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A mathematical model for simulating the transmission of Wuhan novel Coronavirus

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Abstract:

As reported by the World Health Organization, a novel coronavirus (2019-nCoV) was identified as the causative virus of Wuhan pneumonia of unknown etiology by Chinese authorities on 7 January, 2020. In

this study, we developed a Bats-Hosts-Reservoir-People transmission network model for simulating the potential transmission from the infection source (probable be bats) to the human infection. Since the Bats-Hosts-Reservoir network was hard to explore clearly and public concerns were focusing on the transmission from a seafood market (reservoir) to people, we simplified the model as Reservoir-People transmission network model. The basic reproduction number (R_0) was calculated from the RP model to assess the transmissibility of the 2019-nCoV.

Introduction

On 31 December 2019, the World Health Organization (WHO) China Country Office was informed of cases of pneumonia of unknown etiology (unknown cause) detected in Wuhan City, Hubei Province of China, and WHO reported that a novel coronavirus (2019-nCoV) was identified as the causative virus by Chinese authorities on 7 January(1). Potential for international spread via commercial air travel had been assessed(2). Public health concerns have been paid globally on how many people had been infected actually.

In this study, we developed a Bats-Hosts-Reservoir-People (BHRP) transmission network model for simulating the potential transmission from the infection source (probable be bats) to the human infection. Since the Bats-Hosts-Reservoir network was hard to explore clearly and public concerns were focusing on the transmission from a seafood market (reservoir) to people, we simplified the model as Reservoir-People (RP) transmission network model. The basic reproduction number (R_0) was calculated from the RP model to assess the transmissibility of the 2019-nCoV.

The Bats-Hosts-Reservoir-People transmission network model

We assumed that the virus transmitted among the bats population, and then transmitted to an unknown host (probably be wild animals). The hosts were hunted and sent to the seafood market which was defined as the reservoir or the virus. People exposed to the market got the risks of the infection (Figure 1).

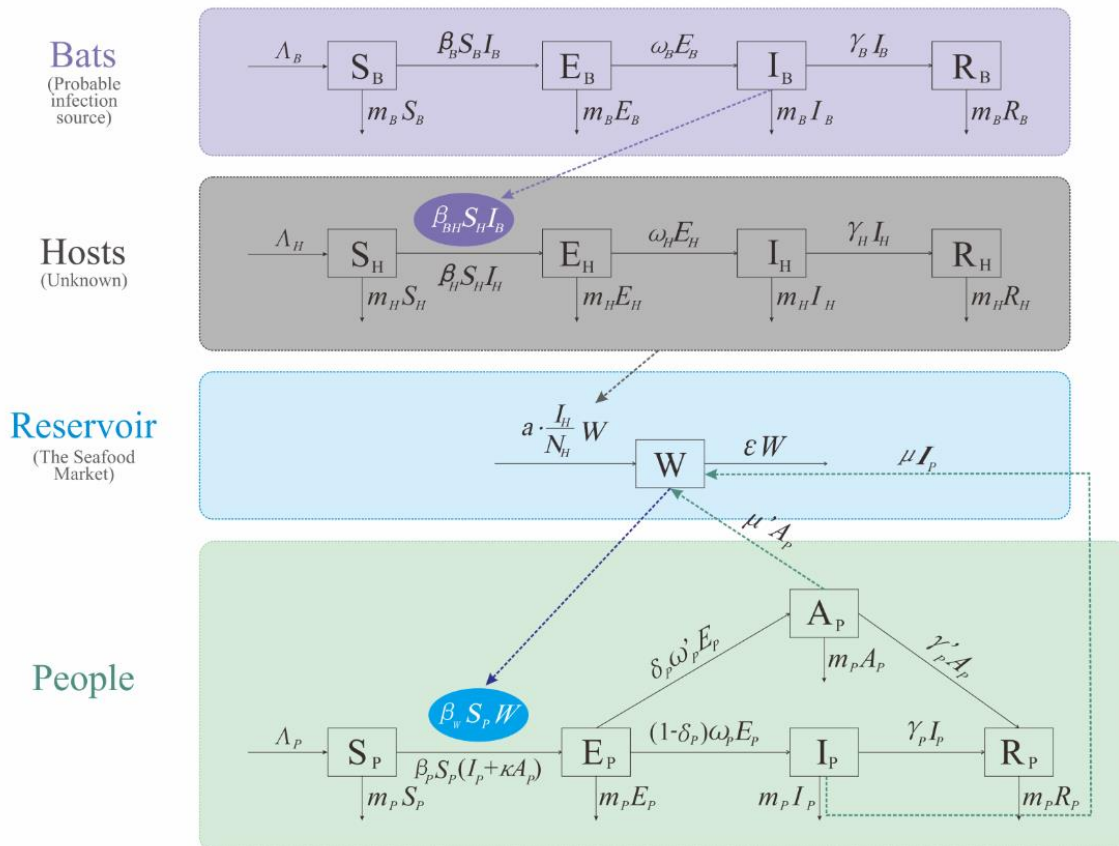


Figure 1. Flowchart of the Bats-Hosts-Reservoir-People transmission network model.

The BHRP transmission network model was based on the following assumptions or facts:

a) The bats were divided into four departments: susceptible bats (S_B), exposed bats (E_B), infected bats (I_B), and removed bats (R_B). The birth rate and death rate of bats were defined as n_B and m_B . In this model, we set $\Lambda_B = n_B \times N_B$ where N_B refer to the total number of bats. The incubation period of bat infection was defined as $1/\omega_B$ and the infectious period of bat infection was defined as $1/\gamma_B$. The S_B will be infected through sufficient contact with I_B , and the transmission rate was defined as β_B .

b) The hosts were divided into four departments: susceptible hosts (S_H), exposed hosts (E_H), infected hosts (I_H), and removed hosts (R_H). The birth rate and death rate of hosts were defined as n_H and m_H . In this model, we set $\Lambda_H = n_H \times N_H$ where N_H refer to the total number of hosts. The incubation period of host infection was defined as $1/\omega_H$ and the infectious period of host infection was defined as $1/\gamma_H$. The S_H will be infected through sufficient contact with I_B and I_H , and the transmission rates were defined as β_{BH} and β_H , respectively.

c) The 2019-nCoV in reservoir (the seafood market) was denoted as W . We assumed that the retail purchases rate of the hosts in the market was a , and that the prevalence of 2019-nCoV in the purchases was I_H/N_H , therefore, the rate of the 2019-nCoV in W imported form the hosts was aWI_H/N_H where N_H was the total number of hosts. We also assumed that symptomatic infected people and asymptomatic infected people could export the virus into W with the rate of μ_p and μ'_p , although this assumption might occur in a low probability. The virus in W will subsequently leave the W compartment at a rate of εW , where $1/\varepsilon$ is the lifetime of the virus.

d) The people were divided into five departments: susceptible people (S_P), exposed people (E_P), symptomatic infected people (I_P), asymptomatic infected people (A_P), and removed people (R_P) including recovered and death people. The birth rate and death rate of people were defined as n_P and m_P . In this model, we set $\Lambda_P = n_P \times N_P$ where N_P refer to the total number of people. The incubation period and latent period of human infection was defined as $1/\omega_P$ and $1/\omega'_P$. The infectious period of I_P and A_P was defined as $1/\gamma_P$ and $1/\gamma'_P$. The proportion of asymptomatic infection was defined as δ_P . The S_P will be infected through sufficient contact with W and I_P , and the transmission rates were defined as β_W and β_P , respectively.

We also assumed that the transmissibility of A_P was κ times that of I_P , where $0 \leq \kappa \leq 1$.

$$\left\{ \begin{array}{l}
 \frac{dS_B}{dt} = \Lambda_B - m_B S_B - \beta_B S_B I_B \\
 \frac{dE_B}{dt} = \beta_B S_B I_B - \omega_B E_B - m_B E_B \\
 \frac{dI_B}{dt} = \omega_B E_B - (\gamma_B + m_B) I_B \\
 \frac{dR_B}{dt} = \gamma_B I_B - m_B R_B \\
 \frac{dS_H}{dt} = \Lambda_H - m_H S_H - \beta_{BH} S_H I_B - \beta_H S_H I_H \\
 \frac{dE_H}{dt} = \beta_{BH} S_H I_B + \beta_H S_H I_H - \omega_H E_H - m_H E_H \\
 \frac{dI_H}{dt} = \omega_H E_H - (\gamma_H + m_H) I_H \\
 \frac{dR_H}{dt} = \gamma_H I_H - m_H R_H \\
 \frac{dS_P}{dt} = \Lambda_P - m_P S_P - \beta_P S_P (I_P + \kappa A_P) - \beta_W S_P W \\
 \frac{dE_P}{dt} = \beta_P S_P (I_P + \kappa A_P) + \beta_W S_P W - (1 - \delta_P) \omega_P E_P - \delta_P \omega'_P E_P - m_P E_P \\
 \frac{dI_P}{dt} = (1 - \delta_P) \omega_P E_P - (\gamma_P + m_P) I_P \\
 \frac{dA_P}{dt} = \delta_P \omega'_P E_P - (\gamma'_P + m_P) A_P \\
 \frac{dR_P}{dt} = \gamma_P I_P + \gamma'_P A_P - m_P R_P \\
 \frac{dW}{dt} = aW \frac{I_H}{N_H} + \mu_P I_P + \mu'_P A_P - \varepsilon W
 \end{array} \right.$$

The parameters of the BHRP model were shown in [Table 1](#).

Table 1. Definition of those parameters in the BHRP model

Parameter	Description
n_B	The birth rate parameter of bats
n_H	The birth rate parameter of hosts

n_P	The birth rate parameter of people
m_B	The death rate of bats
m_H	The death rate of hosts
m_P	The death rate of people
$1/\omega_B$	The incubation period of bats
$1/\omega_H$	The incubation period of hosts
$1/\omega_P$	The incubation period of people
$1/\omega'_P$	The latent period of people
$1/\gamma_B$	The infectious period of bats
$1/\gamma_H$	The infectious period of hosts
$1/\gamma_P$	The infectious period of symptomatic infection of people
$1/\gamma'_P$	The infectious period of asymptomatic infection of people
β_B	The transmission rate from I_B to S_B
β_{BH}	The transmission rate from I_B to S_H
β_H	The transmission rate from I_H to S_H
β_P	The transmission rate from I_P to S_P
β_W	The transmission rate from W to S_P
a	The retail purchases rate of the hosts in the market
μ_P	The shedding coefficients from I_P to W
μ'_P	The shedding coefficients from A_P to W
$1/\varepsilon$	The lifetime of the virus in W
δ_P	The proportion of asymptomatic infection rate of people

κ

The multiple of the transmissibility of A_P to that of I_P .

The simplified Reservoir-People transmission network model

Based on the information we known, we assumed that the 2019-nCoV might be imported to the seafood market in a short time. Therefore, we added the further assumptions as follows:

- a) The transmission network of Bats-Host was ignored.
- b) Based on our previous studies on simulating importation(3, 4), we set the initial value of W as

following impulse function:

$$Importation = impulse(n, t_0, t_i)$$

In the function, n , t_0 and t_i refer to imported volume of the 2019-nCoV to the market, start time of the simulation, and the interval of the importation.

Therefore, the BHRP model was simplified as RP model and is shown as follows:

$$\left\{ \begin{array}{l} \frac{dS_P}{dt} = \Lambda_P - m_P S_P - \beta_P S_P (I_P + \kappa A_P) - \beta_W S_P W \\ \frac{dE_P}{dt} = \beta_P S_P (I_P + \kappa A_P) + \beta_W S_P W - (1 - \delta_P) \omega_P E_P - \delta_P \omega'_P E_P - m_P E_P \\ \frac{dI_P}{dt} = (1 - \delta_P) \omega_P E_P - (\gamma_P + m_P) I_P \\ \frac{dA_P}{dt} = \delta_P \omega'_P E_P - (\gamma'_P + m_P) A_P \\ \frac{dR_P}{dt} = \gamma_P I_P + \gamma'_P A_P - m_P R_P \\ \frac{dW}{dt} = \mu_P I_P + \mu'_P A_P - \varepsilon W \end{array} \right.$$

During the outbreak period, the natural birth rate and death rate in the population was in a relative low level. However, people would commonly travel into and out from Wuhan City due to the Chinese New Year.

Therefore, n_p and m_p refer to the rate of people traveling into Wuhan City and traveling out from Wuhan City, respectively.

The transmissibility of the 2019-nCoV based on the RP model

In this study, we used the basic reproduction number (R_0) to assess the transmissibility of the 2019-nCoV. Commonly, R_0 was defined as the expected number of secondary infections that result from introducing a single infected individual into an otherwise susceptible population(3). If $R_0 > 1$, the outbreak will occur. If $R_0 < 1$, the outbreak will go to an end.

Based on the equations of RP model, we can get the disease free equilibrium point as:

$$\left(\frac{\Lambda_p}{m_p}, 0, 0, 0, 0 \right)$$

$$F = \begin{bmatrix} 0 & \beta_p \frac{\Lambda_p}{m_p} & \beta_p \kappa \frac{\Lambda_p}{m_p} & \beta_w \frac{\Lambda_p}{m_p} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, V^{-1} = \begin{bmatrix} \frac{1}{\omega_p + m_p} & 0 & 0 & 0 \\ A & \frac{1}{\gamma_p + m_p} & 0 & 0 \\ B & 0 & \frac{1}{\gamma'_p + m_p} & 0 \\ B & E & G & \frac{1}{\varepsilon} \end{bmatrix}$$

In the matrix:

$$A = \frac{(1 - \delta_p)\omega_p}{(\omega_p + m_p)(\gamma_p + m_p)}$$

$$B = \frac{\delta_p \omega_p}{(\omega_p + m_p)(\gamma'_p + m_p)}$$

$$D = \frac{(1 - \delta_p)\mu\omega_p}{(\omega_p + m_p)(\gamma_p + m_p)\varepsilon} + \frac{\mu' \delta_p \omega_p}{(\omega_p + m_p)(\gamma'_p + m_p)\varepsilon}$$

$$E = \frac{\mu}{(\gamma_p + m_p)\varepsilon}$$

$$G = \frac{\mu'}{(\gamma'_p + m_p)\varepsilon}$$

By the next generation matrix approach(5), we can get the next generation matrix and R_0 for the RP model:

$$FV^{-1} = \begin{bmatrix} \beta_p \frac{\Lambda_p}{m_p} A + \beta_p \kappa \frac{\Lambda_p}{m_p} B + \beta_w \frac{\Lambda_p}{m_p} D & * & * & * \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$R_0 = \rho(FV^{-1}) = \beta_P \frac{\Lambda_P}{m_P} \frac{(1 - \delta_P)\omega_P}{(\omega_P + m_P)(\gamma_P + m_P)} + \beta_P \kappa \frac{\Lambda_P}{m_P} \frac{\delta_P \omega_P}{(\omega_P + m_P)(\gamma'_P + m_P)} \\ + \beta_W \frac{\Lambda_P}{m_P} \frac{(1 - \delta_P)\mu\omega_P}{(\omega_P + m_P)(\gamma_P + m_P)\varepsilon} + \beta_W \frac{\Lambda_P}{m_P} \frac{\mu' \delta_P \omega_P}{(\omega_P + m_P)(\gamma'_P + m_P)\varepsilon}$$

Author contribution statements:

Tianmu Chen: Methodology, Formal analysis, Writing - original draft, review & editing. **Jia Rui:**

Methodology, Formal analysis. **Zeyu Zhao:** Formal analysis. **Qiupeng Wang:** Formal analysis. **Jing-An**

Cui: Methodology. **Ling Yin:** Methodology.

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