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MODELING AND ANALYZING QUARANTINE STRATEGIES OF EPIDEMIC ON TWO-LAYER NETWORKS: GAME THEORY APPROACH

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The quarantine strategy plays a crucial role in the prevention and control of infectious disease. In this paper, a two-layer network model coupling the transmission of infectious diseases and the dynamics of human behavior based on game theory is proposed. The basic reproduction number of the infectious disease in our proposed model is obtained by the next-generation matrix method and the stability of the disease-free equilibrium is analyzed. Theoretical results show that the spread of infectious diseases can be controlled when the voluntary quarantined individuals reach a certain proportion. The sensitivities of the parameters are analyzed by simulations, and the results show that increasing propaganda can directly accelerate quarantine, and reducing the relative cost of quarantine has a significant effect on preventing the infectious diseases. Increasing the detection rate will lead to overestimating the proportion of undiagnosed infected individuals, and can also promote individuals to quarantine.

Keywords: Human behavior; infectious diseases; two-layer networks.

1. Introduction

The outbreak of coronavirus disease 2019 in many countries has attracted great attention from governments and researchers.[1] Under a variety of defensive measures, the spread of COVID-19 has still not been controlled. Looking back at the entire outbreak, human behavior has played an important role in inhibiting the spread

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of the epidemic.[2] It is found that wearing masks, isolation and other non-drug measures are effective in curbing the epidemic.[3]

Isolation, face masks,[3] and eye protection are key measures to prevent the epidemics.[4] Khan *et al.*[5] formulated a model with quarantine and isolation, in which isolation is one of the states (Q). A novel model of control measures was proposed in Ref. 6, in which quarantined susceptible (Sq) and suspected population (B) were considered. Zhao and Chen[7] developed a Susceptible, Un-quarantined infected, Quarantined infected, Confirmed infected (SUQC) model to characterize the dynamics of COVID-19. The results showed that the quarantine and control measures are effective in preventing the spread of the epidemic. In these papers, isolation is represented as a state that changes at a fixed rate, reducing the randomness of human behavior. Zhao *et al.*[8] developed a compartmental epidemic model based on the classic SEIR model and behavioral imitation through a game theoretical decision-making process to study and project the dynamics of the COVID-19 outbreak in Wuhan, China. These results show that increasing sensitivity to take infection prevention actions and the effectiveness of infection prevention measures are likely to mitigate the COVID-19 outbreak in Wuhan. These papers assume that individuals take protective measures at a fixed rate, but in practice, individuals will adjust their strategies according to the surrounding infection degree and other information. Therefore, our research in this paper uses game theory to describe the human behaviors.

The application of game theory to the coupling model of epidemic disease and human behavior has been studied for a long time.[9] Zhang *et al.*[10] proposed an evolutionary epidemic model coupled with human behaviors where they assume that individuals have three strategies: vaccination, self-protection and laissez faire. They found that increasing the successful rate of self-protection does not necessarily reduce the epidemic size or improve the system payoff. A coupled model of human behavior and disease transmission was proposed in previous work[11] where both individual-based risk assessment and neighbor-based replicator dynamics are taken into account. Their results showed that the change of human behavior can effectively inhibit the spread of the disease. Lim and Zhang[12] experimentally investigated vaccination choices of people in the context of a nonlinear public good game. Ning *et al.*[13] studied the epidemic transmission process using an evolutionary game model of complex networks. There are many researches on individual behavior based on game theory, but they are limited to theoretical research. Meng *et al.*[14] established an SEIRV model and an evolutionary model to analyze the difference between mandatory vaccination method and voluntary vaccination method. Using the SARS-CoV-2 pandemic data from Wuhan, China, their results showed that when the effectiveness rate of vaccination is 0.75, the vaccination cost should not be higher than 0.886 so that the vaccination strategy can be implanted in the population. This paper considers the impact of vaccination on infectious diseases, and studies that quarantine is a better defense strategy before vaccines are developed. A model framework that integrates COVID-19 transmission dynamics with a multi-strategy evolutionary game approach of individual decision-making is developed.[15] The model we proposed only analyzes the dynamics of uniform mixed networks and ignores the influence of networks.

In this paper, a two-layer network model that couples human behavior with epidemics is proposed and studied. The infection process will change accordingly with the changes in human behavior whose dynamics are modeled through game theory. The sensitivity of parameters on infectious diseases and human behavior is analyzed by simulations.

The rest of this paper is organized as follows. The model is introduced in Sec. 2. The simulations are conducted and the results are summarized in Sec. 3. Further discussion is presented in Sec. 4.

2. Methods

In this paper, we present a model of combining epidemics and human behavior based on a two-layer network. The spread of the epidemic is formulated on the actual contact network as one can be infected only through physical contacts. Previous studies have revealed that scale-free networks are closer to real networks.[16] The decision whether individuals choose to quarantine is affected by information about epidemics. Individuals can get information about infectious diseases in various ways, such as social networks, webs, and neighbors. The information, such as cumulative number of infections, cumulative number of deaths, and imported cases from abroad, obtained by each individual is the same, so we assume that human behavior changes on a fully connected network, and the network structure diagram is shown in Fig. 1.

The two-layer network shown in Fig. 1 has the same number of nodes N, and there is a one-to-one correspondence between nodes. The quarantine behavior influences the spread of epidemics, and the spread of epidemics also influences the change

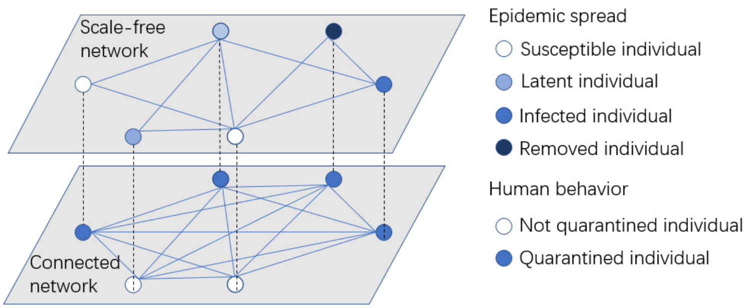

Fig. 1. Network diagram of the model. The upper layer supports epidemic spreading. The lower layer supports human behavior dynamic.

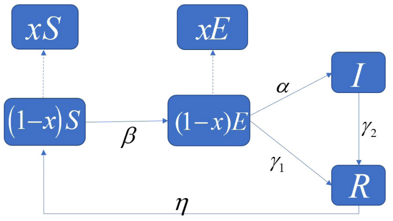

Fig. 2. Schematic diagram of epidemic status transition.

of human behavior. Nodes within a single layer network affect each other, and the corresponding nodes between two-layer networks also affect each other.

2.1. *The epidemic model*

Individuals are divided into four compartments: susceptible (S), undiagnosed infected (E), diagnosed infected (I) and recovered (R). The undiagnosed infected compartment includes latent individuals, asymptomatic infected individuals, undetected infected individuals, etc. The diagnosed infected individuals will be isolated at home or treated in hospital. The schematic diagram of the epidemic is shown in Fig. 2. Here, x represents the probability of individuals taking quarantine measures voluntarily. Susceptible individuals are infected through contacts with undiagnosed infected individuals.

We assume that the diagnosed infected individuals are isolated and have no ability to infect others. The following epidemic model is formulated:

$$\begin{cases} \dot{S}_k(t) = -\beta k(1-x)^2 S_k(t)\Theta(t) + \eta R_k(t), \\ \dot{E}_k(t) = \beta k(1-x)^2 S_k(t)\Theta(t) - (\alpha+\gamma_1)E_k(t), \\ \dot{I}_k(t) = \alpha E_k(t) - \gamma_2 I_k(t), \\ \dot{R}_k(t) = \gamma_1 E_k(t) + \gamma_2 I_k(t) - \eta R_k(t). \end{cases} \tag{2.1}$$

Here, $\Theta(t) = \sum_k kp(k)E_k(t)/\langle k\rangle$, is the probability that any edge points to the undiagnosed infected individuals. $p(k)$ represents the degree distribution of the network. k represents the degree of nodes, and $k = 1, 2, \ldots, N$. $S_k(t)$, $E_k(t)$, $I_k(t)$, $R_k(t)$, respectively, represent the proportion of susceptible, undiagnosed infected, diagnosed infected, and recovered individuals with degree k at time t. Let $S_k(t) + E_k(t) + I_k(t) + R_k(t) = 1$, $k = 1, 2, \ldots, N$. The number of nodes in the network is N, the variable $x(t)$ is the probability of quarantine at time t, it will be explained in detail later. β is the infection rate, α is the rate at which undiagnosed infected individuals are diagnosed, γ_1 is the recovery rate of undiagnosed infected individuals, and γ_2 is the recovery rate of diagnosed infected individuals. η is the rate of loss of immunity of recovered individuals. Let $R_k(t) = 1 - S_k(t) - E_k(t) - I_k(t)$.

The system will become:

$$\begin{cases} \dot{S}_k(t) = -\beta k(1-x)^2 S_k(t)\Theta(t) + \eta(1 - S_k(t) - E_k(t) - I_k(t)), \\ \dot{E}_k(t) = \beta k(1-x)^2 S_k(t)\Theta(t) - (\alpha+\gamma_1)E_k(t), \\ \dot{I}_k(t) = \alpha E_k(t) - \gamma_2 I_k(t). \end{cases} \tag{2.2}$$

Let $E_k = 0$ and $I_k = 0$. The disease-free equilibrium (DFE) of system (2.2) is $E^0 = (1,\dots,1,0,\dots,0,0,\dots,0)$. The next-generation matrix method proposed by Driessche and Watmough in 2002 is adopted to calculate the basic reproduction number.[17] The non-negative matrix, $\mathscr{F}$, of the infection terms and the non-singular M-matrix, $\mathscr{V}$, of the transition terms, are given by

$$\mathscr{F} = \begin{pmatrix} F_{11} & 0 \\ 0 & 0 \end{pmatrix}, \quad \mathscr{V} = \begin{pmatrix} V_{11} & 0 \\ V_{21} & V_{22} \end{pmatrix}.$$

Here,

$$F_{11} = \frac{\beta}{\langle k\rangle}\left(\begin{pmatrix} 1 \\ 2 \\ \vdots \\ N \end{pmatrix}(1\times p(1) 2\times p(2)\cdots N\times p(N))\right),$$

$$V_{11} = -(\alpha+\gamma_1)E, \quad V_{21} = \alpha E, \quad V_{22} = -\gamma_2 E,$$

E is the identity matrix. The basic reproduction number R_0 is equal to the spectral radius of the next-generation matrix $\rho(\mathscr{F}\mathscr{V}^{-1})$, i.e.,

$$R_0 = \frac{\beta\langle k^2\rangle}{(\alpha+\gamma_1)\langle k\rangle}.$$

Theorem 1. *When $R_0 < 1$, the DFE of system (2.2) is stable. When $R_0 > 1$, the DFE of system (2.2) is unstable.*

Proof. The Jacobian matrix of system (2.2) at the DFE is

$$J = \begin{pmatrix} -\eta E & J_1 - \eta E & -\eta E \\ 0 & -J_1 - (\alpha+\gamma_1)E & 0 \\ 0 & \alpha E & -\gamma_2 E \end{pmatrix}. \tag{2.3}$$

Here, 0 is a zero matrix of $N \times N$ and E is the identity matrix of $N \times N$.

$$J_1 = -\frac{\beta}{\langle k\rangle}\left(\begin{pmatrix} 1 \\ 2 \\ \vdots \\ N \end{pmatrix}(1\times p(1) 2\times p(2)\cdots N\times p(N))\right).$$

$-J_1 - (\alpha + \gamma_1)E$ has N identical eigenvalues $-(\alpha + \gamma_1)$ and another eigenvalue $-(\alpha + \gamma_1) + \beta\frac{\langle k^2 \rangle}{\langle k \rangle}$. The eigenvalues of the matrix J are $\lambda_1 = \lambda_2 = \cdots = \lambda_N = -\eta$, $\lambda_{N+1} = \cdots = \lambda_{2N} = -\gamma_2$, $\lambda_{2N+1} = \cdots = \lambda_{3N-1} = -(\alpha + \gamma_1)$, $\lambda_{3N} = -(\alpha + \gamma_1) + \beta\frac{\langle k^2 \rangle}{\langle k \rangle}$. It is obvious that $\lambda_1, \ldots, \lambda_{3N-1} \leq 0$. When $R_0 < 1$, $\lambda_{3N} < 0$, all eigenvalues of J are non-positive and the DFE is stable. Otherwise, the DFE is unstable. □

2.2. *Model with quarantine*

We assume that individuals will decide whether to change their behavior by comparing the payoffs. They update their strategy by Fermi update rule.[18] Individuals compare the payoffs and change strategy by the following probability:

$$w_{i\to j} = \frac{1}{1 + \exp[-\varepsilon(p_j - p_i)]},$$

where ε indicates the individual sensitivity to the payoff differences; p_i represents the payoff of strategy i; and p_j represents the payoff of strategy j. The expression of $w_{i\to j}$ indicates that the larger the ε, the greater impact of the payoff difference on the strategy choice.

Susceptible and undiagnosed infected individuals can decide either to quarantine (Q) or non-quarantine (R). It is assumed that the recovered individuals will have no influence on the quarantine choice. The individuals is divided into four categories based on whether they are voluntarily quarantine: susceptible and quarantine, susceptible and non-quarantine, undiagnosed infected and quarantine, undiagnosed infected and non-quarantine. In practice, there is no difference between susceptible individuals and undiagnosed infected individuals. The variable $x(t)$ is the probability of quarantine at time t.

Suppose the relative cost of quarantine to the cost of infection is q_1 and $0 < q_1 < 1$. For simplicity, the cost of an infected individual is assumed to be 1. For those who do not choose to quarantine, there is a risk of infection. The proportion of undiagnosed infected is unknown, so individuals can only perceive the risk of being infected according to the proportion of diagnosed infected. It is assumed that the perceived risk of infection by non-quarantined individuals is positively correlated with the number of reported infections. The payoffs are summarized as follows:

$$p_i = \begin{cases} -q_1, & \text{quarantine}, \\ -(1 + q_1)\overline{I(t)}, & \text{not quarantine}. \end{cases} \tag{2.4}$$

The notation $\overline{I(t)}$ denotes the average level of diagnosed infected individuals in the network, $\overline{I(t)} = \sum_k p(k)I_k(t)$. $I(t)$ represents the reported infections. Since $\overline{I(t)}$ is close to the reported infection, we use $\overline{I(t)}$ to approximate $I(t)$. Similarly, we defined that $\overline{E(t)} = \sum_k p(k)E_k(t)$.

Individuals who choose quarantine strategies learn strategies of non-quarantine individuals and change their strategy with a certain probability, so that x will decrease:

$$x^- = x(t)(1 - x(t))w_{Q\to R}.$$

Individuals who choose non-quarantine strategies learn strategies of quarantine individuals and change their strategy with a certain probability, so that x will increase:

$$x^+ = x(t)(1 - x(t))w_{R\to Q}.$$

Combining the above two formulas, we get the evolutionary game equation of x as follows:

$$\frac{dx(t)}{dt} = \delta(x^+ - x^-).$$

Here, δ represents the speed of behavior change relative to the speed of epidemic. The human behavior dynamics can be described as follows:

$$\frac{dx}{dt} = \delta x(1 - x)(\omega_{R\to Q} - \omega_{Q\to R}).$$

Because

$$\begin{aligned}\omega_{R\to Q} - \omega_{Q\to R} &= \frac{1}{1 + \exp[-\varepsilon(p_Q - p_R)]} - \frac{1}{1 + \exp[-\varepsilon(p_R - p_Q)]}\\ &= \tanh\left[-\frac{\varepsilon}{2}(p_R - p_Q)\right].\end{aligned}$$

After straightforward algebra calculations, it becomes

$$\frac{dx}{dt} = \delta x(1 - x)\tanh\left(\frac{\varepsilon}{2}(p_Q - p_R)\right).$$

0 and 1 are two constant solutions of the dynamical system.

When $p_Q = p_R$, $I(t) = \frac{q_1}{1+q_1}$, $\frac{dx^*}{dt} = 0$. It is only when $I(t) < \frac{q_1}{1+q_1}$, that $x \to 0$, when $t \to \infty$.

A not-quarantined susceptible individual becomes infected only when he/she comes into contact with an undiagnosed and non-quarantine infected individual. The epidemic model will become:

$$\begin{cases}\dot{S}_k(t) = -\beta k(1 - x)^2 S_k(t)\Theta(t) + \eta(1 - S_k(t) - E_k(t) - I_k(t)),\\ \dot{E}_k(t) = \beta k(1 - x)^2 S_k(t)\Theta(t) - (\alpha + \gamma_1)E_k(t),\\ \dot{I}_k(t) = \alpha E_k(t) - \gamma_2 I_k(t),\\ \dot{x}(t) = \delta x(1 - x)\tanh\left(\frac{\varepsilon}{2}(p_Q - p_R)\right).\end{cases} \tag{2.5}$$

According to the next generation matrix method, the basic reproduction number can be obtained as

$$R_0^* = \frac{\beta(1 - x^*)^2\langle k^2\rangle}{(\alpha + \gamma_1)\langle k\rangle}.$$

When $R_0^* < 1$, the DFE is stable. The expression of $R_0^* = \frac{\beta(1-x^*)\langle k^2\rangle}{(\alpha+\gamma_1)\langle k\rangle} < 1$ gives $x^* > 1 - \frac{1}{\sqrt{R_0}}$. In other words, when the quarantine probability reaches $1 - \frac{1}{\sqrt{R_0}}$, the infectious disease will be controlled. It can be found that this probability is smaller than that of vaccination to meet the needs of group immunization $1 - \frac{1}{R_0}$.[19]

3. Results

Quarantine strategy is one of the most effective methods to control the spread of infectious disease. In this paper, we propose a two-layer network model, in which one layer is the actual contact network to simulate the disease transmission dynamics, and the other layer is the virtual social network to simulate the behavior dynamics of individuals. Starting with a network with five nodes, each time, a new node is added and connected to an existing node according to a preferential connection. Finally, a scale-free network of 1000 nodes is generated. First, we analyze the effects of parameters on infectious diseases and behavior dynamics. Then we focus on the impact of the proportion of undiagnosed infected on infectious diseases and behavioral dynamics. The baseline values of parameters are defined as:[3] $\alpha = 0.4$, $\beta = 0.108$, $\gamma_1 = 0.071$, $\gamma_2 = 0.143$, $\delta = 0.1$, $q_1 = 0.05$, $\eta = 0.01$. The initial values of the proportion of undiagnosed infected and diagnosed infected are 0.0044, respectively.

3.1. *Sensitivity analysis of parameters*

Different policies correspond to different parameter changes. By analyzing the sensitivity of the parameters, we can provide a direction for the prevention of infectious diseases and the control of human behavior. The proportion of total infections is expressed as: $\dot{R}_N(t) = \gamma_1 E_k(t) + \gamma_2 I_k(t)$.

We first analyze the impact of infection rate β, recovery rate γ_1, the relative speed of human behavior changes δ and the relative cost of quarantine q_1 on epidemics and human behavior. The control variable method is used to analyze the sensitivity of parameters. The effect of β, γ_1 on infectious disease and individual behavior was analyzed by taking a 50% variation, respectively. For example, $\beta = 0.05$, $\beta = 0.1$ and $\beta = 0.15$ are used for analysis. Based on the baseline values of the rest of parameters, the corresponding time series of the proportion of infected individuals and the proportion of total infections are obtained according to different values of β, as shown in the first diagram of Figs. 3 and 4. We take $\delta = 0.1, 0.3, 0.5$. When $\delta = 0.1$, the rate of behavior changes slower than the spread of infections diseases, when $\delta = 0.5$, the rate of behavior changes faster. Similarly, we take $q_1 = 0.05, 0.25, 0.45$. The time series of the proportion of diagnosed infected individuals and the proportion of total infections can be obtained through repeated iterations of the model, as shown in Figs. 3 and 4.

The lines in Fig. 3 show how the proportion of undiagnosed infected individuals changes over time under different parameters. In Fig. 3, we can find that as β and

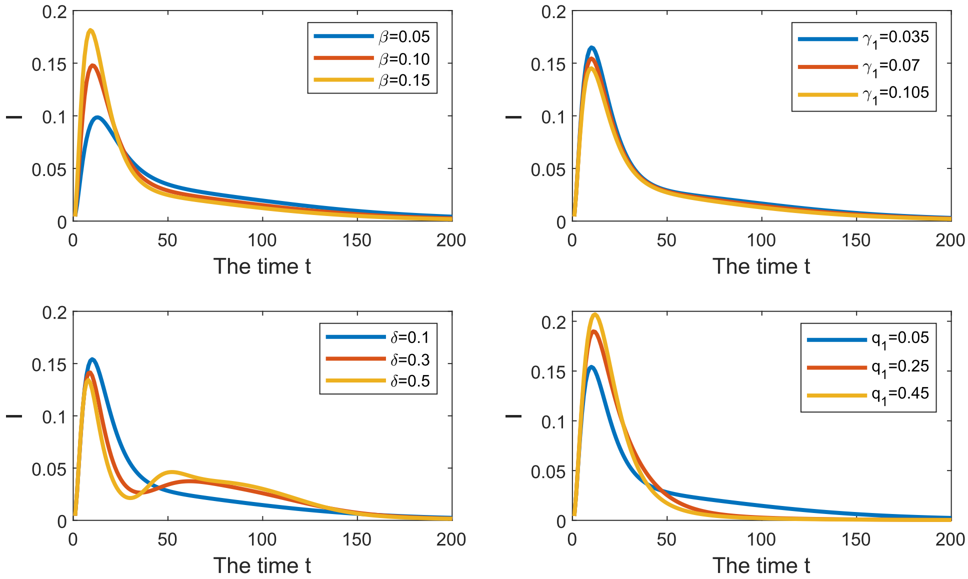

Fig. 3. Time series of the proportion of infected individuals under different β, γ_1, δ and q_1.

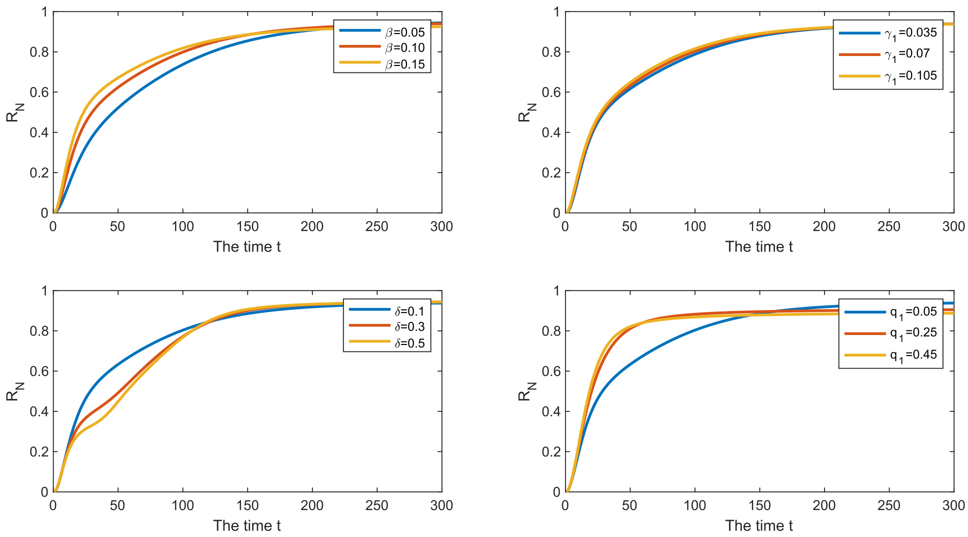

Fig. 4. Time series of the proportion of total infectious under different β, γ_1, δ and q_1.

q_1 increase, the peak of I will increases. As δ and γ_1 increase, the peak of I will decrease. That is, as the infection rate and the relative cost of quarantine increase, the number of infected individuals increases. As the relative cost of quarantine increases, the proportion of quarantine decreases and the proportion of infected individuals increases. The number of infected individuals decreases as the rate of individual behavior change increases or the recovery rate increases.

In Fig. 4, the proportions of total infection are described under different parameters. It can be seen that the recovery rate has little effect on it. β and δ mainly affect its rate of change and have little effect on the total number of final infections. Next, the effects of parameters on the dynamics of individual behavior will be analyzed.

The same method is used to analyze the effects of parameters on individual behavioral dynamics. The variable x indicates the proportion of susceptible and undiagnosed infected who choose the quarantine strategy. By fixing other parameters, the influence of a single parameter on individual behavior is analyzed.

With the increase of β, the proportion of infected individuals increases, and so does the risk of infection of non-quarantined individuals. Therefore, more individuals will choose quarantine. The impact of recovery rate is just the opposite. As recovery rate increases, the proportion of infected individuals decreases, and so does the risk of non-quarantine. Therefore, the proportion of quarantine individuals decreases. As can be seen from Fig. 5, the effects of q_1 and δ on the rate of individual behavior change are opposite to the proportion of infected individuals. When $q_1 = 0.05$, many individuals choose quarantine at the beginning. But when $q_1 = 0.25, 0.45$, the proportion of quarantine decreases rapidly. That is because of the increase in the relative cost of quarantine, quarantine will not be the optimal strategy, so more people choose not to quarantine. Therefore, reducing the relative

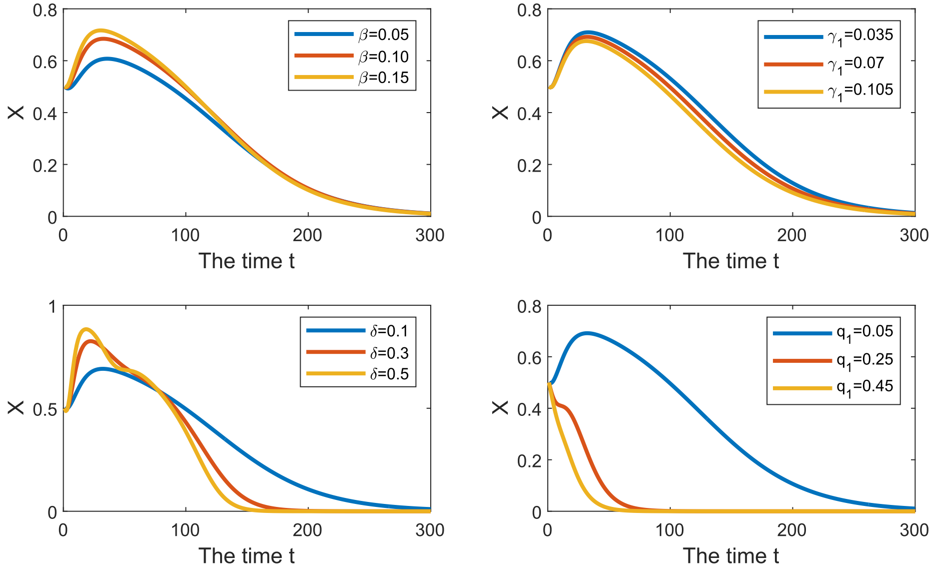

Fig. 5. Time series of the proportion of quarantined individuals under different β, γ_1, δ and q_1.

cost of quarantine can effectively promote quarantine and reduce the proportion of infected individuals. With the increase of δ, individuals can respond to the changes of infectious diseases more timely. Therefore, as δ increases, the proportion of quarantine individuals reaches a steady value faster.

Increasing the publicity and education of the harm of infectious diseases and speeding up the dissemination of information about infectious diseases can increase the rate of human behavior change. Based on Figs. 3 and 5, it is found that the decrease of q_1 and increase of δ can not only promote people to quarantine as soon as possible, but also help prevent the spread of infectious diseases.

It is discovered that secondary wave occurs when δ changes. To analyze this phenomenon, the dynamics of infectious diseases and behavioral changes are analyzed by increasing the value of δ.

In Fig. 6, the time series of the undiagnosed infected (E), diagnosed infected (I), the probability of individuals taking quarantine measures voluntarily (x) and the total infectious (R_N) are analyzed. It can be found that a more rapid change in behavior leads to waves of infections and waves of behavior also. The larger the value of δ, the more waves and the larger the peaks. From the last subgraph of Fig. 6, it can be found that with the increase of δ, although it leads to waves, the proportion of total infection decreases.

3.2. *Sensitivity analysis of undiagnosed infected*

In the model, we use the proportion of diagnosed infected individuals to assess the risk of infection. But in fact, the risk of infection depends on the proportion

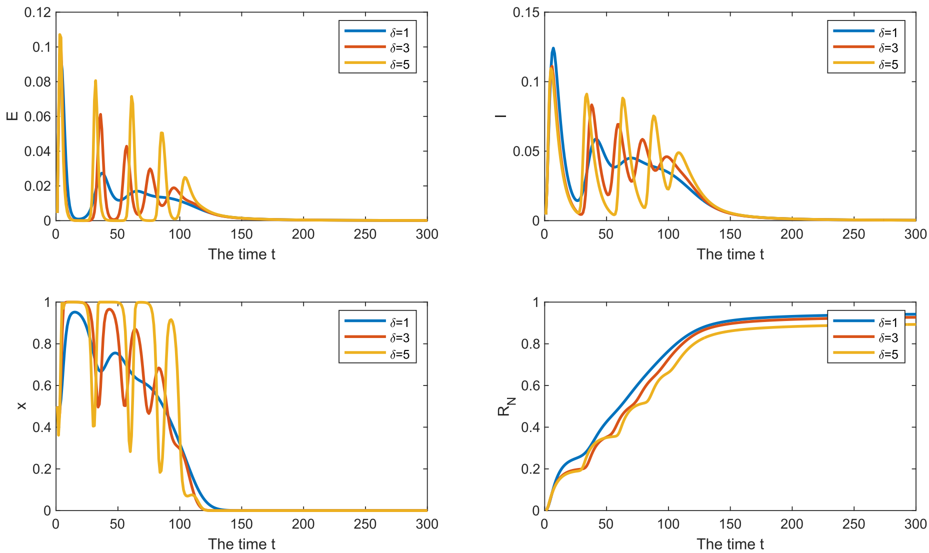

Fig. 6. Effect of parameter δ on infectious diseases and individual behavior.

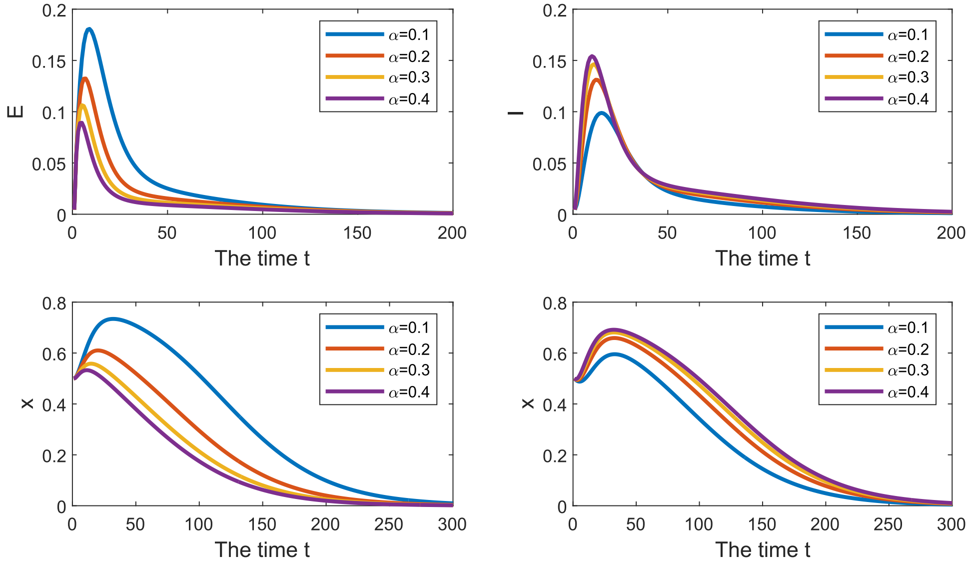

Fig. 7. Influence of detection rate on infectious diseases and behavior dynamics.

of undiagnosed infected individuals. High or low assessments of the proportion of undiagnosed infected individuals affect behavior dynamics. We will analyze it by simulations. The values of other parameters are the same as baseline values.

Undiagnosed infected individuals pose a greater risk to susceptible individuals than diagnosed infected individuals. Everyone knows the presence of undiagnosed infected individuals, but the proportion is unknown. The key parameter α influence the size relation between the proportion of undiagnosed infected individuals and the proportion of diagnosed infected individuals. We take $\alpha = 0.1, 0.2, 0.3, 0.4$. The time series of E and I are obtained through iterative model, and shown in Fig. 7.

In Fig. 7, the lines in the bottom two panels are time series of behavioral dynamics when the values of E and I are used to assess the risk of infection, respectively. Through comparison, it is found that the impact of α on infectious diseases is consistent with that on behavioral dynamics. When $\alpha = 0.3, 0.4$, individuals will overestimate the proportion of undiagnosed infected individuals. Individuals underestimate the proportion of undiagnosed infections when $\alpha = 0.1$. As α increases, E increases and I decreases. This is because as the detection rate increases, more undiagnosed infected individuals will be transferred to the diagnosed compartment. At the same time, the proportion of quarantine individuals who use I to assess the risk of infection will increase. Therefore, increasing the detection rate can promote individuals to quarantine.

Initial values also affect the proportion of undiagnosed infected individuals and diagnosed infected individuals. Next, we will analyze the effect of initial value of

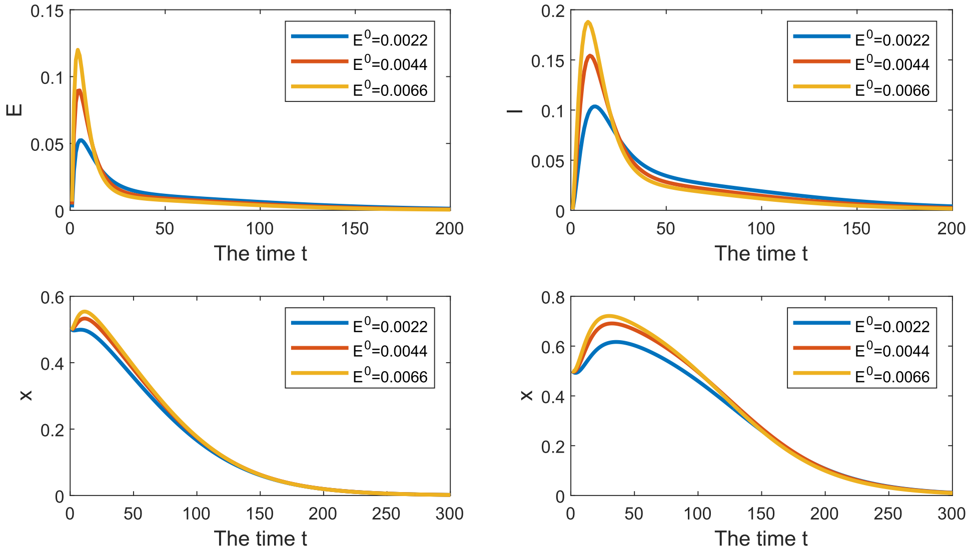

Fig. 8. Influence of the initial value of E on infectious diseases and behavior dynamics.

E on behavior dynamics. We take $E_0 = 0.0022, 0.0044, 0.0066$. A similar method is used to analyze, as shown in Fig. 8.

In Fig. 8, we can find that with the increase of the initial value of E, the proportion of undiagnosed infected individuals and the diagnosed infected individuals increases. Meanwhile, the proportion of quarantine individuals increases. It is found that the proportion of diagnosed infected individuals is always bigger than the proportion of undiagnosed infected individuals. The proportion of quarantine when the values of E are used to assess the risk of infection is always bigger than when the values of I are used to assess the risk of infection. We can also find that the initial value of E does not affect the size relation between E and I and has little affect on the behavior dynamics.

4. Discussion

In this paper, game theory is used to analyze individual decision on taking quarantine measures in the process of infectious diseases spreading. The influences of parameters on the proportion of infected individuals and proportion of quarantine individuals are analyzed by using the control variable method. The effects of undiagnosed infected individuals on behavior dynamics are analyzed by using different risk assessment.

Through theoretical analysis, the basic reproduction number is obtained and the stability of DFE is analyzed. The results of parameters analysis showed that the greater the infection rate, the more infected individuals will be, and individuals will accelerate to choose to quarantine. Reducing the relative cost of quarantine can effectively suppress the spread of infectious diseases. Increasing propaganda can effectively improve the awareness of prevention and directly affect the speed of defense behavior. Increasing detection rate can effectively promote individuals to quarantine. Because it is difficult to distinguish between susceptible and undiagnosed infected individuals, undiagnosed infected individuals have a great impact on the prevention and control of infectious diseases.

The study of prevention strategies is of great significance to the control of infectious diseases. The quarantine strategy can effectively inhibit the spread of infectious diseases, but freedom is lost. Other non-pharmacologic interventions can also effectively suppress the spread of infectious diseases, but these studies need to consider individual connections. The behavior of each individual is also different due to different living habits. In the future, we will consider more about the game between individuals and neighbors.

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