Analysis of COVID-19 based on SEIR epidemic models in a multi-patch environment

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Abstract  In this paper, an $n$-patch SEIR epidemic model for the coronavirus disease 2019 (COVID-19) is presented. It is shown that there is unique disease-free equilibrium for this model. Then, the dynamic behavior is studied by the basic reproduction number. Some numerical simulations with three patches are given to validate the effectiveness of the theoretical results. The influence of quarantined rate and population migration rate on the basic reproduction number is also discussed by simulation.

Keywords COVID-19 · $n$-patch SEIR epidemic model · Basic reproduction number · Quarantine strategy · Migration rate

1 Introduction

The coronavirus disease 2019 (COVID-19) has spread to more than 200 countries worldwide, which has a significant impact on economy development, social stability and people’s daily life. According to the data on December 30, 2020 of World Health Organization, the number of confirmed cases has increased to 80,155,187 and the number of confirmed deaths cases has increase to 1,771,128 [1].

In fact, COVID-19 is one of the most serious viruses for human beings. How to reduce or control the spread of this epidemic has attracted much attention from various communities [2,3,4,5,6,7,8]. Zhu et al. [9] isolated COVID-19 from pneumonia patient samples and found that it belongs to the seventh member of the coronavirus family. Linton et al. [10] obtained that an average incubation period is 5 days for COVID-19 by statistical analysis of epidemic data. Chen et al. [11] presented a transmission network model and calculated the basic reproduction number of the model, which showed that COVID-19 has a higher infection rate.
than SARS but less than MERS. Saha et al. [12] proposed an SEIRS epidemic model to explore coronavirus infection and suggested that susceptible individuals can avoid infection by taking appropriate precautions. Quaranta et al. [13] performed a multi-scale dynamic analysis of COVID-19 outbreak in Italy to show changes at different geographic scales. Leung et al. [14] established a susceptible-exposed-infectious-recovered (SEIR) model and the basic reproduction was estimated. Du et al. [15] presented a hybrid artificial intelligence (AI) model for COVID-19 outbreak prediction. However, it is rare to establish a multi-patch epidemic model to study the impact of population migration and quarantine on the basic reproduction number.

With the rapid development of transportation, population migration among different regions has been one of the important factors to study the spread of epidemic. Hethcote [16] presented a model for migration between the two patches and studied the impact for migration on infectious diseases. Sattenspiel and Herring [17] presented a population flow model with \( n \)-patch and studied the dynamic behavior of the model. Driessche and Arino [18] established an epidemic patch model for \( n \) cities and analyzed the impact of population mobility on spatial distribution. Cui et al. [19] proposed a spatial infectious disease model with migration which has the potential value for disease control. Li [20] showed that pattern transition from stationary pattern to patch invasion appears to be possible in a fully deterministic parasite-host model. Arino et al. [21] found that infection during transport increases the possibility that the disease persists in both patches and amplifies prevalence. A two-patch SEIRS epidemic model is proposed by Liu et al. [22] to study the impact of travel on the spatial spread of dog rabies between patches with different level of disease prevalence. Zhang et al. [23] focused on a delayed multi-group SIS epidemic model with nonlinear incidence rates and patch structure. Driessche and Salmani [24] gave an SEIRS model of \( p \)-patch and analyzed the stability of the disease-free equilibrium point. The effects of heterogeneity in groups, patches and mobility patterns on \( R_0 \) and disease prevalence were explored by Bichara et al. [25]. The dynamics of an SIS epidemic model with asymmetric connectivity matrix was analyzed by Chen et al. [26] and it showed that the basic reproduction number \( R_0 \) was strictly decreasing with respect to the dispersal rate of the infected individuals. How to study the spread of COVID-19 in a multi-patch environment is an interesting and important topic.

Inspired by above discussion, in this paper, a \( n \)-patch SEIR epidemic model is formulated. The paper is organized as follows. In Section 2, the SEIR model with \( n \)-patch for COVID-19 is proposed. In section 3, the basic reproduction number associated with quarantined rate and population migration rate is given, and the stability of the model is studied. In Section 4, based on the data of Wuhan, Huanggang and Huangshi, a numerical simulation with three patches is given, which shows that appropriate quarantine strategy and control of the migration rate are important strategies to reduce the spread of COVID-19. Conclusions are made in Section 5.

**Notations:** \( \rho(A) \triangleq \max_{i=1,2,\ldots,n} |\lambda_i| \) and \( s(A) \triangleq \max_{i=1,2,\ldots,n} \text{Re}(\lambda_i) \), where \( \lambda_1, \lambda_2, \ldots, \lambda_n \) are the eigenvalues of matrix \( A \); \( \mathbf{0} \) denotes the \( 3 \times 3 \) zero matrix.
2 The n-patch SEIR model for COVID-19

The population in the $i$-th patch is stratified as susceptible ($S_i$), exposed ($E_i$), infectious ($I_i$), quarantined ($Q_i$), hospitalized ($H_i$) and recovered ($R_i$). By tracing close contacts, some individuals exposed to the virus are quarantined. If the close contacts are infected individuals, they will be sent directly to the hospital. Thus, we only consider quarantining the exposed individuals. It is assumed that the self-quarantined susceptible individuals who stay in safe areas have no contact with infected individuals. The disease transmission in each patch is shown in Figure 1.

Fig. 1 The disease transmission in each patch.

Based on the SEIR epidemic model, the n-patch SEIR epidemic model for COVID-19 is formulated as follows.

$$\begin{align*}
\frac{dS_i}{dt} &= b_i - \beta_i S_i (1 - z_i)(v_i E_i + I_i) - \mu_i S_i + \sum_{j \neq i} (a_{ij} S_j - a_{ji} S_i), \\
\frac{dE_i}{dt} &= \beta_i S_i (1 - z_i)(v_i E_i + I_i) - (q_i + \sigma_i + \mu_i) E_i + \sum_{j \neq i} (b_{ij} E_j - b_{ji} E_i), \\
\frac{dI_i}{dt} &= \sigma_i E_i - (\delta_i + \gamma_i + \theta_i) I_i + \sum_{j \neq i} (c_{ij} I_j - c_{ji} I_i), \\
\frac{dQ_i}{dt} &= q_i E_i - (\alpha_i + \mu_i) Q_i, \\
\frac{dH_i}{dt} &= \alpha_i Q_i + \delta_i I_i - (\eta_i + g_i) H_i, \\
\frac{dR_i}{dt} &= \gamma_i I_i + \eta_i H_i - \mu_i R_i + \sum_{j \neq i} (d_{ij} R_j - d_{ji} R_i), i = 1, 2, \ldots, n,
\end{align*}$$

where $\beta_i$, $v_i$, $z_i$, $q_i$, $\sigma_i$, $\delta_i$, $\gamma_i$ and $\eta_i$ represent the disease transmission coefficient, the contact rate regulator of exposed individuals, the self-quarantined rate of susceptible individuals, the quarantined rate of exposed individuals, the transition rate of exposed individuals to infected individuals, the transition rate of infected individuals to hospitalized individuals, the recovery rate of the infectious individuals and the recovery rate of hospitalized individuals, respectively. $b_i$, $\mu_i$, $\theta_i$ and $g_i$ are the number of births per unit time, the natural death rate, the death
rate of infected individuals and the death rate of hospitalized individuals in the $i$-th patch, respectively. The migration rates of susceptible, exposed individuals, infectious and removed individuals from the $j$-th patch to the $i$-th patch are denoted by $a_{ij}$, $b_{ij}$, $c_{ij}$ and $d_{ij}$, respectively. It is clear that all these parameters are non-negative.

Remark 1 Different with the model in [27], the natural birth rate, the number of births per unit time, the death rate of hospitalized individuals and the self-quarantined rate of susceptible are taken into consideration. Moreover, people can migrate between any two patches.

3 Main results

In order to discuss the dynamic behavior of system (1), we firstly introduce the following definition.

Definition 1 [28] Let $A = [a_{ij}] \in R^{n \times n}$, where $a_{ij} < 0$ if $i \neq j$, and the sum of each column element of the matrix is positive, then the matrix is a nonsingular $M$ matrix and $A^{-1} \geq 0$.

Lemma 1 System (1) has unique disease-free equilibrium.

Proof. By the definition of the disease-free equilibrium, substituting $I_i = 0$ ($i = 1, 2, \cdots, n$) into (1), we have

$$
\begin{align*}
&b_i - \beta_i S_i (1 - z_i) v_i E_i - \mu_i S_i + \sum_{j \neq i} (a_{ij} S_j - a_{ji} S_i) = 0, \\
&\beta_i S_i (1 - z_i) v_i E_i - (q_i + \sigma_i + \mu_i) E_i + \sum_{j \neq i} (b_{ij} E_j - b_{ji} E_i) = 0, \\
&\sigma_i E_i = 0, \\
&q_i E_i - (\alpha_i + \mu_i) Q_i = 0, \\
&(\alpha_i Q_i + g_i) H_i = 0, \\
&\eta_i H_i - \mu_i R_i + \sum_{j \neq i} (d_{ij} R_j - d_{ji} R_i) = 0, i = 1, 2, \cdots, n.
\end{align*}
$$

Then

$$
\begin{align*}
&b_i - \mu_i S_i + \sum_{j \neq i} (a_{ij} S_j - a_{ji} S_i) = 0, \\
&-\mu_i R_i + \sum_{j \neq i} (d_{ij} R_j - d_{ji} R_i) = 0, i = 1, 2, \cdots, n,
\end{align*}
$$

that is

$$
\begin{align*}
&G_1 S = B, \\
&G_2 R = 0,
\end{align*}
$$

where

$$
S = (S_1, S_2, \cdots, S_n)^T, B = (b_1, b_2, \cdots, b_n)^T, R = (R_1, R_2, \cdots, R_n)^T.
$$
Therefore, \( \sum_{j \neq i} x_{ji} \geq 0 \) and \( G_1^{-1} \geq 0 \). Therefore, \( (2) \) has unique solution \( S^0 = (S_0^0, S_0^0, \cdots, S_n^0) \) \( G_1^{-1}B \) and \( R^0 = 0 \).

Thus, system (1) has unique disease-free equilibrium \( C_0 = (S^0, 0, 0, 0, 0, 0) \).

The proof is completed.

**Lemma 2** \( \Gamma = \{ (S_1, E_1, I_1, Q_1, H_1, R_1, \cdots, S_n, E_n, I_n, Q_n, H_n, R_n) \in \mathbb{R}^{6n} | N(t) \leq \frac{\bar{B}}{\mu^*}, 0 \leq S_i \leq S_i^0, i = 1, 2, \cdots, n \} \) is a positively invariant set for system (1).

where \( \bar{B} = \sum_{i=1}^{n} b_i, \mu^* = \min \{ \mu_i, \theta, g_i \} \), and \( N(t) = \sum_{i=1}^{n} (S_i + E_i + I_i + Q_i + H_i + R_i) \).

**Proof.** In term of system (1), we have

\[
\dot{N}(t) = \bar{B} - \sum_{i=1}^{n} (\mu_i S_i + \mu_i E_i + \theta_i I_i + \mu_i Q_i + g_i H_i + \mu_i R_i) + \sum_{j \neq i} \sum_{i=1}^{n} (a_{ij} S_j - a_{ji} S_i) + \sum_{j \neq i} (b_{ij} S_j - b_{ji} S_i) + \sum_{j \neq i} (c_{ij} S_j - c_{ji} S_i) + \sum_{j \neq i} (d_{ij} S_j - d_{ji} S_i)
\]

\[
= \bar{B} - \sum_{i=1}^{n} (\mu_i S_i + \mu_i E_i + \theta_i I_i + \mu_i Q_i + g_i H_i + \mu_i R_i)
\]

\[
\leq \bar{B} - \mu^* N(t).
\]

Therefore

\[
N(t) \leq (N(0) - \frac{\bar{B}}{\mu^*})e^{-\mu^* t} + \frac{\bar{B}}{\mu^*},
\]

where \( N(0) \) is initial population.

Therefore, \( N(t) \leq \frac{\bar{B}}{\mu^*} \) if and only if \( N(0) \leq \frac{\bar{B}}{\mu^*} \).

From the first equation of system (1), we have

\[
\frac{dS_i}{dt} \leq b_i - \mu_i S_i + \sum_{j=1}^{n} (a_{ij} S_j - a_{ji} S_i) = (G_1 S^0 - G_1 S)_i,
\]

where \( G_1 \) and \( G_2 \) are nonsingular M-matrix, then \( G_1^{-1} \geq 0 \) and \( G_1^{-1} \geq 0 \). Therefore, \( (2) \) has unique solution \( S^0 = (S_0^0, S_0^0, \cdots, S_n^0) \) \( G_1^{-1}B \) and \( R^0 = 0 \).
where \((G_i S^0 - G_i S_i)\) is the \(i\)th element of \(G_i S^0 - G_i S\).
Therefore \(\frac{dS_i}{dt} \leq 0\) if and only if \(S_i = S^0\), \(i = 1, 2, \cdots, n\).

The proof is completed.

Based on Lemma 2, the dynamical properties of the system (1) are studied only in \(\Gamma\). Now, we are in the position to discuss the basic reproduction number of the system (1).

Define \(F = \begin{bmatrix} F_{11} & F_{12} \\ 0 & 0 \end{bmatrix}\) and \(V = \begin{bmatrix} V_{11} & 0 \\ V_{21} & V_{22} \end{bmatrix}\), where
\[
F_{11} = \text{diag}(v'_1, v'_2, \cdots, v'_n), \quad v'_i = (1 - z_i)\beta_i v_i S^0_i,
\]
\[
F_{12} = \text{diag}(u_1, u_2, \cdots, u_n), \quad u_i = (1 - z_i)\beta_i S^0_i,
\]
where \(z_i \in (0, 1)\).

\[
V_{11} = \begin{bmatrix}
(q_1 + \sigma_1 + \mu_1) + \sum_{j \neq 1} b_{1j} & -b_{12} & \cdots & -b_{1n} \\
-b_{21} & (q_2 + \sigma_2 + \mu_2) + \sum_{j \neq 2} b_{2j} & \cdots & -b_{2n} \\
\vdots & \vdots & \ddots & \vdots \\
-b_{n1} & -b_{n2} & \cdots & (q_n + \sigma_n + \mu_n) + \sum_{j \neq n} b_{jn}
\end{bmatrix},
\]
\[
V_{21} = \begin{bmatrix}
(\delta_1 + \gamma_1 + \theta_1) + \sum_{j \neq 1} c_{1j} & -c_{12} & \cdots & -c_{1n} \\
-c_{21} & (\delta_2 + \gamma_2 + \theta_2) + \sum_{j \neq 2} c_{2j} & \cdots & -c_{2n} \\
\vdots & \vdots & \ddots & \vdots \\
-c_{n1} & -c_{n2} & \cdots & (\delta_n + \gamma_n + \theta_n) + \sum_{j \neq n} c_{jn}
\end{bmatrix},
\]
\[
V_{22} = \begin{bmatrix}
(q_1 + \sigma_1 + \mu_1) + \sum_{j \neq 1} b_{1j} & -b_{12} & \cdots & -b_{1n} \\
-b_{21} & (q_2 + \sigma_2 + \mu_2) + \sum_{j \neq 2} b_{2j} & \cdots & -b_{2n} \\
\vdots & \vdots & \ddots & \vdots \\
-b_{n1} & -b_{n2} & \cdots & (q_n + \sigma_n + \mu_n) + \sum_{j \neq n} b_{jn}
\end{bmatrix}.
\]

By using the method in Driessche and Watmough [28], the basic reproduction number \(R_0\) can be determined by computing the spectral radius of matrix
\[
FV^{-1} = \begin{bmatrix} F_{11}V_{11}^{-1} & F_{12}V_{21}^{-1} \\ 0 & V_{22}^{-1} \end{bmatrix},
\]
that is \(R_0 = \rho(FV^{-1}) = \rho(F_{11}V_{11}^{-1} - F_{12}V_{21}^{-1}V_{22}^{-1})\).

Lemma 3 [29] If \(J_1\) is a nonnegative matrix and \(J_2\) is a nonsingular matrix, then
\[
s(J_1 - J_2) < 0 \iff \rho(J_1J_2^{-1}) < 1\] and \(s(J_1 - J_2) > 0 \iff \rho(J_1J_2^{-1}) > 1\).

Theorem 1 The disease-free equilibrium \(C_0\) is globally asymptotically stable if \(R_0 < 1\) and the disease-free equilibrium \(C_0\) is unstable if \(R_0 > 1\).

Proof. From the second equations and the third equations of system (1), we have
\[
\dot{X} = (F - V)X,
\]
where \(X = (E_1, E_2, \cdots, E_n, I_1, I_2, \cdots, I_n)^T\).

Since \(F\) is a nonnegative matrix and \(V\) is a nonsingular matrix, it follows from Lemma 3 that
\[
S(F - V) > 0 \iff R_0 = \rho(FV^{-1}) > 1.
\]

Thus, the disease-free equilibrium \(C_0\) is unstable if \(R_0 > 1\).
Next, we prove $C_0$ is globally asymptotically stable if $R_0 < 1$. Since
\[ V^{-1}F = V^{-1}FV^{-1}V, \]
then $V^{-1}F$ is similar to $FV^{-1}$. Therefore,
\[ \rho(V^{-1}F) = \rho(FV^{-1}) = R_0. \]
Since $V^{-1}F$ is a nonnegative irreducible matrix, by Perron-frobenius theorem [28], $V^{-1}F$ have a positive left eigenvector $x$ and
\[ xV^{-1}F = \rho(V^{-1}F)x. \]
Let $x = (e_1, e_2, \ldots, e_n, r_1, r_2, \ldots, r_n)$, then
\[ (e_1, e_2, \ldots, e_n, r_1, r_2, \ldots, r_n)V^{-1}F = R_0(e_1, e_2, \ldots, e_n, r_1, r_2, \ldots, r_n). \]
Let $W = \sum_{i=1}^{n} k_i E_i + \sum_{i=1}^{n} l_i I_i$ be a candidate Lyapunov function, where $(k_1, k_2, \ldots, k_n, l_1, l_2, \ldots, l_n) = (e_1, e_2, \ldots, e_n, r_1, r_2, \ldots, r_n)V^{-1}$. Then, calculate the derivative of $W$ along the solution of system (1), we have
\[ W = \sum_{i=1}^{n} (k_i \frac{dE_i}{dt} + l_i \frac{dI_i}{dt}) \]
\[ = \sum_{i=1}^{n} k_i \left[ \beta_i S_i(1 - z_i)(v_i E_i + I_i) - (q_i + \sigma_i + \mu_i)E_i + \sum_{j \neq i}^{n} (b_{ij}E_j - b_{ji}E_i) \right] \]
\[ + \sum_{i=1}^{n} l_i \left[ \sigma_i E_i - (\delta_i + \gamma_i + \theta_i)I_i + \sum_{j \neq i}^{n} (c_{ij}I_j - c_{ji}I_i) \right] \]
\[ \leq \sum_{i=1}^{n} k_i \left[ \beta_i s_i^0(1 - z_i)(v_i E_i + I_i) - (q_i + \sigma_i + \mu_i)E_i + \sum_{j \neq i}^{n} (b_{ij}E_j - b_{ji}E_i) \right] \]
\[ + \sum_{i=1}^{n} l_i \left[ \sigma_i E_i - (\delta_i + \gamma_i + \theta_i)I_i + \sum_{j \neq i}^{n} (c_{ij}I_j - c_{ji}I_i) \right] \]
\[ = (k_1, k_2, \ldots, k_n) [(F_{11} - V_{11}) E + F_{12} I] - (l_1, l_2, \ldots, l_n)(V_{21} + V_{22} I) \]
\[ = (e_1, e_2, \ldots, e_n, r_1, r_2, \ldots, r_n)V^{-1}(F - V)X \]
\[ = (e_1, e_2, \ldots, e_n, r_1, r_2, \ldots, r_n)(V^{-1}F - E)X \]
\[ = (e_1, e_2, \ldots, e_n, r_1, r_2, \ldots, r_n)(R_0 - 1)X, \]
where $E = (E_1, E_2, \ldots, E_n)^T$, and $I = (I_1, I_2, \ldots, I_n)^T$. If $R_0 < 1$, then $W \leq 0$, and $W = 0$ if and only if $S_i = s_i^0$ or $E_i = 0$, $I_i = 0$, $i = 1, 2, \ldots, n$. Thus, $C_0$ is globally asymptotically stable if $R_0 < 1$.
The proof is completed.

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4 Numerical simulations

In this section, some numerical simulations on a three-patch SEIR epidemic model are presented to verify the theoretical results. The effects of migration rate and quarantined rate on the basic reproduction number are also discussed. The model is as follows.

\[
\begin{align*}
\frac{dS_i}{dt} &= b_i - \beta_i S_i (1 - z_i) (v_i E_i + I_i) - \mu_i S_i + \sum_{j \neq i} a_{ij} S_j - a_{ji} S_i, \\
\frac{dE_i}{dt} &= \beta_i S_i (1 - z_i) (v_i E_i + I_i) - (\sigma_i + \mu_i) E_i + \sum_{j \neq i} (b_{ij} E_j - b_{ji} E_i), \\
\frac{dI_i}{dt} &= \sigma_i E_i - (\delta_i + \gamma_i + \theta_i) I_i + \sum_{j \neq i} (c_{ij} I_j - c_{ji} I_i), \\
\frac{dQ_i}{dt} &= q_i E_i - (\alpha_i + \mu_i) Q_i, \\
\frac{dR_i}{dt} &= \gamma_i I_i + \eta_i H_i - \mu_i R_i + \sum_{j \neq i} (d_{ij} R_j - d_{ji} R_i),
\end{align*}
\]  

(3)

where \( i = 1, 2 \) and 3 represent Wuhan, Huanggang, and Huangshi, respectively. It is assumed that \( a_{ij} = b_{ij} = c_{ij} = d_{ij} = p_{ij}, i, j = 1, 2, 3 \), and \( i \neq j \), where \( p_{ij} \) is the migration rate from the \( j \)-th patch to the \( i \)-th patch. The migration matrix is \( P = (p_{ij}) \), where \( p_{ii} = 0, i = 1, 2, 3 \). The data are mainly from Hubei Provincial Health Commission, National Bureau of Statistics, Baidu Migration and related literature. According to the data of Hubei Provincial Bureau of Statistics [30], \( \mu_i \) and \( b_i \) are obtained. It is assumed that \( \gamma_i = \eta_i, \theta_i = q_i \) from January 10 to January 25 because of the lack of medical awareness of COVID-19 in the early stages of its development. The values of \( \theta_i \) and \( \gamma_i \) are taken as the average death rate and cure rate of confirmed infected persons in Hubei Province from January 10 to January 25 [31], respectively. The values of \( q_i \) and \( \eta_i \) are taken as the average death rate and cure rate of confirmed infected persons in Hubei Province from January 10 to March 31 [31], respectively. At the early stage of the city closure in Wuhan, it is assumed that \( (R_0^1, R_0^2, R_0^3) = (3.66, 2.28, 2.26) \) [27] and \( z_i = q_i = 0, i = 1, 2, 3 \), where \( R_0^i \) represent the reproduction number in the \( i \)-th patch. According to the above parameters, the disease transmission coefficients can be calculated by MATLAB. The parameters of system (3) are shown in Table 1.

|       | \( i = 1 \)          | \( i = 2 \)          | \( i = 3 \)          | source       |
|-------|----------------------|----------------------|----------------------|--------------|
| \( \beta_i \) | \( 2.5 \times 10^{-8} \) | \( 1.35 \times 10^{-8} \) | \( 3.13 \times 10^{-8} \) | Parameter estimation |
| \( v_i \)     | 1.5                  | 1.5                  | 1.5                  | [27]          |
| \( \sigma_i \) | 0.2                  | 0.2                  | 0.2                  | [10]          |
| \( \mu_i \)   | \( 3.18 \times 10^{-5} \) | \( 1.44 \times 10^{-5} \) | \( 1.5 \times 10^{-5} \) | data          |
| \( \delta_i \) | 0.1328               | 0.1328               | 0.1328               | [27]          |
| \( \gamma_i \) | 0.042                | 0.042                | 0.042                | data          |
| \( \theta_i \) | 0.01                 | 0.01                 | 0.01                 | data          |
| \( g_i \)     | 0.004                | 0.004                | 0.004                | data          |
| \( b_i \)     | 360                  | 191                  | 84                   | data          |
| \( \eta_i \)  | 0.055                | 0.055                | 0.055                | data          |
| \( \alpha_i \) | 0.1259               | 0.1259               | 0.1259               | [27]          |
Table 1 Parameter data and sources of Wuhan, Huanggang and Huangshi in Hubei Province, China.

Case I: Migration of people is not restricted and quarantine strategy is not taken.

Let \( q_i = 0, z_i = 0, i = 1, 2, 3 \), and \( P = P_0 = \begin{bmatrix} 0 & 0.007 & 0.0016 \\ 0.004 & 0 & 0.0011 \\ 0.0026 & 0.0009 & 0 \end{bmatrix} \), where \( P_0 \) is taken as the average of the migration rate of each city from January 10, 2020 to January 25, 2020 on Baidu migration [32]. With the chosen parameters, the basic reproduction number \( R_0 = 5.0312 \) > 1, which implies that the disease-free equilibrium is unstable by Theorem 1.

In Fig. 2, the simulation started on January 10, 2020. Assume the initial number of susceptible individuals is equal to the number of permanent residents in the city. Since there were no infectious people in Huanggang and Huangshi on January 10, 2020, other initial values for Huanggang and Huangshi are zero. Thus, \( (S_1(0), S_2(0), S_3(0)) = (11081000, 6330000, 2740700) \) [30], \( (E_1(0), I_1(0), Q_1(0), H_1(0), R_1(0)) = (600, 410, 20, 41, 2) \) [27] and \( (E_i(0), I_i(0), Q_i(0), H_i(0), R_i(0)) = (0, 0, 0, 0, 0), i=2,3 \). Fig. 2(a)-(c) implies that outbreaks will occur in these three cities and Fig.2(d) implies that the disease will persist and become endemic.

Fig. 2 Time evolution of individuals when \( P = P_0, q_i = 0, z_i = 0, i = 1, 2, 3 \).

Case II: Migration of people is restricted and quarantine strategy is taken.
Let \( q_i = 0.5, z_i = 0.3, i = 1, 2, 3, \) and \( P = \begin{bmatrix}
0 & 0.001 & 0.001 \\
0.001 & 0 & 0.001 \\
0.001 & 0.001 & 0
\end{bmatrix}. \) Then the disease-free equilibrium \( C_0 = (S^0, 0, 0, 0, 0), \) where \( S^0 = (1.0383 \times 10^7, 1.0387 \times 10^7, 1.0349 \times 10^7). \) By calculating, we have \( R_0 = 0.8304 < 1. \) Therefore, the disease-free equilibrium is asymptotic stability by Theorem 1.

Assume these conditions are the same as those in case I. The simulation results are shown in Fig. 3. Fig. 3(a)-(c) shows the number of infected individuals in each city is gradually decreasing and finally the disease disappears. Fig. 3(d) shows the trajectories converge to the disease-free equilibrium \( C_0. \)

**Fig. 3** Time evolution of individuals when \( P = 0, q_i = 0.5, z_i = 0.3, i = 1, 2, 3. \)

In the following, the effect of migration rate and quarantined rate on \( R_0 \) is discussed by numerical simulations, respectively.

First, we assume that \( q_i = 0.4, z_i = 0.2, i = 1, 2, 3 \) and the migration rate between any two cities is the same. The effect of migration rate on \( R_0 \) is shown in Fig. 4. Fig.4(a) shows \( R_0 \) decreases with the increasing of migration rate at the beginning and then increases with the increase of migration rate. This is because that there is no infectious people in Huanggang, and Huangshi at the beginning, and then there are many people begin to be infected since there is no constricted on migration. In Fig. 4(b), we can find that \( R_0 \) decreases with the increasing of migration rate when migration rate exceeds certain threshold. This is an interest-
ing phenomenon. But how to explain this phenomenon by theoretical analysis is difficult in the frame of this paper. We left it for future study.

![Graph](image1)

**Fig. 4** The effect of migration rate on $R_0$.

Second, the simulation for the effect of quarantined rate on $R_0$ for $P = P_0$ and $P = 0$, respectively, is shown in Fig. 5.

![Graph](image2)

**Fig. 5** The effect of quarantined rate on $R_0$.

In Fig. 5, the red solid represent quarantined rate of exposed individuals where $P = P_0$, $z_i = 0$, $i = 1, 2, 3$; black solid represent self-quarantined rate of susceptible individuals where $P = P_0$, $q_i = 0$, $i = 1, 2, 3$; blue solid represent both kinds of quarantine strategies are performed simultaneously where $P = P_0$, $q_i = z_i$, $i = 1, 2, 3$; red dotted represent quarantined rate of exposed individuals where $P = 0$, $z_i = 0$, $i = 1, 2, 3$; black dotted represent self-quarantined rate of susceptible individuals where $P = 0$, $q_i = 0$, $i = 1, 2, 3$; blue dotted represent both kinds of quarantine strategies are performed simultaneously where $P = 0$, $q_i = z_i$, $i = 1, 2, 3$. 
Fig. 5 shows $R_0$ decreases with the increase of quarantined rate. Compared with self-quarantine of susceptible individuals, quarantine of exposed individuals has a greater effect on $R_0$. The simultaneous execution of both quarantine strategies has the greatest impact on $R_0$. Moreover, stricter quarantine strategy need to be enforced when $P = P_0$ than when $P = 0$ to make the epidemic disappears. Therefore, to control the transmission of COVID-19 better, self-quarantine of susceptible and quarantine of exposed need to be executed, and the population migration needs to be properly controlled.

5 Conclusion

In this paper, based on epidemiological characteristics of COVID-19 and government intervention strategy, an n-patch SEIR epidemic model is presented. It is shown that system (1) has unique disease-free equilibrium $C_0$. Moreover, $C_0$ is globally asymptotically stable if $R_0 < 1$ and it is unstable if $R_0 > 1$. A three-patch SEIR epidemic model is formulated to explore the effect of migration rate and quarantined rate on the basic reproduction number. The numerical results show that appropriate controls on migration and quarantined rate are necessary to prevent outbreaks.

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Conflict of interest

The authors declare that they have no conflict of interest.

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