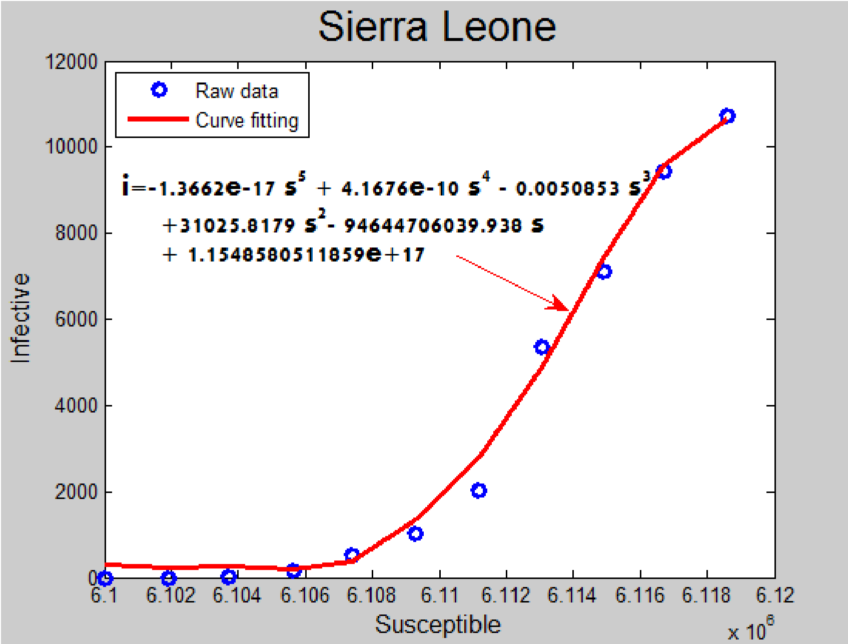

Fig. 3 The relationship between the Infective and Susceptible in Sierra Leone

Seen from Figure 2 and Figure3, We can clearly observe that the Ebola virus infections in Guinea and Sierra Leone increase every month, which image is growing as a line from March, 2014 to January, 2015. Combined with the world health organization official website statistics, they calculated that in March 2014 to January 2015, the average monthly death rate is as high as 64.98%, 55.97%, 30.78%. It demonstrates that hygiene and medical standards in the areas that need to be improved, the effort in response to the Ebola virus need to be strengthened, changes in infectious disease dynamics model can be analyzed and forecast the spread of the Ebola virus corresponding trend. In consequence, it is very urgent to take effective measures to establish a realistic, rational and useful model.

3. The foundation of SEIR model

3.1 Assumptions and Notations

Taking into account the isolation and treatment are two important measures to control the epidemic of Ebola virus, and we establish a combination of isolation and treatment model. There will be the incubation period of about 12 days after considering the Ebola virus infection. For isolation and treatment of infected people, the corresponding infected population can be divided into two categories: infectious disease people and without treatment due to infectious disease people. Meanwhile, S represents Susceptible, E represents Lurker. And some infected people can produce immunity after treatment [7]. The model is established on the basis of these equations as shown below:

$$\begin{cases} \dfrac{dS}{dt} = \Lambda - \beta I_u S - \mu S + \delta(1-p)E + \sigma(1-q)I_u + \mu_2 I_t \\ \dfrac{dE}{dt} = \beta I_u S - (\mu+\delta)E \\ \dfrac{dI_u}{dt} = \delta pE - (\mu+\sigma+\mu_1)I_u \\ \dfrac{dR}{dt} = XI \end{cases} \tag{5}$$

Where Λ is susceptible S input rate, including birth and immigration, and we assume that all inputs into the S-Class p and q , respectively, for the development of latent proportion of infected person I_u and I_t treated, μ_1 and μ_2 are constants, respectively for I_u and I_t the infected persons screened for active treatment and cure of proportion .The parameters in the model are non-negative. It can be known from the model that all answers with non-negative initial value existing and being non-negative in equation (5).The basic reproductive number of the model obtained by using the renewable matrix is

$$R_0 = \frac{\beta\Lambda\delta p}{\mu(\mu+\delta)(\mu+\sigma+\mu_1)} \tag{6}$$

3.2 Results & Analysis of the Model

The basic reproduction number R_0 is when a primary case was introduced to the average number of cases occurred in uninfected populations of secondary cases [8]. When R_0 is greater than 1, the infection may spread in the population, the value of R_0 is represented the faster spread rate. Doubling time is based on the reproduction number and spacing estimates generations. Estimate R_0 help assess disease control efforts required to pay, the propagation velocity fluctuates over time effects and control measures implemented by the way.

We according to the time sequence of the incidence of cases (as in the process of drawing the popular weekly number of new cases curve) and the estimated incidence of cases on behalf of the spacing distribution to estimate R_0. Then, calculate the average estimate R_0 January 2015 to February 2015 this time, which is based on case reports the estimated time to be used to predict future cases.

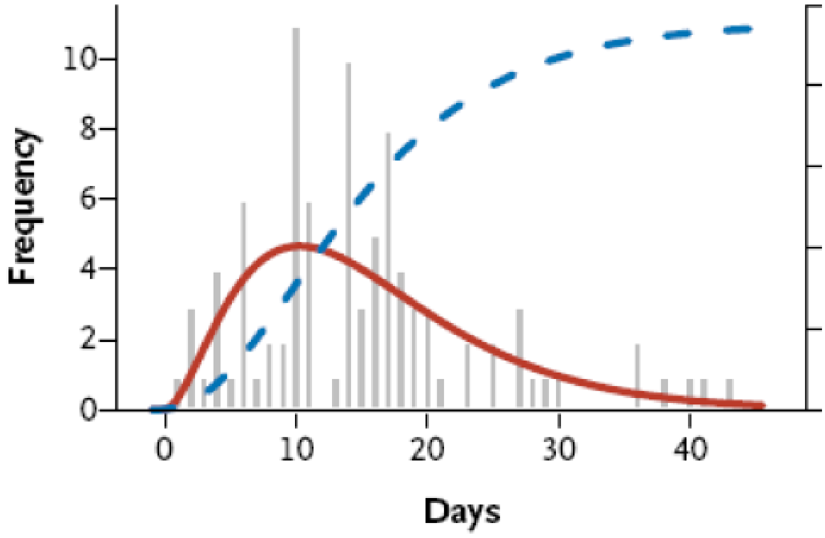

Fig. 4 Infections and infectious cases

The basic reproductive number R_0 (blue curve) and on behalf of the pitch (gray histogram) and the best fit (γ) probability density function (red curve). On behalf of the spacing of 15.3 days, may indicate that the outbreak in isolated cases of inadequate measures, resulting in a higher spread events occur late in the disease process of proportion.

4. Conclusion

Ebola Virus Disease (EVD; formerly known as Ebola hemorrhagic fever) is a serious, often fatal human disease outbreaks, high mortality rate of up to 90%. Ebola virus through close contact with infected animal blood, secretions, organs or other body fluids and spread to humans, and then be spread by person to person spread in human society. According to SEIR model, we implement the way of combining segregate control with therapy on infected persons. Therefore, we can predict that the number of infected persons will grow rapidly.

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