WEP
Warwick
Evans
Publishing

International Journal of Computer Science and Information Technology
ISSN: 3005-9682 (Print), ISSN: 3005-7140 (Online) | Volume 2, Number 2, Year 2024
DOI: https://doi.org/10.62051/ijcsit.v2n2.42
Journal homepage: https://wepub.org/index.php/IJCSIT/index

A Two-layer Coupled Network Disease Transmission Model Considering Multiple Messages

Yang Li, Gengxin Sun, Sheng Bin*

College of Computer Science and Technology, Qingdao University, Qingdao, China
*Corresponding Author: binsheng@qdu.edu.cn

ABSTRACT

In order to discuss the coupling dynamics relationship between disease propagation and information diffusion more accurately, we propose a $SIR-UAOE_1E_2$ information-disease two-layer coupling network propagation model, which takes into account individual heterogeneity and the mutual influence of nodes, introducing hesitant individuals. The impact of various behavioral factors of observing individuals on disease transmission under the influence of various information was explored through simulation experiments. The results show that enhancing the correctness of observing individual behavior decisions, improving their sensitivity to disease information, and enhancing their response intensity to infected neighbors, would play a positive role in suppressing disease outbreaks.

KEYWORDS

Two-layer network; Propagation model; Hesitant individual; Threshold model; Microscopic Markov chain

1. INTRODUCTION

With the rapid development of globalization and the popularity of social networks, information diffusion has become an important influence on disease transmission. Traditional models of infectious disease transmission focus on the dynamics of disease transmission and the influence of network topology on the transmission process[1-5]. However, it should not be overlooked that during an epidemic spread, a wide range of information related to the disease also spreads among the population and prompts people to take some preventive measures[6-10], and these behaviors ultimately affect the scale of the epidemic spread and the overall direction of the epidemic. Therefore, how to more accurately understand the interactions between information diffusion and disease spread will be an important future research topic in the field of complex networks.

Funk et al.[11] were the first to study the impact of epidemic-related awareness on epidemic transmission on a single-layer network, and found that the acquisition of disease-related awareness is crucial during the transmission of infectious diseases, and the spread of related awareness affects the scale and speed of disease transmission. With the development of science and technology, information can be spread quickly and far through online media such as WeChat and Weibo, while diseases must be spread through physical contact in reality. Considering that information dissemination and disease dissemination have different ways and modes, researchers began to use two-layer coupled networks to study the relationship between information dissemination and disease dissemination, in which one layer is the information dissemination layer, which is used to represent the dissemination of disease-related information, and the other layer is the disease dissemination layer, which is used to represent the dissemination of infectious diseases, and the nodes in the two layers of the network correspond to each other one by one, with different topologies between them. 2013. Granell C et al.[12] investigated the effect of information dissemination on disease transmission on a two-layer coupled network and found that disease-related information and network topology affect the scale of disease transmission. In recent years, the application of coupled networks in infectious disease propagation has gained widespread attention. In 2019, Xia[13] and Wang[14] et al. added R (recover) nodes to the SIS model and investigated the impact of information dissemination coupled with the SIR model for spreading. It was found that the wider the information dissemination and the higher the information awareness rate, the more effective the disease control was.2022 Wang[15] et al. further enriched the structure of the model by proposing a model named sUAU-tSIS to better study the interaction between awareness and disease, which found that the phenomenon of group synergy promotes the diffusion of disease-related awareness and thus suppresses the spread of epidemics. Recently, the literature at[16] has used the case of the United States under the Covid-19 pandemic, where cumulative diagnostic data from the United States was used as the disease transmission layer, and retweets of Covid-19-related articles on Twitter were considered as the information diffusion layer, and a real dataset was compared with the model, and it was found that effective dissemination of scientific information slowed down the progression of the pandemic, and that major social events that were not related to the disease distracted people from it, thus increasing the disease's attention. attention to the disease, thus increasing the scale of disease spread.

Existing coupled network models, however, only consider the influence of positive disease-related information on disease transmission. With the rapid development of science and technology, the dissemination of information has become more and more extensive, and the sources and types of information have become more and more diversified. During the spread of epidemics, not only positive prevention messages such as "reduce going out and wear masks" spread on the Internet, but also negative messages. If such negative messages are widely spread on the Internet, it will have a serious impact on epidemic prevention. 2020, Huang et al.[17] constructed a two-layer coupled model of SI I12 S-SEIS to study the effects of knowledge and rumours on disease transmission, and the results showed that the spread of knowledge can eliminate rumours and infectious diseases, and the penetration rate of knowledge plays a key role. 2021, Wang et al. [18]studied the effects of positive and negative prevention messages on disease transmission, and found that the spread of epidemics and outbreaks could be suppressed by promoting the spread of positive prevention messages and inhibiting the spread of negative prevention messages. A large proportion of these studies were conducted under the dichotomous assumption that individuals either endorse disease-related messages and take preventive measures accordingly, or do not receive epidemic-related messages, which cannot explain the wide range of attitudes and behaviours exhibited by individuals in response to epidemics. Recent research and reality suggest that some members of society do not take preventive measures after hearing about epidemic-related information.

Therefore, in order to better adapt to the current complex information environment, this paper takes into account the variability in the sensitivity and response intensity of individuals facing epidemics. In the information dissemination layer, new E(wait-and-see) individuals are added, which are individuals who are aware of the disease-related information but do not take relevant preventive measures. As the epidemic spreads and related information continues to spread, the attitudes of these watchful nodes are easily influenced by neighbouring nodes, and people's attitudes may shift when most of the nodes in the neighbourhood do not agree with their own viewpoints or the proportion of infected people in the neighbourhood nodes is higher, and in this paper we use a threshold model to represent the influence of neighbouring nodes on the attitudes of individuals. In addition to this during a pandemic spreading in a big way, the relevant organizations also publish information about the disease and the correct response online, in this paper this is attributed to the influence of mass media on the spread of the disease. In summary, this paper proposes a SIR-UAOE$_1$E$_2$ two-layer coupled network model of information and disease, which takes into account the coupled propagation of multiple disease information and multi-state disease, and introduces the wait-and-see individuals in the information layer, and also takes into account the influences of the neighbouring nodes and the mass media on the attitudes of the individuals, so as to simulate the coupled propagation evolution process of the disease information and the disease in the real world in a more realistically and accurately way. coupled propagation evolution process. This study is of great significance for the accurate understanding of the disease transmission mechanism in the social network environment, and can provide a theoretical basis for public health departments to formulate effective disease control strategies.

2. SIR−UAOE$_1$E$_2$ OVERVIEW OF THE COUPLED PROPAGATION MODEL

Considering the diversity of individuals spreading information, and in order to make the state of nodes in the information layer more relevant to the real situation, this paper proposes a coupled network spreading model that takes into account the heterogeneity of individuals, the influence of neighbouring nodes and mass media. As shown in Figure 1, the model is a two-layer network model, with the upper layer being a virtual social network for disease-related information dissemination, and the lower layer being a realistic contact network representing the spread of infectious diseases. Each node in the network represents an entity, and the solid lines between individual nodes represent entities interconnected with each other. The individual entities of the upper and lower layers of the network present one-to-one correspondence and are connected by dotted lines. Both layers of the network are undirected unweighted graphs, but their topology structures are different because in real life, information spreads and diffuses in a different way than diseases.

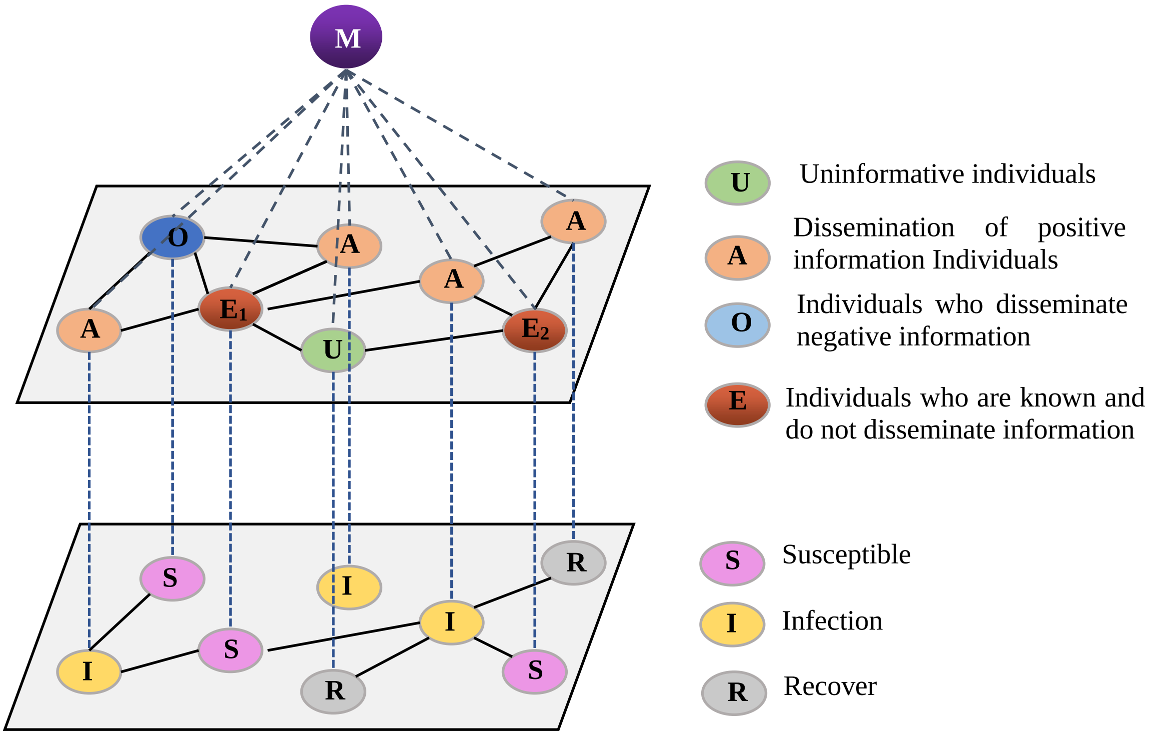
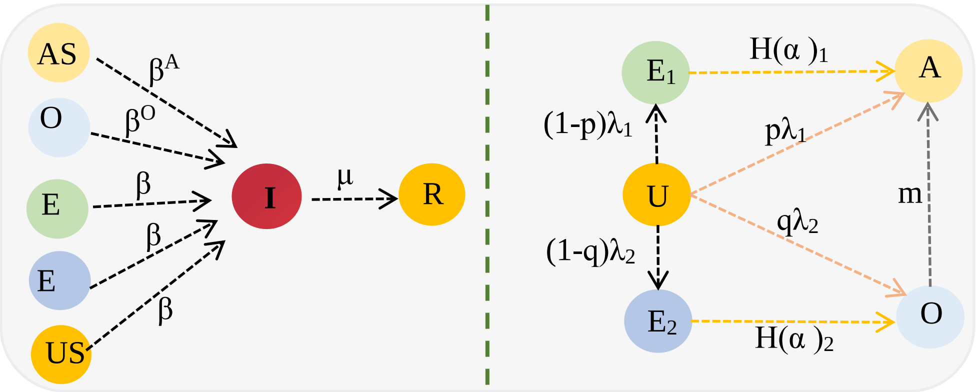


Figure 1. SIR-UAOE$_1$E$_2$ Coupled Propagation Model

In this paper, a UAOE1E2 information dissemination model is proposed in the information layer. The nodes in this layer are categorized as uninformed individuals (U), known and spreading positive message individuals (A), known and spreading negative message individuals (O), known positive message but not spreading (E$_1$), and known negative message but not spreading (E$_2$). The state of individuals in the message layer affects the process by which susceptible individuals in the disease layer are infected with the disease by their neighbors, where the protective measures taken by individuals who spread positive messages are more effective than those taken by individuals who spread negative messages, whereas the probability of contracting the infectious disease does not change for individuals who are not aware of any messages and for wait-and-see individuals because they do not take protective measures.

As shown in Figure 2(a) AS state individuals, OS state individuals are affected by different types of messages and will have probability of $\gamma_1 \beta$, $\gamma_2 \beta$ respectively to be infected, and because of being infected, both of them will be changed to AI state which is the proponent of the positive message, where $0 \leq \gamma_1 < \gamma_2 \leq 1$, and γ_1, γ_2 denote the effectiveness factor of the measures for the AS and OS individuals respectively. In the physical layer, the disease propagation conforms to the healthy-infected-immune (SIR) model, and there exist three states: healthy state (S), infected state (I), and immune state (R). At each t time step, a healthy state individual has a probability of β to be infected if it comes into contact with a neighbouring node in the infected state; an infected individual reverts to the immune state with a probability of μ. Since an individual that has been infected with a disease possesses an antibody, in this paper it is assumed that an immune state individual will not be infected again.

The node state transition schematic of the information layer is shown in Figure 2(b). Positive information and negative information spread in the population with probabilities of λ_1 and λ_2, respectively. After individuals in state U hear about disease-related information, due to individual differences in sensitivity to disease prevention and perceived severity of the disease, some people will recognise one of the information and take appropriate preventive measures to reduce their risk of being infected; while some people will not take disease information after hearing about it due to their disbelief in the existence of disease preventive measures. For an individual with state E, considering the herd mentality and the influence of neighbouring nodes, the individual may switch between E and A/O. A threshold model is used in this layer to describe the transition of the state in the personal information layer, where $\alpha1$, $\alpha2$ are the local transition rates.



(a) Physical layer node state transition (b) Message layer node state transitions

Figure 2. State Transition Diagram

The transition rule is defined as follows: if an individual is in state E1 and the sum of the number of his virtual layer neighbors that are in state A or in state I in the physical layer as a proportion of the total number of neighbors in the virtual and physical layers exceeds the local transition rate $\alpha1$, then the individual will transition to state A. Suppose, when a person receives two messages at the same time, considering the cost problem individual will prefer the negative preventive behaviour. And as time passes, people will forget the positive and negative messages with the probability of $\delta1$, $\delta2$. Under the influence of mass media, individuals in the O and E_2 states will directly switch to the A state with a probability of m. Table 1 lists the descriptions of all symbols.

Table 1. Description of All Symbols

notation	descriptions
t	time step
$\lambda 1$ /$\lambda 2$	Rate of dissemination of positive/negative information
$\alpha 1$ /$\alpha 2$	Local conversion rate of positive/negative messages
$\delta 1$ /$\delta 2$	Positive/negative information forgetting rate
β_i^X	Disease transmission rate at state node X
u	Disease recovery rate
$\gamma 1$ /$\gamma 2$	Attenuation factors of positive/negative prophylaxis on disease transmission
p	Proportion of individuals with known positive information who took positive preventive measures
q	Proportion of individuals with known negative information who took negative precautions
m	Mass media information dissemination rate
A	Neighbourhood matrix of the information dissemination layer network
B	Neighbourhood matrix of the epidemic transmission layer network
a_{ij}	Elements of the adjacency matrix A
b_{ij}	Elements of the adjacency matrix B
$r_i^A(t)$	Probability that individual i is not informed of positive information by any neighbour at moment t
$r_i^O(t)$	Probability that individual i is not informed of negative information by any neighbour at moment t
$\theta_i^{X\to Y}(t)$	The probability that individual i transitions from state X to state Y at the message layer in moment t
$q_i^U(t)$	Probability that individual i of state U is not infected by the disease at moment t
$q_i^A(t)$	Probability that individual i of state A is not infected by the disease at moment t
$q_i^O(t)$	O the probability that state individual i is not infected by the disease at moment t
$q_i^{E_1}(t)$	E1 Probability that state individual i is not infected by the disease at moment t
$q_i^{E_2}(t)$	E2 Probability that state individual i is not infected by the disease at moment t
$p_i^{XY}(t)$	Probability that individual i is in XY at moment t

3. CONSTRUCTION OF COUPLED PROPAGATION DYNAMICS EQUATIONS

In this study, MMC was used to construct the message-disease coupling dynamics equations. Let the probability that any individual i is in the state US, AS, OS, E1S, E2S, AI, AR, UR, E1R are $p_i^{US}(t)$, $p_i^{AS}(t)$, $p_i^{OS}(t)$, $p_i^{E_1S}(t)$, $p_i^{E_2S}(t)$,$p_i^{AI}(t)$,$p_i^{AR}(t)$,$p_i^{UR}(t)$, $p_i^{E_1R}(t)$, and the satisfaction probability is 1. In the information layer, the individual i with state U, assuming that the probability that he does not get positive or negative information from the neighbor node at the t time step is$r_i^A(t)$ and $r_i^O(t)$. Use aij to represent the information layer adjacent matrix element of the information, if there is a connection between i and j, aij is 1, and otherwise 0:

$$\begin{cases} r_i^A(t) = \prod_j [1 - a_{ij} P_j^A(t) \lambda_1]. \\ r_i^O(t) = \prod_j [1 - a_{ij} P_j^O(t)(t) \lambda_2]. \end{cases} \tag{1}$$

where $p_j^A(t) = p_i^{AS}(t) + p_i^{AI}(t) + p_i^{AR}(t)$, denotes the probability that moment t node j is A state.$p_j^O(t) = p_i^{OS}(t)$, denotes the probability that moment t node j is in state O.

For an individual in state U, if it is not affected by any message at time t, it remains in its original state; if it is affected by a positive message, a proportion p of individuals change to state A, and a proportion (1-p) change to state E_1; if it is affected by a negative message, a proportion q of individuals change to state O, and a proportion (1-q) change to state E_2; and the probability of the transition is as equation (2). The transition probabilities between other states are as in the following equation:

$$\begin{cases} \theta_i^{U \to U}(t) = r_i^A(t) r_i^O(t). \\ \theta_i^{U \to A}(t) = \{1 - r_i^A(t) - [1 - r_i^A(t)][1 - r_i^O(t)]\} p. \\ \theta_i^{U \to O}(t) = [1 - r_i^O(t)] q. \\ \theta_i^{U \to E_1}(t) = \{1 - r_i^A(t) - [1 - r_i^A(t)][1 - r_i^O(t)]\} (1 - p). \\ \theta_i^{U \to E_2}(t) = [1 - r_i^O(t)](1 - q). \end{cases} \tag{2}$$

$$\begin{cases} \theta_i^{E_1 \to U}(t) = \delta_1. \\ \theta_i^{E_1 \to A}(t) = H(\alpha_1 - \frac{\sum_j a_{ji} p_j^A(t) + \sum_j b_{ji} p_j^I(t)}{\sum_j a_{ji} + \sum_j b_{ji}}). \end{cases} \tag{3}$$

$$\begin{cases} \theta_i^{E_2 \to U}(t) = \delta_2. \\ \theta_i^{E_2 \to O}(t) = H(\alpha_2 - \frac{\sum_j a_{ji} P_j^O(t)}{\sum_j a_{ji}} + \frac{\sum_j b_{ji} P_j^I(t)}{\sum_j b_{ji}}). \\ \theta_i^{E_2 \to A}(t) = m. \end{cases} \tag{4}$$

$$\begin{cases} \theta_i^{A \to U}(t) = \delta_1. \\ \theta_i^{A \to E_1}(t) = H(\alpha_1 - \frac{\sum_j a_{ji} P_j^{E_1}(t)}{\sum_j a_{ji}}). \end{cases} \tag{5}$$

$$\begin{cases} \theta_i^{O \to U}(t) = \delta_2. \\ \theta_i^{O \to E_2}(t) = H(\alpha_2 - \frac{\sum_j a_{ji} P_j^{E_2}(t)}{\sum_j a_{ji}}). \\ \theta_i^{O \to A}(t) = m. \end{cases} \tag{6}$$

In a disease network, denoted byb_{ij} denote the elements of the disease layer adjacency matrix, assume that the probability that an uninformed node i is not infected by any of its neighbouring nodes at the moment t is denoted as$q_i^U(t)$, the probability that node i, which is known and disseminates positive messages at the moment t, is not infected by any of the neighbour nodes is denoted as$q_i^A(t)$, the probability that node i, which is known and disseminates message information at moment t, is not infected by any neighbouring node is denoted as$q_i^O(t)$ The probability that a watchful individual is not infected by any neighbouring node at time t is the same as that of an uninformed individual because he/she does not take any protective measures, although he/she is aware of the information about the disease, is then obtained:

$$\begin{cases} q_i^A(t) = \prod_j [1 - b_{ji} P_j^I(t) \beta_i^A]. \\ q_i^O(t) = \prod_j [1 - b_{ji} P_j^I(t) \beta_i^O]. \\ q_i^U(t) = q_i^{E_1}(t) = q_i^{E_2}(t) = \prod_j [1 - b_{ji} P_j^I(t) \beta_i^U]. \end{cases} \quad (7)$$

In order to further investigate the behaviour of the coupled information-disease propagation dynamics, a state transfer probability tree as shown in Figure 3 was constructed based on the state transition schematic shown in Figure 2. Figure 3 depicts the transfer probability tree of nine states, where the root node of each tree represents the state of the node at moment t and the leaf nodes represent the state at the next moment.

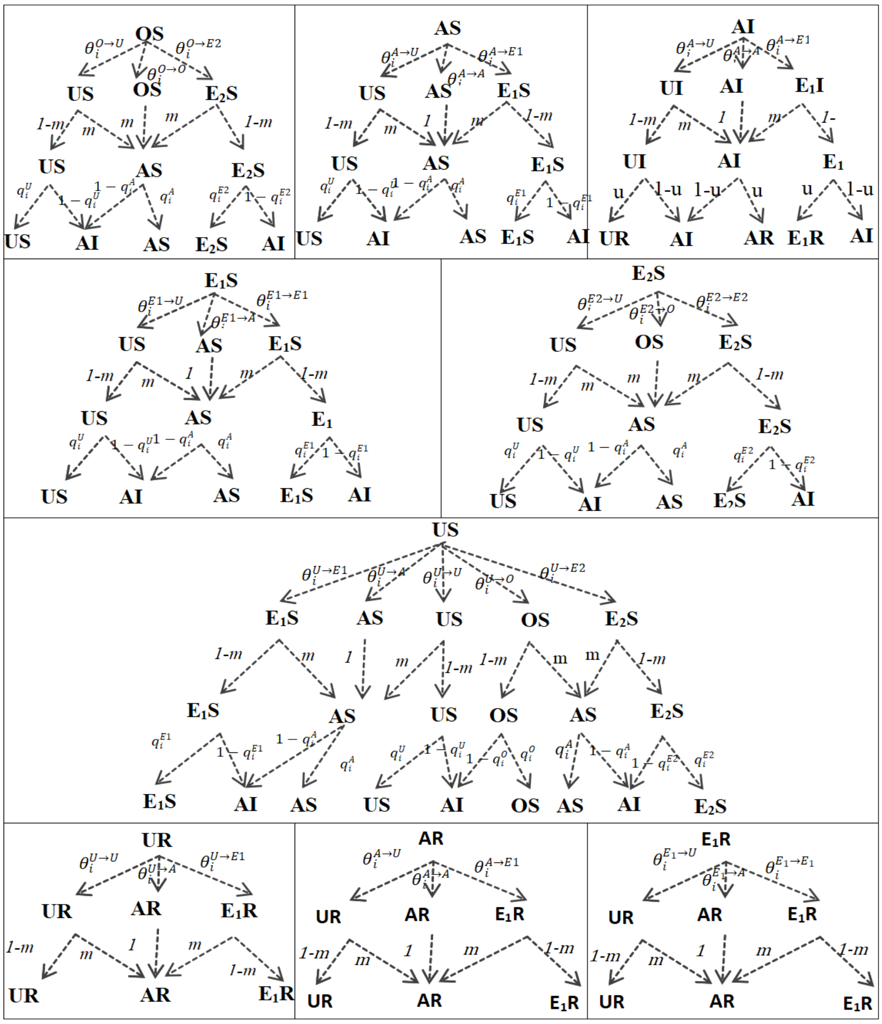


Figure 3. Probability Transfer Tree of SIR-UAOE$_1$E$_2$ Mode

According to the state transition probability tree in Figure 3 and the MMC method, the state evolution equation can be obtained as:

$$
\left\{
\begin{aligned}
&P_i^{US}(t+1)=P_i^{US}(t)\theta_i^{U\to U}(1-m)q_i^U+P_i^{AS}(t)\theta_i^{A\to U}(1-m)q_i^U+P_i^{OS}(t)\theta_i^{O\to U}(1-m)q_i^U\\
&\qquad +P_i^{E_1S}(t)\theta_i^{E_1\to U}(1-m)q_i^U+P_i^{E_2S}(t)\theta_i^{E_2\to U}(1-m)q_i^U.\\
&P_i^{AS}(t+1)=P_i^{US}(t)\{\theta_i^{U\to A}q_i^A+\theta_i^{U\to O}mq_i^A\}+P_i^{AS}(t)\theta_i^{A\to A}q_i^A+P_i^{OS}(t)\theta_i^{O\to O}mq_i^A+\\
&\qquad P_i^{E_1S}(t)\theta_i^{E_1\to A}q_i^A+P_i^{E_2S}(t)\theta_i^{E_2\to A}mq_i^A.\\
&P_i^{OS}(t+1)=P_i^{US}(t)\theta_i^{U\to O}(1-m)q_i^O.\\
&P_i^{E_1S}(t+1)=P_i^{US}(t)\theta_i^{U\to E_1}(1-m)q_i^{E_1}+P_i^{AS}(t)\theta_i^{A\to E_1}(1-m)q_i^{E_1}+P_i^{E_1S}(t)\theta_i^{E_1\to E_1}(1-m)q_i^{E_1}.\\
&P_i^{E_2S}(t+1)=P_i^{US}(t)\theta_i^{U\to E_2}(1-m)q_i^{E_2}+P_i^{OS}(t)\theta_i^{O\to E_2}(1-m)q_i^{E_2}+P_i^{E_2S}(t)\theta_i^{E_2\to E_2}(1-m)q_i^{E_2}.\\
&P_i^{AI}(t+1)=P_i^{US}(t)\{\theta_i^{U\to E_1}[(1-m)(1-q_i^{E_1})+m(1-q_i^A)]+\theta_i^{U\to A}(1-q_i^A)+\theta_i^{U\to U}[(1-m)\\
&\qquad (1-q_i^U)+m(1-q_i^A)]+\theta_i^{U\to O}[(1-m)(1-q_i^O)+m(1-q_i^A)]+\theta_i^{U\to E_2}(1-m)(1-\\
&\qquad q_i^{E_2})\}+P_i^{AS}(t)\{\theta_i^{A\to U}[(1-m)(1-q_i^U)+m(1-q_i^A)]+\theta_i^{A\to A}(1-q_i^A)+\theta_i^{A\to E_1}[m\\
&\qquad (1-q_i^A)+(1-m)(1-q_i^{E_1})]\}+P_i^{OS}(t)\{\theta_i^{O\to U}[(1-m)(1-q_i^U)+m(1-q_i^A)]+\theta_i^{O\to O}\\
&\qquad m(1-q_i^A)+\theta_i^{O\to E_2}[m(1-q_i^A)+(1-m)(1-q_i^{E_2})]\}+P_i^{E_1S}(t)\{\theta_i^{E_1\to U}[(1-m)(1-q_i^U)\\
&\qquad +m(1-q_i^A)]+\theta_i^{E_1\to A}(1-q_i^A)+\theta_i^{E_1\to E_1}[m(1-q_i^A)+(1-m)(1-q_i^{E_1})]\}+P_i^{E_2S}(t)\{\theta_i^{E_2\to U}\\
&\qquad [(1-m)(1-q_i^U)+m(1-q_i^A)]+\theta_i^{E_2\to O}m(1-q_i^A)+\theta_i^{E_2\to E_2}[m(1-q_i^A)+(1-m)(1-q_i^{E_2})\\
&\qquad]\}+P_i^{AI}(t)\{\theta_i^{A\to U}[(1-m)(1-u)+m(1-u)]+\theta_i^{A\to A}(1-u)+\theta_i^{A\to E_1}[(1-m)(1-u)+\\
&\qquad m(1-u)]\}.\\
&P_i^{AR}(t+1)=P_i^{AI}(t)\{\theta_i^{A\to U}mu+\theta_i^{A\to A}mu\}+P_i^{AR}(t)\{\theta_i^{A\to U}m+\theta_i^{A\to A}+\theta_i^{A\to E_1}m\}+P_i^{UR}(t)\{\theta_i^{U\to U}m\\
&\qquad +\theta_i^{U\to A}+\theta_i^{U\to E_1}m\}+P_i^{E_1R}(t)\{\theta_i^{E_1\to E_1}m+\theta_i^{E_1\to A}+\theta_i^{E_1\to U}m\}.\\
&P_i^{UR}(t+1)=P_i^{AI}(t)\theta_i^{E_1\to U}(1-m)u+P_i^{AR}(t)\theta_i^{A\to U}(1-m)+P_i^{UR}(t)\theta_i^{U\to U}(1-m)+P_i^{E_1R}(t)\theta_i^{E_1\to U}\\
&\qquad (1-m).\\
&P_i^{E_1R}(t+1)=P_i^{AI}(t)\theta_i^{A\to E_1}(1-m)u+P_i^{AR}(t)\theta_i^{A\to E_1}(1-m)+P_i^{UR}(t)\theta_i^{U\to E_1}(1-m)+P_i^{E_1R}(t)\theta_i^{E_1\to E_1}\\
&\qquad (1-m).
\end{aligned}
\right.
\tag{8}
$$

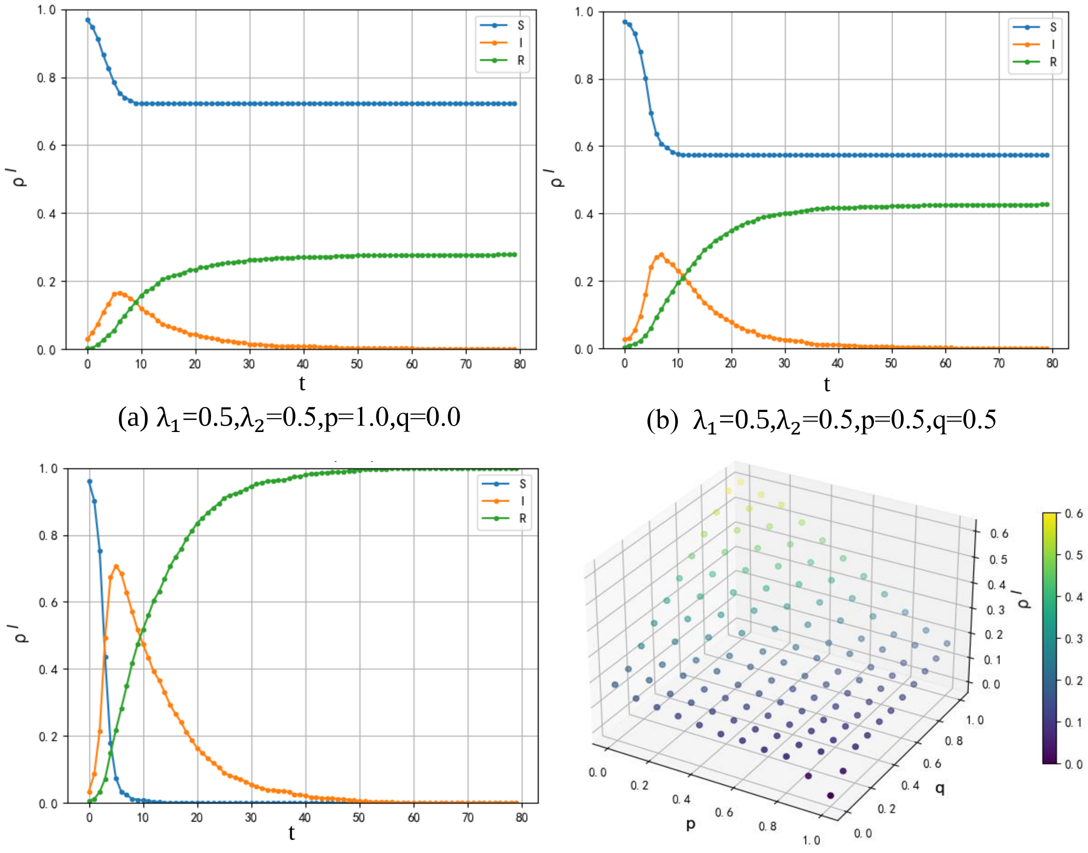
4. SIMULATION EXPERIMENT AND RESULT ANALYSIS

In order to investigate the effect of the presence of watchful individuals under the influence of two competing message propagation on the spread of the disease in a two-layer coupled network, a number of simulation experiments are carried out in this chapter. The experiments use the configuration model in B´ ela Bollob´ as [19] to generate a BA network with an average degree of 6 and a power index of 3 to construct the information layer network, and a WS small-world network to construct the contact layer network. The final simulation results are averaged after simulating 200 MMCA propagation evolutions, assuming that the values of ρ^I, ρ^A and ρ^O states at the initial moments of the disease propagation and the information propagation are 0.01, 0.01, and 0.01, respectively.

4.1. Impact of behavioral changes at the watch node on disease transmission

Considering the variability of individuals' susceptibility in the face of epidemics and the intensity of their response to infected neighbouring nodes, in this experiment, the impact of different behaviors of watchful nodes on the trend and scale of disease spread in the SIR-UAOE$_1$E$_2$ model is verified. The results obtained are shown in Figure 4.

From Figures 4(a)-(c), it can be seen that the change in status of the watchful individuals affects the scale of disease transmission to varying degrees. If the watchful individuals listen to the negative disease prevention message and become advocates of the negative message, the disease transmission will peak at a faster rate. The higher the proportion of watchful individuals who become negative prevention message spreading individuals, the larger the scale of disease spread, when disease control requires higher cost and time. When the watchful node becomes a proponent of positive prevention messages, the spread of the disease slows down. The higher the proportion of watchful individuals become positive prevention message spreading individuals, the smaller the peak of the disease and the scale of infection. And the more effective the prevention measures taken by individuals, the smaller the scale and peak of disease transmission. Figure 4(d) shows that the scale of disease transmission changes with the proportion of watchful individuals changing into individuals with negative prevention messages and individuals with positive prevention messages, and the above conclusion can be drawn more intuitively from this figure.



(a) λ_1=0.5,λ_2=0.5,p=1.0,q=0.0

(b) λ_1=0.5,λ_2=0.5,p=0.5,q=0.5

(c) λ_1=0.5,λ_2=0.5,p=0.0,q=1.0

(d) λ_1=0.5,λ_2=0.5

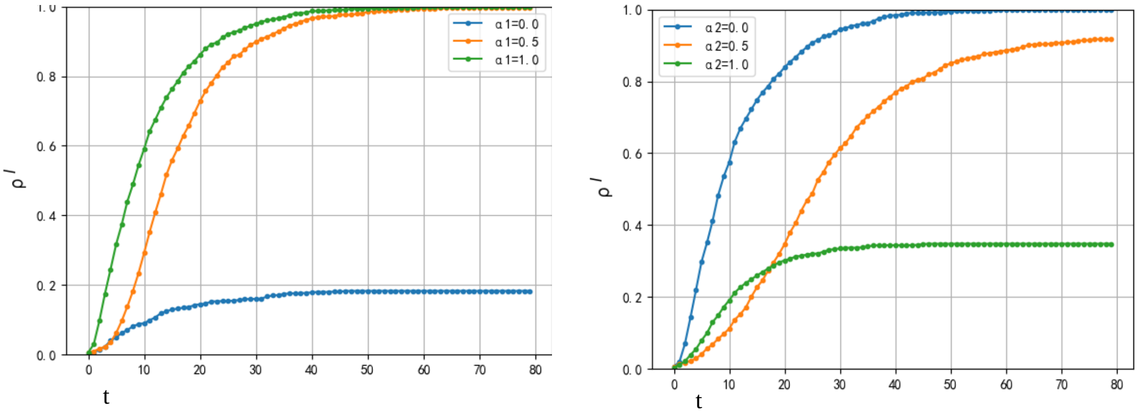
Figure 4. The Impact of Hesitant Individual Behavioral Factors (p and q) on Disease Transmission

The results of this experiment show that the behaviour of the watchful individuals is crucial to the disease transmission process. In real-life disease prevention and control, in addition to focusing on individuals who spread misinformation, we should also focus on watchers, and we should disseminate disease-related knowledge and effective protective measures to them, so that they can become supporters of positive prevention messages and take effective self-protection measures as much as possible, thus slowing down the scale of outbreaks and the pressure of disease prevention and control.

When a new epidemic has just emerged, as the epidemic is not yet confirmed, people may not believe in the existence of the epidemic when they hear about it, will not take any protective measures and are in a wait-and-see mode. Once an epidemic is confirmed, people should immediately take the initiative to become disseminators of positive disease prevention information, raise their awareness of disease protection, take effective protective measures to reduce their risk of being infected, and minimize the physical hazards and economic losses brought about by sudden outbreaks of epidemics.

4.2. Impact of local conversion rates on disease transmission

Considering that the attitudes of watchful individuals are affected by the state of neighbouring nodes, the effect of local switching rate on the scale of disease transmission is investigated in this section. As shown in Figure 5(a), the scale of disease spreading βI increases as $\alpha 1$ increases, suggesting that boosting people's sensitivity to positive disease prevention messages or increasing the intensity of people's response to infected neighbors can slow down large-scale disease outbreaks. When $\alpha 1$ is smaller, the easier it is to switch from E1 individuals to A individuals, when more individuals will take effective disease prevention measures, thus slowing down the scale of disease outbreaks. And Figure 5(b) illustrates that in the face of the complex social network environment, people should improve their information recognition, make correct behavioral decisions, and improve their awareness of protection, so as to reduce the risk of being infected.



(a) Impact of α_1 on the scale of disease transmission (b) Impact of α_2 on the scale of disease transmission

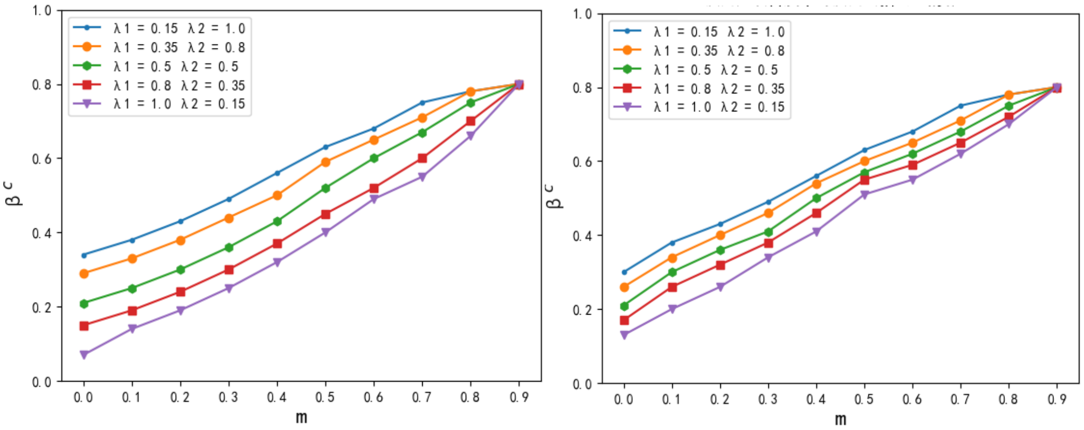
Figure 5. Effect of Local Conversion Rates (α_1 and α_2) on Disease Transmission: $\lambda_1 = 0.5, \lambda_2 = 0.5, \delta_1 = 0.3, \delta_2 = 0.3$

4.3. Effect of multiple information dissemination rates, mass media disease literacy, and individual information sensitivity on disease thresholds

In the context of today's spreading epidemics, disease-related information is widely spread in social networks, and the accuracy of the messages cannot be guaranteed. Based on this situation, many people may choose to believe in negative disease prevention messages and take wrong actions when they are faced with a large amount of disease information, which is very unfavourable to disease spreading. This experiment explores how the popularization of people's knowledge about diseases by the mass media will affect the spread of diseases.

As shown in Figure 6, the disease threshold βc increases with the popularity of disease knowledge in mass media, suggesting that enhancing people's knowledge of diseases can slow down large-scale disease outbreaks. When $\lambda 1$, $\lambda 2$ are the same, the epidemic threshold in Figure 6(b) is lower than that in Figure 6(a), which implies that enhancing individuals' sensitivity to disease-related information is also an effective way to inhibit mass outbreaks of diseases.

In Figure 6(a), (b), for fixed λ_2, γ_1, γ_2 and m, the threshold βc gradually increases as λ_1 increases from 0.15 to 1.0. Fixing λ_1, the threshold β_c As λ_2 increases from 0.15 to 1.0, the threshold βc gradually decreases. It indicates that the outbreak of epidemic is suppressed by promoting the spread of positive prevention messages and suppressing the spread of negative prevention messages. When λ_1, λ_2 and m are constant, the threshold βc increases as γ_1 and γ_2 decrease. Therefore, increasing people's sensitivity to disease information is also an effective measure to suppress mass outbreaks.



(a) $\gamma_1 = 0.5$, $\gamma_2 = 1.0$ (b) $\gamma_1 = 0.0$, $\gamma_2 = 0.5$

Figure 6. Effect of Multiple Information Dissemination Rate, Disease Knowledge Prevalence M and Individual Information Sensitivity on Disease Thresholds

5. SUMMARY

In this paper, on the basis of the traditional disease-information interaction propagation model, considering the individual sensitivity to epidemics and the variability of reaction strength to infected neighbors, we propose a SIR-UAOE$_1$E$_2$ message-disease two-layer coupled network model, which considers the disease propagation process under the influence of multiple messages and introduces watchful individuals at the message layer. Secondly, the state transfer probability tree of this model is constructed by using MMCA, and the role of the behavioral choices of the watchful individuals in disease propagation is investigated through a large number of simulation experiments. The experimental conclusions show that applying some kind of intervention to watchful individuals to enhance the correctness of their behavioral decisions and the intensity of their reaction to infected neighbors, as well as to increase the media's knowledge of the disease to the general public, is an effective way to slow down the outbreak of the disease. In the context of the frequent occurrence of infectious diseases and the rapid development of the Internet, the model provides a new way of thinking for the study of current disease transmission, and provides a reference for the use of transmission models in order to curb the practical problems of large-scale disease transmission.

CONFLICTS OF INTEREST

We have no conflict of interest.

REFERENCES

[1] ANDERSON R M, MAY R M, ANDERSON B. 1992 Infectious diseases of humans: dynamics and control [M]. USA: Oxford University Press, 1992:127.

[2] HETHCOTE H W. The mathematics of infectious diseases [J]. Siam Review, 2000, 42(4): 599-653.

[3] GRABOWSKI A, KOSINSKI R A. Epidemic spreading in a hierarchical social network [J]. Physical Review E, 2004, 70(3) : 031908.

[4] YANG H, GU C G, TANG M, et al. Suppression of epidemic spreading in time-varying multiplex networks [J]. Applied Mathematical Modelling, 2019, 75 : 806-818.

[5] DAVIS J T, PERRA N, ZHANG Q, et al. Phase transitions in information spreading on structured populations [J]. Nature physics, 2020, 16(5): 590-596.

[6] WANG B, GOU M, HAN Y X. Impacts of information propagation on epidemic spread over different migration routes [J]. Nonlinear Dynamics, 2021, 105(4): 3835-3847.

[7] WEN T. Evaluating the Vulnerability of Communities in Social Networks by Gravity Model [J]. arXiv, 2019, arXiv:1912.07293.

[8] FERGUSON N. Capturing human behaviour [J]. Nature, 2007, 446 (7137): 733.

[9] WANG Z, ANDREWS M A, WU Z X, et al. Coupled disease-behaviour dynamics on complex networks: a review [J]. Physics of Life Reviews, 2015, 15: 1-29.

[10] WANG Z, BAUCH C T, BHATTACHARYYA S, et al. Statistical physics of vaccination [J]. Physics Reports, 2016, 664:1-113.

[11] FUNK S, GILAD E, WATKINS C, et al. The spread of awareness and its impact on epidemic outbreaks [J]. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106 (16):6872-6877.

[12] GRANELL C, GOMEZ S, ARENAS A. Dynamical interplay between awareness and epidemic spreading in multiplex networks [J]. Physical Review Letters, 2013, 111 (12):128701.

[13] XIA C Y, WANG Z S, ZHENG C Y, et al. A new coupled disease-awareness spreading model with mass media on multiplex networks [J], Information Sciences: an International Journal, 2019, 471:185-200.

[14] WANG Z S, XIA C Y. Co-evolution spreading of multiple information and epidemics on two-layered networks under the influence of mass media [J], Nonlinear Dynamics, 2020,102(4): 3039-3052.

[15] WANG H, ZHANG H F, ZHU P C, et al. Interplay of simplicial awareness contagion and epidemic spreading on time-varying multiplex networks [J]. Chaos: An Interdisciplinary Journal of Nonlinear Science, 2022, 32(8):083110.

[16] YANG B, LIU C, CHENG X, et al. Understanding users' group behavioral decisions about sharing articles in social media: an elaboration likelihood model perspective [J]. Group Decision and Negotiation,2022, 31(4): 819-842.

[17] HUANG H, CHEN Y, MA Y, Modelling the competitive diffusions of rumor and knowledge and the impacts on epidemic spreading[J]. Applied Mathematics and Computation, 2021, 388:125536.

[18] WANG Z, XIA C, CHEN Z, et al. Epidemic propagation with positive and negative preventive information in multiplex networks [J]. IEEE Transactions on Cybernetics,2020, 51 (3): 1454-1462.

[19] GUO H, XU L. Research on the application of big data visualisation technology in urban road congestion [J]. European Journal of Remote Sensing, 2022,11: 1-12.