

The Spread of Ebola Virus Based On SEIHCR Model

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Abstract. The spread of virus is based on some mathematical models. An epidemic model SEIHCR was build up to take the special features of Ebola into consideration. These are treatments from hospital, infectious corpses and intensified contact tracing. This model is developed from the traditional SEIR model. The model's result, whose parameters are decided by using computer simulation, matches perfectly with the data reported by WHO, suggesting the validity of the improved model.

1. Introduction

Ebola virus disease, formerly known as Ebola haemorrhagic fever, is a severe, often fatal illness in humans. The current outbreak in West Africa, (first cases notified in March 2014), is the largest and most complex Ebola outbreak since the Ebola virus was first discovered in 1976. It started in Guinea and later spread across land borders to Sierra Leone and Liberia^[1]. The analysis of the spread of epidemic has been a universal concern. Moreover, there have been a lot of research into the studies of the 2014 Ebola epidemic in West Africa^[2].

2. The Traditional Epidemic Model

The transmission of virus follows SEIR (susceptible-exposed-infections-recovered) dynamics and can be described by the following set of ordinary differential equations^[3]:

$$\begin{cases} \dot{S}(t) = -\beta S(t)I(t)/N \\ \dot{I}(t) = \sigma E(t) - \gamma I(t) \\ \dot{E}(t) = \beta S(t)I(t)/N - \sigma E(t) \\ \dot{R}(t) = \gamma I(t) \\ CUM = \sigma E(t) \end{cases} \quad (1)$$

Where:

$S(t)$ is the number of susceptible individuals at time t ,

$I(t)$ is the number of infectious individuals at time t ,

$E(t)$ is the number of exposed individuals at time t ,

$R(t)$ is the number of removed individuals at time t ,

$CUM(t)$ is the cumulative number of Ebola cases from symptoms onset,

N is the size of total population,

$1/\gamma$ is the average duration of infectiousness.

$1/\sigma$ is the average duration of incubation,

β is the transmission rate per person day. β is constant in absence of control interventions.

However, β is assumed to decay exponentially at rate k ^[4] after control measures are introduced at time $t \geq \tau$. That is,

$$\beta(t) = \begin{cases} \beta_0 & t < \tau \\ \beta_0 e^{-k(1-\tau)} & t \geq \tau \end{cases} \quad (2)$$

3. The Improved Model

The SEIR model is a basic model to predict the spread of disease. However, for the specific case of Ebola, we have to take other important factors into consideration. The things mainly considered are as follows.

- 1) The potential threat posed by infectious corpses and the provision of hospital care;
- 2) The involvement of contact tracing (CT).

Figure 1 shows a schematic presentation of the improved model SEIHCR, indicating the compartmental states and the transition rates among the states.

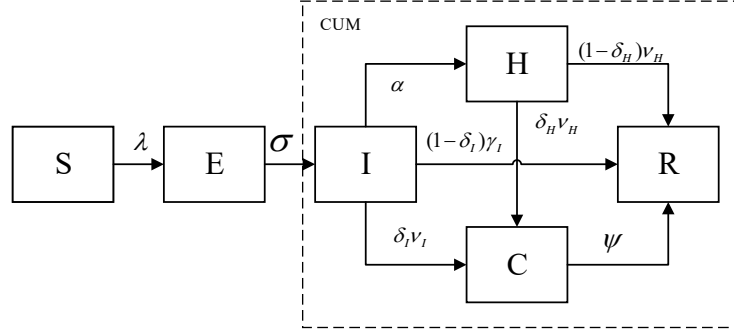


Figure 1. Compartmental flow of the SEIHCR model

The traditional model SEIR should be modified^[5], and the improved SEIHCR(CT) model can be written as

$$\begin{cases} \dot{S}(t) = -\beta_I S(t)I(t)/N - \beta_H S(t)H(t)/N - \beta_C S(t)C(t)/N \\ \dot{E}(t) = \beta_I S(t)I(t)/N + \beta_H S(t)H(t)/N + \beta_C S(t)C(t)/N - \sigma E(t) \\ \quad - \kappa(\alpha I(t) + \psi C(t))\pi_E \omega_E(E(t)/N) \\ \dot{I}(t) = \sigma E(t) - \alpha I(t) - (1-\delta_I)\gamma_I I(t) - \delta_I \nu_I I(t) \\ \quad - \kappa(\alpha I(t) + \psi C(t))\pi_I \omega_I(I(t)/N) \\ \dot{H}(t) = \alpha I(t) - (1-\delta_H)\gamma_H H(t) - \delta_H \nu_H H(t) \\ \dot{C}(t) = \delta_I \nu_I I(t) + \delta_H \nu_H H(t) - \psi C(t) \\ \dot{R}(t) = (1-\delta_I)\gamma_I I(t) + (1-\delta_H)\gamma_H H(t) + \psi C(t) \end{cases} \quad (3)$$

where:

$C(t)$ is the number of contaminated deceased at time t ,

$H(t)$ is the number of hospitalized individuals at time t ,

β_I is the transmission rate outside hospital,

β_C is the transmission rate due to improper handling of deceased, and

$$\lambda = \beta_I \frac{I(t)}{N} + \beta_H \frac{H(t)}{N} + \beta_C \frac{C(t)}{N} \quad (4)$$

β_H is the transmission rate inside hospital,

λ is the total transmission rate,

α is the rate of infectious individuals to be identified/isolated,

$1/\gamma_H$ is the average time from symptoms onset to recovery inside hospital,

$1/\nu_H$ is the average time from symptoms onset to death inside hospital,

δ_H is the fatality rate inside hospital,

$1/\gamma_I$ is the average time from symptoms onset to recovery outside hospital,

$1/\nu_I$ is the average time from symptoms onset to death outside hospital,

δ_I is the fatality rate outside hospital,

$1/\psi$ is the average time until deceased is properly handled,

κ is the average number of contacts traced per identified/isolated infectious individual,
 π_E is the probability a contact traced exposed individual is isolated without causing a new case,
 ω_E is the ratio probability that contact traced individual is infectious at time of originating case identification to the probability a random individual in the population is infectious.

Test the validity of the ultimate model, and compare the calculated data with the actual data. The cumulative number of individuals can be obtained by

$$CUM(t + \Delta t) = CUM(t) + \int_t^{t+\Delta t} \sigma E(s) ds \quad (5)$$

Equation (3) is improved from the original model SEIR and it is an ultimate model. Name it the SEIHCR model to illustrate its improvement and differences from the traditional SEIR model. The transition SEIR to SEIHCR shows how basic model can be greatly improved based on other factors and my understanding toward this problem.

4. Determining Parameters in SEIHCR Model

4.1. Estimation of R_0

In order to obtain the reproduction number R_0 , a method is used. The method is as follows.

$$R_0 = \rho(FV^{-1}) \quad (6)$$

where:

$\rho(A)$ denotes the spectral radius of a matrix A ,

F is the rate of appearance of new infections,

V is the rate of transfer of individuals by all other means.

F and V that are corresponded with the SEIHCR model are

$$F = \begin{pmatrix} -(\beta_I SI / N + \beta_H SH / N + \beta_C SC / N) \\ \beta_I SI / N + \beta_H SH / N + \beta_C SC / N \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, V = \begin{pmatrix} 0 \\ -\sigma E \\ \sigma E - \alpha I \\ \alpha I - \gamma_H H - \nu_H H \\ \nu_I I + \nu_H H - \psi C \\ \gamma_I I + \gamma_H H + \psi C \end{pmatrix} \quad (7)$$

4.2. Determination of other parameters

The values of the parameters $\beta_I, \beta_H, \beta_C, \alpha$ and ψ are estimated for the three countries using a least square curve fitting algorithm. The parameters $\sigma, \gamma_I, \gamma_H, \nu_I, \nu_H, \delta_I, \delta_H$ are borrowed from existing references^[6].

The basic reproduction number of the SEIHCR model is given by the following formula, computed by the next-generation method:

$$R_0 = \frac{\beta_I}{\alpha + (1 - \delta_I)\gamma_I + \delta_I\nu_I} + \frac{\beta_H}{(1 - \delta_H)\gamma_H + \delta_H\nu_H} + \frac{\beta_C}{\psi} \quad (8)$$

Among all these parameters, β_I is constant in absence of control interventions, just as β from the SEIR model. After control measures are introduced at time $t \geq \tau$, β_I is assumed to decay exponentially at rate k ^[7], That is,

$$\beta_I(t) = \begin{cases} \beta_{I0} & t < \tau \\ \beta_{I0}e^{-k(t-\tau)} & t \geq \tau \end{cases} \quad (9)$$

Since k and γ_H are both related to the efficacy of medicine, we assume their relationship to be

$$\gamma_H = \theta k \quad (10)$$

where θ is assumed to be 3.2 based on experience.

5. Result of the SEIHCR Model

The dotted is used to represent the actual data of the cumulative numbers found in the WHO situation reports^[8] and the solid line to represent our calculated number from Equation (3) of the SEIHCR model. The start day of the simulation is defined as Day 1st.

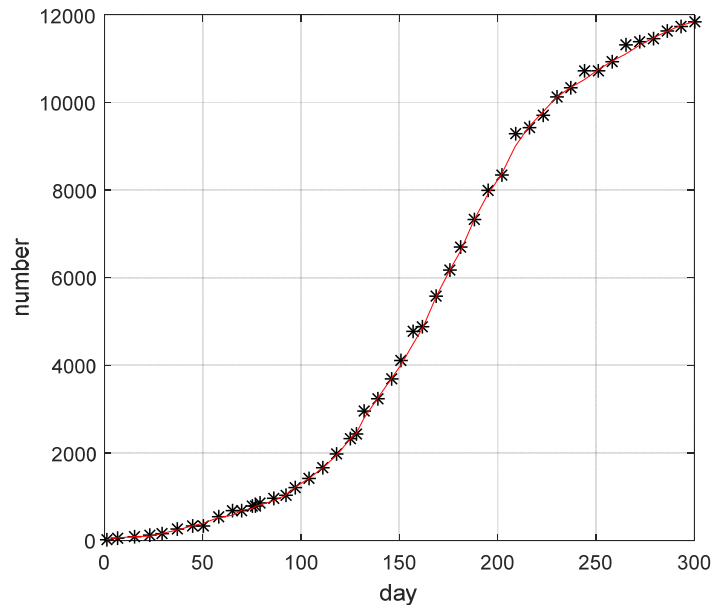


Figure 2. Simulation of cumulative cases in Sierra Leone from May 27th, 2014 to Feb 4th, 2015. The parameter values are $N = 6000000$, $\beta_{I0} = 0.31$, $\beta_H = 0.0001$, $\beta_C = 0.125$, $\alpha = 0.2$, $\gamma_I = 1/21$, $\nu_I = 1/8$, $\nu_H = 1/31$, $\psi = 1/5.5$, $\kappa = 0$, $k = 0.015$, $\tau = 160$

These simulations are accomplished by varying combinations of parameters. The calculated data become more smoothly and closely approximate to the actual reported data with the simulation for Sierra Leone being the perfect approximation

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