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Frontiers

Analysis of epidemic spreading process in multi-communities

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ARTICLE INFO

Article history:

Received 29 November 2017

Revised 24 January 2018

Accepted 4 February 2018

Available online 20 March 2018

Keywords:

Multiplex networks

Virtual layer

Intra-contact

Susceptible-infected-recovered (SIR) model

Inter-contact

ABSTRACT

In practice, an epidemic might be spreading among multi-communities; while the communities are usually intra-connected. In this manuscript, each community is modeled as a multiplex network (i.e., virtual layer and physical one). The connections inside certain community are referred as inter-contacts while the intra-contacts denote the connections among communities. For the epidemic spreading process, the traditional susceptible-infected-recovered (SIR) model is adopted. Then, corresponding state transition trees are determined and simulations are conducted to study the epidemic spreading process in multi-communities. Here, the effect of incorporating virtual layer on the range of individual affected by the epidemic is pursued. As illustrated, multi-summits are incurred if the spreading in multi-communities is considered; furthermore, the disparity between summits varies. This is affected by various factors. As indicated, the incorporation of virtual layer is capable of reducing the proportion of individuals being affected; moreover, disparity of different summits is likely to be increased regarding with scenarios of excluding virtual layer. Furthermore, the summit is likely to be postponed if virtual layer is incorporated.

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1. Introduction

The isolated networks are widely investigated to study the relationship between network topology and network activity [1]. Nevertheless, in practice, a network is usually classified into several communities while a community is composed of a group of nodes in the network while the community is more densely connected than with the other nodes of the network. For instance, the World-wide Airport Network is composed of Airport Network of US, Airport Network of India, Airport Network of China and so forth. Moreover, community detection methods are presented and standards are proposed in order to measure the community partition [2–4]. This indicates most networks are not isolated but interacting with each other, being referred to as a *network of networks* (NoN). Within each individual network, the connectivity links are maintained to represent various connections (often called *inter-contacts*); whereas links are added to connect each network to others (being referred to as *intra-contacts*) [5]. This type of networks is capable of modeling a number of real-world systems, for instance, the European air transport system [6], the global cargo ship network [7], living organisms [8–10] and social networks [11,12].

Recently, researchers started to investigate a special class of NoN, while each node possesses different types of links on dif-

ferent layers [13], being referred to as Multiplex networks. Multiplex networks are widely adopted in various areas, among which, the epidemic spreading process is a rapidly evolving topic [14–16]. In [16,17], a two-layered multiplex network is presented in order to analyze the epidemic spreading process, while the application of this two-layered network model is also thoroughly investigated [18,19]. In this model, the two layers are referred to as a virtual layer and a physical one respectively. The physical layer is composed of individuals while the links represent the corresponding practical body contacts. For the virtual layer, it is consisting of virtual nodes (with each node corresponding to an individual on the physical layer); here, the connections indicate relationships incurred by various social ties, such as phone call, twitter, Wechat and etc. On the virtual layer, the information about the epidemic is spreading among nodes; whereas on the physical layer, biological elements carrying the virus of epidemic are exchanged among individuals through physical contacts.

In order to investigate the epidemic spreading process, various models are presented, for instance, susceptible-infected (SI), susceptible-infected-susceptible (SIS), susceptible-infected-recovered (SIR) and etc. [1,20]. In [21], the SIR model is adopted for the analysis of epidemic spreading process in multilayered networks. While in [14], the SIS model is applied to investigate the epidemic spreading process in multilayered networks. Furthermore, in [22], the SIS model is investigated in multiplex networks using a contact-contagion formulation. While in order to improve the evaluation efficiency, stochastic analysis is performed to pre-

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dict the long run behaviors of multiplex networks with the adoption of the proposed stochastic architectures for SIS model in [23]. For this class of disease as H1N1 (Swine Influenza), H5N1 (Avian Influenza) or the SEVERE Acute Respiratory Syndrome (SARS) [24], the favorite approach to describe the spreading process is the SIR model. For SIR model, an infected individual is able to be recovered from an infected state due to the effect of medical treatments or self-rehabilitation.

As discussed previously, a network is composed of a number of communities. Hence, in practice, the epidemic might be spreading among different communities; whereas the communities are usually intra-connected due to the existence of frequent communications among individuals. Thus, the epidemic spreading processes in multi-communities are widely investigated. In [25], an analytical approach is presented and dynamic interactions between two different SIR propagation processes are thoroughly investigated. In [26], the scenario of recurrent epidemics is studied which is an extension from a single community. Furthermore, in [27], the epidemic spreading process is investigated to reproduce the synchronized and mixed outbreak patterns in two communities.

For the epidemic spreading process in multi-communities, there usually exist multi-summits (here, each indicates a larger proportion of individuals being affected by the epidemic). Nevertheless, the summits of the epidemic spreading process in multi-communities are likely to occur at different time. As indicated by previous studies, the disparity of different summits is likely to be affected by a number of factors, such as infectivity probabilities, recovery probability, network topology and etc. Nevertheless, it is still of great interest to investigate the problem of minimizing the range of individuals being affected by the epidemic. Hence, in this manuscript, the evolution process is further investigated which is spreading in two intra-connected communities. Here, the adopted model to mimic the spreading process is the traditional SIR model. Furthermore, each community is characterized by a two-layered multiplex model. Thus, the effect of incorporating virtual layer on the epidemic spreading process is pursued with the analysis of illustrative examples.

Overall, the contributions of this manuscript are summarized as follows:

1. The epidemic spreading process in two communities is investigated while each community is modeled with the adoption of a two-layered multiplex network;
2. The factors that affect the evolution process is thoroughly incorporated, especially the consideration of virtual layer which provides a potential efficient means to control the epidemic spreading process.

The rest of the paper is organized as follows. Section 2 presents some hypothesis used in this manuscript. While the fundamentals of multiplex networks are presented in Section 3; furthermore, the state transition tree is also derived. Then, the construction process of the intra-communities is given in Section 4. Corresponding result and analysis are presented in Section 5. Finally, Section 6 concludes the paper.

2. Assumptions

Here, some assumptions are listed as follows:

- 1) An individual becomes aware of the epidemic due to communications with neighbors, this occurs with a probability of λ ;
- 2) The infected individual is aware of the epidemic immediately;
- 3) For the seasonal epidemic, an individual is likely to forget the awareness and becomes unaware again in the future. This happens with a probability of δ ;

- 4) For a susceptible individual, if he or she is aware of the epidemic, then the infectivity is reduced by a factor of γ , as preventive measures are to be taken. Hence, if the original infectivity is β^U , then the reduced probability is $\gamma\beta^U$;
- 5) The infected individual is recovered with a probability of μ .

3. Methods

3.1. Two-layered multiplex networks

In this manuscript, the epidemic is spreading among multi-communities while each community is indicated by a two-layered multiplex network consisting of a virtual layer and a physical one respectively. The nodes on the virtual layer can exchange information related with the epidemic with each other through virtual contacts; while biological elements carrying the virus are transmitted among individuals through physical contacts. For an illustration, a system consisting of two communities (for instance, A and B) is presented in Fig. 1. As in Fig. 1, *intra-contacts* between the two communities are denoted by dotted lines through which the intra-communication is conducted. For certain community, the connections among nodes on the virtual or individuals on the physical layer might be totally different. Here, the connections in certain layer are represented by corresponding topology.

For the presented model in this work, the information transition process on the virtual layer and epidemic spreading process on the physical layer are relevant processes. As to the virtual layer, if an individual is aware of the epidemic, then preventive measures can be taken which reduces the infectivity by a factor accordingly; this is referred to as self-protection. Furthermore, if an individual on the physical layer is infected, then he or she becomes aware of the epidemic immediately; this indicates the self-awareness ability of the individual.

In order to investigate the epidemic spreading process, the SIR model is adopted in this manuscript. For the physical layer, an individual is anticipated to be in one of the three states, i.e., *susceptible* (**S**) in which the individual is free of the epidemic but might be infected via physical contacts with the infected neighbors, *infected* (**I**) in which the individual is infected by the epidemic and can affect its susceptible individuals, and *recovered* (**R**) in which the individual is recovered from the epidemic through applying medical treatment. For simplicity, the recovered individual is assumed to be immune to the epidemic in this manuscript. Then, the state transition for the individual on the physical layer is derived as $S \rightarrow I \rightarrow R$.

Whereas, for the virtual layer, corresponding node for certain individual is likely to be in one of the following two states, i.e., *unaware* (**U**) in which the individual has no information regarding with the epidemic, *aware* (**A**) in which the susceptible individual is already aware of the epidemic and preventive measures can be taken to protect himself (for instance, reducing the frequency of outside activities, wearing face masks, washing hands frequently to remove the possible virus, taking the vaccination, doing exercises and so forth [28–30]). The individual without awareness will be aware of the epidemic due to the information transition process on the virtual layer; moreover, due to the assumption of seasonal epidemic, an individual with awareness will forget the epidemic. Hence, corresponding transition on the virtual layer is anticipated to be $U \leftrightarrow A$.

Overall, in the proposed model, each individual (including corresponding node on the virtual layer) falls into the following state combinations, i.e., **US**, **UI**, **UR**, **AS**, **AI** and **AR**. Fig. 2 illustrates the possible transitions between the state combinations of individuals for community A, the outgoing arrow from a given node at time t points to the possible successor state at time step $t+1$ where $X_{PA}Y_{VA}$ means that the state of the individual on the physical layer is in X state and the corresponding node on virtual layer for the in-

Fig. 1. An illustration of two communities with intra-connections. Each community is modeled as a two-layered multiplex network. Dashed lines indicate that each individual on the physical layer corresponds to a node on the virtual layer; the solid lines show the inter-connections at each layer while the dotted lines denote the intra-connections among the individuals in the investigated two communities.

Fig. 2. Possible transitions between the states from a given state at time step t to the possible successor state at time step $t + 1$ for certain individual in community A.

Fig. 3. An illustration of node $x_{i,j}$ and its neighbors listed as $x_{i1,j}$, $\dots$, $x_{il,j}$, $\dots$, $x_{im,j}$.

dividual of community A is in Y state and. As to the corresponding probabilities for individual i , they are denoted as p_i^{US} , p_i^{UI} , p_i^{UR} , p_i^{AS} ,

Fig. 4. Transition probability trees for states of an individual in certain community (a) AI, (b) US and (c) AS per time step. AI, UI, US, AS, AR and UR indicate the possible states of certain individual. U: unaware; A: aware; S: susceptible; I: infected; R: recovered.

represented by corresponding topology.

Fig. 5. Possible transitions between the states of two selected individuals through an intra-connection from a given state at time step t to the possible successor state at time step $t + 1$. Here, P and V indicate physical and virtual layers respectively.

p_i^{AI} and p_i^{AR} respectively. Whereas in community B, similar possible transitions can be obtained accordingly.

3.2. Infection process

For the investigated system, a susceptible individual is likely to be infected in two ways. The first one is incurred by physical contacts with the infected neighbors via inter-contact inside the same community. Whereas, the other one is incurred by physical contacts with infected individuals from the other community if corresponding intra-contact exists.

Fig. 6. Average value of the proportion of infected individuals, the experiment is performed for 10 runs.

Table 1

Possible state combinations for two individuals from different communities before updating incurred by inter-connection.

	S_B	I_B	R_B
S_A	$S_A S_B$	$S_A I_B$	$S_A R_B$
I_A	$I_A S_B$	$I_A I_B$	$I_A R_B$
R_A	$R_A S_B$	$R_A I_B$	$R_A R_B$

3.2.1. Infection via intra-contact

For two randomly selected individuals from different communities, corresponding state of one individual (usually susceptible) might be affected by the state of the other if intra-connection between the two nodes exists. Here, the infection processes among the individuals from different communities are assumed to be occurred at the end of each time step.

As stated previously, the possible states of an individual on the physical layer are listed as S , I and R . Then, possible state combinations for the above two individuals are presented in Table 1.

Here, let X_m and X'_m indicate the states of the investigated individual in community m before and after updating through the intra-connection respectively, where $X \in \{S, I, R\}$ and $m \in \{A, B\}$. As indicated by the results in Table 1, if $X_A X_B \in \{S_A S_B, S_A R_B, I_A I_B, I_A R_B, R_A S_B, R_A I_B, R_A R_B\}$, then corresponding state remains, i.e., $X'_A = X_A$ and $X'_B = X_B$. For instance, if $X_A X_B = I_A I_B$, then both individuals are infected; hence, even if the intra-connection exists, corresponding state will not be changed. For the scenarios of $X_A X_B \in \{S_A I_B, I_A S_B\}$, then the susceptible individual is likely to be affected by the infected one. Corresponding updating process is presented in Fig. 5.

With incorporation of virtual layer, the infectivity probability (denoted by β_{AB}) for intra-community infection is related with the state of corresponding node for the investigated susceptible individual on the virtual layer. This is due to the reason that if the susceptible individual is aware of the epidemic, then he or she is likely to take preventive measures i.e., self-protection. Hence, for a susceptible individual in community A with an infected neighbor in community B (i.e., $S_A I_{PB}$), if he or she is unaware of the epidemic (i.e., scenario (a) in Fig. 3), then it is likely to be infected with a probability of β_{AB} ; otherwise, corresponding state combination remains with a probability of $1 - \beta_{AB}$. Nevertheless, if the susceptible individual is aware of the epidemic (as depicted by Fig. 3(b)), then the infection probability is to be reduced with a factor of γ_{AB} ($0 \leq \gamma_{AB} \leq 1$) (i.e., corresponding infectivity probability equals to $\gamma_{AB} \beta_{AB}$). Otherwise, the state combination of $S_A I_{PB}$ remains with a probability of $1 - \gamma_{AB} \beta_{AB}$. For the state combination of $I_{PA} S_{PB}$, similar analysis can be performed.

3.2.2. Infection via inter-contact

Then, the infection process through inter-contacts inside certain community is illustrated as follows. Here, certain community is presented for an illustration.

In a two-layered multiplex network, there are a number of neighbors for certain node on the virtual layer or certain individual on the physical one, i.e., $x_{i,j}$ ($j = \{1, 2\}$), here 1 and 2 indicate the virtual and physical layer respectively. If certain node is aware of (or infected by) certain epidemic, then the source of infection can be any neighbors. Thus, it is highly necessary to consider all the neighbors in order to determine the infectivity probability or information transition probability for certain individual. For $x_{i,j}$, the total number of its neighbors is assumed to be m . Fig. 3 shows an illustration of node $x_{i,j}$ and its m neighbors.

Similar as [17], for the scenario of certain individual being not informed by any neighbors from the same community, the corresponding probability is indicated by r_i . Then, for the case of being not infected by any neighbors from the same community if $x_{i,j}$ is aware, the probability is represented by q_i^A . As to the scenario of individual $x_{i,j}$ being not infected by any neighbors from the same community if $x_{i,j}$ is unaware, the probability is denoted as q_i^U . The above defined probabilities are described as follows

$$\begin{cases} r_i = \prod_{l=1}^m (1 - \lambda p_l^A) \\ q_i^A = \prod_{l=1}^m (1 - \gamma \beta^U p_l^{AI}) \\ q_i^U = \prod_{l=1}^m (1 - \beta^U p_l^{AI}) \end{cases} \quad (1)$$

where m represents the total number of neighbors for individual $x_{i,j}$. Here, for individual l , $p_l^A = p_l^{AI} + p_l^{AS} + p_l^{AR}$. The parameters for (1) are the same as those introduced in Section 2. With provided parameters, corresponding transition probability trees for state combinations of an individual are further presented in Fig. 4 according to the analysis of possible transitions presented in Fig. 2. As in Fig. 4, the state updating process is divided into two sub-steps, i.e., state updating process on the virtual layer and state updating process on the physical layer.

For the virtual layer, the state switching of either $U \rightarrow A$ or $A \rightarrow U$ occurs. If the initial state combination is US (as in Fig. 4(b)), then the individual will be informed by his neighbors of the epidemic with a probability of $1 - r_i$ where r_i denotes the probability of being not informed by any neighbors from the same community. Hence, corresponding state combination is likely to be AS with a probability of $1 - r_i$ and remains to be US with a probability of r_i . Assuming the initial state combination is AI or AS , then the individual is likely to become unaware of the epidemic with a probability of δ ; hence, the corresponding state remains with a probability of $1 - \delta$. This is used to mimic the seasonal property and the fact of forgetting the awareness for the individual. For simplicity, in this manuscript, the recovered individual is supposed to be immune to the disease and aware of the epidemic with a probability of 1; furthermore, the recovered individual remains to be aware of the epidemic during the investigated time interval, thus the state combination of UR and AR is not neglected.

$$\begin{cases} p_i^{US}(t+1) = p_i^{US}(t) * r_i * q_i^U + p_i^{AS}(t) * \delta * q_i^U \\ p_i^{AR}(t+1) = p_i^{AI}(t) * \{\mu * \delta + (1 - \mu) * \delta\} \\ p_i^{AS}(t+1) = p_i^{US}(t) * (1 - r_i) * q_i^A + p_i^{AS}(t) * (1 - \delta) * q_i^A \\ p_i^{AI}(t+1) = p_i^{AI}(t) * (1 - \mu) + p_i^{US}(t) * \{(1 - r_i) * (1 - q_i^A) + r_i * (1 - q_i^U)\} \\ \quad + p_i^{AS}(t) * \{\delta * (1 - q_i^U) + (1 - \delta) * (1 - q_i^A)\} \end{cases} \quad (2)$$

Then, the updating process in the physical layer is studied. Given a state combination of AS , this indicates the susceptible individual is already aware of the epidemic; thus, the susceptible individual will be infected with a probability of $1 - q_i^A$ and the state combination of AS will be remained with a probability of q_i^A (refer to formula (1) to determine the value). Whereas for the state

Fig. 7. Proportion of individuals who are aware of the epidemic.

combination of US, the susceptible individual (who is unaware of the epidemic) will be infected with a probability of $1 - q_i^U$ (in this manuscript, the individual is immediately aware of the epidemic once infected, this indicates UI becomes AI immediately with a probability of 1), whereas US remains with a probability of q_i^U (refer to formula (1) to determine the value). If the state combination is AI, then the individual will become healthy again (i.e., recovered) with a probability of μ , this might be due to personal self-healing or medical treatment; otherwise, he or she remains to be in the state of AI. For simplicity, we assume the recovered individual is immediately aware of the infected fact. This indicates the state combination of UI becomes AI immediately with a probability of 1.

According to the above analysis, the corresponding state transition probabilities can be summarized as formula (2) where $p_i^{US}(t+1)$, $p_i^{AS}(t+1)$, $p_i^{AI}(t+1)$ and $p_i^{AR}(t+1)$ denote the probabilities of the corresponding states of individual i after evolving inside the community. Then, the probabilities of p_i^{US} , p_i^{AR} , p_i^{AS} , p_i^{AI} can be determined accordingly (here, $p_i^{UR} = 0$ and $p_i^{UI} = 0$ due to the pre-assumptions).

Let $p_{i,A}^S(t)$, $p_{i,A}^I(t)$ and $p_{i,A}^R(t)$ be the probabilities for node i in network A being in the states of S, I and R at the investigated time t respectively. Similarly, the corresponding state probabilities for node j in network B are obtained as $p_{j,B}^S(t)$, $p_{j,B}^I(t)$ and $p_{j,B}^R(t)$ accordingly. The state probabilities should meet the following rela-

tionships.

$$\begin{cases} p_{i,A}^S(t) + p_{i,A}^I(t) + p_{i,A}^R(t) = 1 \\ p_{j,B}^S(t) + p_{j,B}^I(t) + p_{j,B}^R(t) = 1 \end{cases} \quad (3)$$

where the values can be determined with the adoption of the variables in formula (2), for instance, $p_{i,A}^R(t) = p_i^{UR} + p_i^{UR}$.

4. Community network construction

For community A , the multiplex network is consisting of two layers with the degree distributions being denoted as $P_{AV}(k)$ and $P_{AP}(k)$ for the virtual and physical layers respectively, while for community B , the degree distributions are provided as $P_{BV}(k)$ and $P_{BP}(k)$ for the virtual and physical layers respectively. As to the connections between the physical layers of communities A and B , corresponding degree distribution is represented as $P_{ABP}(k)$. Hence, the average degrees of the physical and virtual layers for communities A and B are obtained as $\langle k_{AP} \rangle$, $\langle k_{AV} \rangle$, $\langle k_{BP} \rangle$ and $\langle k_{BV} \rangle$ respectively, whereas the average degree for the intra-community connections is denoted as $\langle k_{ABP} \rangle$. Here, for simplicity, only two communities are incorporated; if multi-communities are investigated, similar analysis can be performed accordingly.

Here, we first generate two separated physical layers for A (through Barabási–Albert (BA) scale-free network generating algorithm) and B (through Erdős–Rényi (ER) random network generating algorithm) respectively with the same size of N and the pre-specified degree distributions. Then corresponding virtual layers can be determined accordingly, there is a connection between each individual on the physical layer and corresponding node on the virtual layer. Then, the virtual layers are connected with the provided degree distributions.

Later, links should be added between the individuals from the physical layer for community A and those for community B . This process is done as follows:

- 1) Firstly, two individuals are randomly chosen from physical layers for community A and B ;
- 2) The two individuals are connected if there is no connection between them;

Fig. 8. Illustration of infected individuals at different time step.

Table 2
Parameters of the investigated system.

$\langle k_{AP} \rangle = 6$	$\langle k_{AV} \rangle = 6.5$	$\langle k_{BP} \rangle = 6$	$\langle k_{BV} \rangle = 6.5$
$\langle k_{ABP} \rangle = 1$	$N = 1000$	$\lambda = 0.8$	$\mu = 0.1$
$\beta_{AB} = 0.005$	$\gamma_{AB} = 0.8$	$\beta^U = 0.1$	$\gamma = 0.1$
$\delta = 0.1$	$N_I = 10$		

Table 3
Obtained time point for achieving the maximum of infected individuals in the spreading process for different communities.

	With virtual layer			Without virtual layer		
	T_A	T_B	ΔT	T_A	T_B	ΔT
1	14	51	37	7	28	21
2	13	54	41	4	22	18
3	15	52	37	7	24	17
4	13	49	36	6	27	21
5	12	48	36	7	29	22
Avg. of ΔT	/	/	37.4	/	/	20

- 3) The above processes are repeated until the anticipated average intrs-community degree is met.

For simplicity, a system consisting of two communities is investigated in this work; if more communities are incorporated, similar construction process can be applied with minor modification.

5. Results analysis

Two communities (i.e., A and B) are considered in this manuscript while *intra-contacts* exist. Each community is represented by a two-layered multiplex network consisting of a physical layer and a virtual one. For simplicity, two communities are of the same number of individuals (i.e., N), thus the total number of individuals in the investigated system equals to $2N$.

Simulations are conducted to investigate the epidemic spreading process the adoption of MC simulation. Stable output is obtained if reasonable simulation runs are used. Initially, a number of N_I individuals in community A are randomly selected to be infected. During the epidemic transition process, individuals in community B are infected due to intra-connections. Simulation stops if stationary states of the system are achieved or the investigated time steps are reached. Corresponding parameters are listed as in Table 2.

With the parameters in Table 2, simulations can be performed with the obtained results being depicted in Fig. 6. Here, the average value is obtained for 10 simulations. For comparison, the scenario of excluding the virtual layer is also investigated. As per by the simulation results, the incorporation of virtual layer is capable of reducing the proportion of infected individuals to a large extent. This phenomena is consistent with common sense as once an individual is aware of the epidemic, various preventive measures are taken to reduce the infectivity.

For the investigated system with provided parameters in Table 2, there are two summits occurred, being referred to as M curve. For different experiment, the summits are likely to come at different time step. This is due to the different nodes being selected for initial infection and the stochastic fluctuations of simulation based approaches. Furthermore, disparity of the summits of the epidemic spreading process in different communities is also presented in Table 3 for different experiments. Here, five simulations are conducted and presented for simplicity. As shown by the obtained time step of the summits, we can see the summit for communities without the virtual layer always comes later than that for the scenario with virtual layer. This indicates that the incorporation of virtual layer is able to postpone the summit of the

Fig. 9. Simulation results for different topologies for communities A and B. ($\langle k_{ABP} \rangle = 0.8$).

epidemic spreading process. Furthermore, as indicated by the results, for the scenario with virtual layer, the average value of disparity is obtained as 37.4; nevertheless, if the virtual layer is not incorporated, the corresponding average value is obtained as 20. This shows the disparity between two summits is likely to be enlarged if the virtual layer is investigated.

Furthermore, the trend of proportion of individuals with awareness is illustrated in Fig. 7 for certain simulation. As indicated by the results, we can draw the conclusion that the proportion is becoming stationary with the increasing of the mission time. This is due to the reason that with the proceeding of the evolving process, the infected individuals are close to zero; most individuals fall into the state combination of AR; this can be indicated by Fig. 4. Furthermore, the increase of proportion of individuals with awareness in the virtual layer for community A (which is infected first) is faster than that for community B.

Furthermore, the states of the 2000 nodes are presented in Fig. 8 for different time steps for certain simulation. As in Fig. 8, the proportion of infected and reversed individuals in A is much larger than that in B. This indicates the previous conclusion that the epidemic spreading faster in community A. This is due to the reason that the average degree of intra-community is much smaller than the degree distributions of communities A and B, thus the infectivity among communities is largely affected by the average degree of intra-contacts.

As stated previously, the disparity of the two summits for the M curve is affected by a number of factors, such as topology of community, intra-degree distribution, infectivity probability inside community, intra-infectivity probability, existence of virtual layer, self-protection and etc. The effects of system topology on the disparity of the summits of spreading in different communities are investigated. The obtained results are presented in Fig. 9; here, the parameters remain as in Table 2. As per by the results in Fig. 9, we can draw the conclusion that the system topology plays an important role in affecting the epidemic spreading process in multi-communities. If the effects of other factors are focused, similar analysis can be performed.

Moreover, the nodes on different virtual layers for different communities might be also intra-connected; this is consistent with practice, for instance, two individuals from different countries might only be friends through internet tools such as twitter. If the intra-connections are incorporated, then similar analysis can be performed with minor modification of the probability transition tree. The incorporation of intra-connection between the different virtual layers is anticipated to capable of reducing the infection of the communities further.

6. Conclusion

In practice, the epidemic might spread in various communities, while the communities might be interacted with each other.

Hence, it is of interest to investigate the epidemic spreading process in multi-communities. For each community, a two-layered multiplex network model is adopted, i.e., virtual layer and physical layer, to investigate the epidemic spreading process. In this manuscript, the SIR model is adopted to describe the infectious process. If virtual layer is incorporated, then corresponding state transition tree is derived. Then, MC simulation is performed to investigate the epidemic spreading process. As indicated, the incorporation of virtual layer is capable of reducing the proportion of infected individuals to a large extent. This is consistent with common sense as individuals are more likely to take protective measures if they already know the epidemic. Furthermore, the occurrence of the maximum value of the transition process in certain community can be postponed if the virtual layer is considered. Moreover, the difference between the summits of different trends is able to be reduced greatly by incorporating the virtual layer.

Acknowledgement

This work was supported in part by the National Science Foundation of China (Grant no. 61601371 and no. 61371024), Aviation Science Fund of China (Grant no. 2016ZD53035), Industry-Academy-Research Cooperation Project of AVIC (Grant no. cxy2013XGD14), Fundamental Research Funds for the Central University under Grant 3102016QD042 and Open Fund of the Key Laboratory for Reliability Physics and Application Technology of Electronic Components.

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