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Dynamical behavior of epidemic on complex networks with population mobility*

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In this paper, we study the dynamical behaviour of epidemic on complex networks with population mobility. In our model, the number of people on each node is unrestricted as the nodes of the network are considered as cities, communities, and so on. Because people can travel among different cities, we study the effect of population's mobility on the epidemic spreading. In view of the population's mobility, we suppose that the susceptible individual can be infected by an infected individual in the same city or other connected cities. Simulations are presented to verify our analysis.

Keywords: complex network, mobility, heterogeneity, epidemic threshold
PACC: 0250, 0565, 0520, 8000

1. Introduction

In the past few years, complex networks have attracted an increasing attention, because many real-life technological, social and biological systems have complex network-like structures. Some important examples include the Internet, the World Wide Web (WWW), and scientific-collaboration networks, etc. A main quantity that characterizes the structure and dynamics of such networks is the so called degree distribution $P(k)$, the probability that a randomly chosen node within the network has degree k. In order to understand the mechanism of network formation, Watts and Strongatz proposed a model for complex networks:[1] small-world network, whose degree distribution $P(k)$ obeys the Poisson distribution. This kind of networks is viewed as homogenous networks. However, Barabási and Albert address another new model of complex networks: scale-free network (BA).[2] In such network the degree distribution $P(k)$ obeys a power law $P(k) \backsim k^{-\gamma}$. In contrast to the SW model, the scale-free network is a heterogenous network.

An interesting dynamical process on complex networks is the spread of epidemics. The SIS (susceptible-infected-susceptible) model and the SIR (susceptible-infected-recovered/removed) model are considered as the convenient way to describe the fundamental mechanism of diseases.[3] For the SIS epidemic model, each individual can exist in two states: S-susceptible and I-infected. A susceptible individual can become infected at certain rate λ when it is in contact with some infected individuals, while infected individuals may recover and become susceptible again at certain rate γ. For the SIR model, recovery (class R) individuals have permanent immunity, so that they can never get disease again or pass it again.

Many researchers have studied the spread of epidemics on complex networks,[4−18] and tried to understand how the structure, such as the degree distribution, influences the spreading. When epidemics spread on homogenous networks, the results both for SIS and SIR models are that the transmission of an infectious

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agent can be characterized by the epidemic threshold λ_c. The disease will break out when the infection rate $\lambda > \lambda_c$; otherwise, the contagion is self-limiting. However, when epidemics spread on heterogenous networks, the most striking result is that for SIS and SIR models the epidemic threshold λ_c is null if the size of a heterogenous network is sufficiently large.[4−6]

Many good results about epidemic diseases on networks have been obtained. However, most previous research papers assumed that a node is an individual. As a result, the deeper structure of networks were neglected, such as the mobility of individuals between different cities was ignored. Most recently, Vittoria Colizza *et al* studied the behaviour of two basic types of reaction–diffusion processes ($B \to A$ and $B + A \to 2B$),[7] they supposed that a node of the network can be occupied by any number of individuals and the individuals can diffuse along the link between nodes. The two basic reaction-diffusion processes can be used to model the spreading of epidemic diseases with SIS model.[7] In the epidemic terminology, a node can be viewed as a city, i.e, all people have the same degree k if they live in the same city (the node with degree k), and the diffusion of particles among different nodes can be considered as the travel of people among different cities. They supposed that the infection may happen inside a city, however, the infection may also happen in different cities by other media, e.g., for the Avian Influenza, different places' poultry can be infected by migratory birds even though the poultry have no mobility.

We suppose that the infection can also happen in different cities, and study the effect of this kind of epidemic spreading on the epidemic threshold. This can be done by introducing a probability of spreading of the infection to the neighbouring nodes without the need of diffusion of infected particles. In fact, as we will show, this mechanism is in part equivalent to the diffusion of the particles.

The rest of this paper is organized as follows: In Section 2, in order to find out the effect of mobility of individuals, we first consider the epidemic spreading only take place inside a city and mobility is denied, then the mobility of individuals in different cities is considered in Section 3 and Section 4. In Section 3, we only discuss that the epidemic spreading happens in different cities, we neglect the spreading of the disease inside a city. In Section 4, both kind of spreadings are considered. We discuss two cases of infection taking place in different cities. Firstly, the infection rate is proportional to $\Theta_1 = \Sigma_{k'} \frac{P(k'|k)I_{k'}}{k'}$;[12,15] secondly, the infection rate is proportional to $\Theta_2 = \Sigma_{k'} P(k'|k)I_{k'}$.[4,5] Section 5 our analysis is confirmed with numerical simulations. Finally, conclusions are given in Section 6.

In this paper, we assume that the complex network is uncorrelated. It means that the conditional probability $P(k'|k)$ that a link departing from a node of degree k points to a node of degree k' is independent of k, i.e., $P(k'|k) = k'P(k')/\langle k\rangle$, where $\langle k\rangle = \Sigma_k P(k)k$.

2. Epidemic spreading without mobility of individuals

In order to find out the effect of mobility of individuals, we first assume that mobility is zero. In this case, the dynamics equations are:

$$\begin{aligned} \frac{\mathrm{d}I_k(t)}{\mathrm{d}t} &= \alpha k S_k \Theta_i + \beta S_k I_k - \mu I_k, \\ \frac{\mathrm{d}S_k(t)}{\mathrm{d}t} &= -\alpha k' S_{k'} \Theta_i - \beta S_k I_k + \mu I_k, \quad i = 1, 2, \end{aligned} \tag{1}$$

where μ is the rate for infected individuals becoming susceptible again, and $P(k'|k)$ is the conditional probability that a node with degree k is connected to a node with degree k'. β and α are the epidemic rates inside a city and among different cities respectively. The term $\beta S_k I_k$ means the infection coming from same city, and the term $\alpha k' S_{k'} \Theta_i$ stands for the density of S_k which is infected by other cities' infected individuals. Here we should note that the total density $S_k + I_k$ is not changed because there is no mobility of individuals among different cities (this case is different from the discussion in the following sections where we consider the mobility, as a result, the individual's degree may change), so we can let $S_k + I_k = 1$.

Let $\frac{\mathrm{d}I_k(t)}{\mathrm{d}t} = 0$, from the first equation of Eqs.(1) one has

$$\begin{aligned} &\alpha k S_k \Theta_i + \beta S_k I_k - \mu I_k \\ =&(1 - I_k)[\alpha k \Theta_i + \beta I_k] - \mu I_k = 0, \end{aligned} \tag{2}$$

namely,

$$I_k = \frac{-(\alpha k\Theta_i + \mu - \beta) + \sqrt{(\alpha k\Theta_i + \mu - \beta)^2 + 4\alpha\beta k\Theta_i}}{2\beta}, \quad i = 1, 2. \tag{3}$$

The case $I_k < 0$ is omitted for realistic reason.

Here we assume that $\beta/\mu < 1$. Under this condition, the epidemic disease for standard SIS model will not be prevalent:[3] the disease is self-limiting. However, we will demonstrate that the epidemic can prevail when the heterogeneity of network is considered.

We impose a self-consistent condition for Θ_2, we have

$$\begin{aligned}\Theta_2 &= \Sigma_{k'} P(k'|k) I_{k'} \\ &= \Sigma_{k'} P(k') k' \frac{-(\alpha k'\Theta_2 + \mu - \beta) + \sqrt{(\alpha k'\Theta_2 + \mu - \beta)^2 + 4\alpha\beta k'\Theta_2}}{2\beta\langle k\rangle}.\end{aligned} \tag{4}$$

$\Theta_2 = 0$ is always a solution for Eq.(4). In order to obtain a non-zero solution for Θ_2, the condition

$$\frac{\mathrm{d}}{\mathrm{d}\Theta_2}(\Sigma_{k'} P(k') k' \frac{-(\alpha k'\Theta_2 + \mu - \beta) + \sqrt{(\alpha k'\Theta_2 + \mu - \beta)^2 + 4\alpha\beta k'\Theta_2}}{2\beta\langle k\rangle})|_{\Theta_2=0} > 1 \tag{5}$$

must be satisfied. This inequality implies

$$\frac{\alpha\langle k^2\rangle}{\langle k\rangle(\mu - \beta)} > 1, \quad \text{i.e.,} \quad \frac{\alpha}{\mu - \beta} > \frac{\langle k\rangle}{\langle k^2\rangle}, \tag{6}$$

this condition demonstrates that epidemic diseases will always become endemic for a heterogenous network with sufficiently large size.

For the case Θ_1, by using the same method, we obtain

$$\frac{\alpha}{\mu - \beta} > 1, \tag{7}$$

this case suggests that the epidemic threshold is irrelevant to the topology of the network, which is similar to the results in Ref.[12].

In the following sections, we take into account the mobility of individuals in different cities, so the individuals' degrees may change, that is, the total density $S_k + I_k$ is not an invariant, but the average density $n = \Sigma_k P(k)(S_k + I_k)$ is an invariant.

3. Spreading of epidemic among different cities

Let V denote the size of the network, N_{S} and N_{I} are the numbers of susceptible and infective individuals respectively, so the total number of individuals in the network is $N = N_{\mathrm{S}} + N_{\mathrm{I}}$ and $n = N/V$ is the average density of people. Because the number of individuals on each node is a random non-negative integer, set a_i and b_i as the numbers of S and I stores on node i. In order to take into account the heterogenous quality of networks we have to explicitly consider the presence of nodes with very different degree k. A convenient representation of the system is therefore provided by the following quantities:

$$S_k = (\Sigma_{i|k_i=k} a_i)/v_k, \quad I_k = (\Sigma_{i|k_i=k} b_i)/v_k, \tag{8}$$

where v_k is the number of nodes with degree k and the sums run over all nodes i having degree k_i equal to k.

For simplicity, we assume that the mobility of people is unitary time rate 1 along one of the links departing from the node in which they are at a given time.[7] This implies that at each time step an individual occupies in the node with degree k will travel to another city with probability $1/k$.

Now the dynamics of epidemic spreading can be described as follows:

$$\begin{aligned}\frac{\mathrm{d}I_k(t)}{\mathrm{d}t} &= -I_k(t) + k\Sigma_{k'} P(k'|k)\frac{1}{k'}[(1-\mu)I_{k'}(t) + \alpha k' S_{k'}\Theta_i], \\ \frac{\mathrm{d}S_k(t)}{\mathrm{d}t} &= -S_k(t) + k\Sigma_{k'} P(k'|k)\frac{1}{k'}[S_k(t) + \mu I_{k'}(t) - \alpha k' S_{k'}\Theta_i], \quad i = 1, 2.\end{aligned} \tag{9}$$

We now give the explanation of the right-hand side terms of the first equation of Eqs.(9). The first term $-I_k$ is obtained by considering that at each time step the infected people lived in a city of degree k move to other cities with unitary rate, and the positive term $k\Sigma_{k'}P(k'|k)\frac{1}{k'}[(1-\mu)I_{k'}(t)+\alpha k'S_{k'}\Theta_i]$ contributing to the infected individual density is obtained by summing up the contribution of all individuals moving to the city of degree k from their neighbours of any degree k', including the new infected individuals generated by the term $\alpha k'S_{k'}\Theta_i$ $(i=1,2)$. The right-hand side terms of the second equation of Eqs.(9) have the similar explanation.

By considering the stationary sate of Eqs.(9), we have

$$\begin{aligned} I_k(t) &= k\Sigma_{k'}P(k'|k)\frac{1}{k'}[(1-\mu)I_{k'}(t)+\alpha k'S_{k'}\Theta_i],\\ S_k(t) &= k\Sigma_{k'}P(k'|k)\frac{1}{k'}[S_{k'}(t)+\mu I_{k'}(t)-\alpha k'S_{k'}\Theta_i],\\ & i=1,2. \end{aligned} \tag{10}$$

As shown in Eqs.(9) the average density $n=N/V$ is an invariant constant.

Combining

$$I=\Sigma_k P(k)I_k, \quad S=\Sigma_k P(k)S_k \tag{11}$$

and the assumption $P(k'|k)=k'P(k')/\langle k\rangle$(that is, the network is an uncorrelated network), we obtain

$$\begin{aligned} I_k(t) &= \frac{k}{\langle k\rangle}[(1-\mu)I+\alpha T_1\Theta_i],\\ S_k(t) &= \frac{k}{\langle k\rangle}[S+\mu I-\alpha T_1\Theta_i], \quad i=1,2, \end{aligned} \tag{12}$$

where $T_1=\Sigma_k P(k)kS_k$.

Manipulating the operator$\Sigma_k P(k)$ on both sides of Eqs.(12), we obtain

$$\begin{aligned} I &= (1-\mu)I+\alpha T_1\Theta_i,\\ S &= S+\mu I-\alpha T_1\Theta_i, \quad i=1,2, \end{aligned} \tag{13}$$

that is,

$$\mu I=\alpha T_1\Theta_i, \quad i=1,2. \tag{14}$$

From Eqs.(12)

$$\begin{aligned} T_1 &= \Sigma_k P(k)kS_k\\ &= \Sigma_k P(k)k\frac{k}{\langle k\rangle}[S+\mu I-\alpha T_1\Theta_i]\\ &= \frac{\langle k^2\rangle}{\langle k\rangle}S. \end{aligned} \tag{15}$$

For the case of Θ_1, since

$$\Theta_1=\Sigma_{k'}\frac{P(k'|k)I_{k'}}{k'}=\frac{I}{\langle k\rangle}. \tag{16}$$

By inserting Eqs.(15), (16) into Eq.(14), we obtain

$$\mu I=\alpha\frac{I}{\langle k\rangle}\frac{\langle k^2\rangle}{\langle k\rangle}S=\alpha I\frac{\langle k^2\rangle}{\langle k\rangle^2}(n-I), \tag{17}$$

that is,

$$I\left(\mu-\alpha\frac{\langle k^2\rangle}{\langle k\rangle^2}(n-I)\right)=0. \tag{18}$$

In order to get a positive I, we let

$$\left(\mu-\alpha\frac{\langle k^2\rangle}{\langle k\rangle^2}(n-I)\right)=0.$$

So the threshold for the average density is

$$n_{c_1}=\frac{\mu\langle k\rangle^2}{\alpha\langle k^2\rangle}. \tag{19}$$

From Eqs.(12), we have

$$\begin{aligned} \Theta_2 &= \Sigma_{k'}P(k'|k)I_{k'}\\ &= \frac{\Sigma_{k'}k'P(k')I_{k'}}{\langle k\rangle}\\ &= \frac{\Sigma_{k'}k'P(k')\frac{k'}{\langle k\rangle}[(1-\mu)I+\alpha T_1\Theta_2]}{\langle k\rangle}\\ &= \frac{\langle k^2\rangle}{\langle k\rangle^2}I. \end{aligned} \tag{20}$$

The same method can be used to Θ_2, and the threshold is

$$n_{c_2}=\frac{\mu\langle k\rangle^3}{\alpha\langle k^2\rangle^2}. \tag{21}$$

From the Eq.(20) and Eq.(21), we conclude that the epidemic is always endemic for sufficiently large heterogenous networks. Moreover, the prevalence of epidemics with infection rate $\alpha k\Theta_2$ is greater than the infection rate $\alpha k\Theta_1$.

4. Epidemic spreading within and between cities

In this section, we assume that the epidemic disease not only occurs within individual cities but also between connected cities. And we also consider two types of epidemic spreadings inside the same cities. In the case of type 1, we consider that each a_i individuals may be infected by all the b_i individuals in the same cities. In this case, the epidemic rate is β when

the spreading of the epidemic disease happens in the same cities. This case is discussed in Section 4.1. In the case of type 2, we consider that each individual has a finite number of contacts with others, in this case the epidemic rate has to be rescaled by the total number of individuals in city i, i.e., β/n_i is the epidemic rate in the same cities, where $n_i = a_i + b_i$ is the total number of individuals in the city i. This case is discussed in Section 4.2.

4.1. The epidemic rate is β inside the same cities

In this case, the number of infected individuals generated by the infection taking place in node of the degree class k is $\beta S_k I_k$. Let $T_k = S_k I_k$, we have

$$T = \Sigma_k P(k) T_k = \Sigma_k P(k) S_k I_k. \tag{22}$$

Then the dynamics of epidemic spreading can be written as

$$\begin{aligned}
\frac{\mathrm{d}I_k(t)}{\mathrm{d}t} &= -I_k(t) + k\Sigma_{k'} P(k'|k)\frac{1}{k'}[(1-\mu)I_{k'}(t) + \beta T_k + \alpha k' S_{k'}\Theta_i], \\
\frac{\mathrm{d}S_k(t)}{\mathrm{d}t} &= -S_k(t) + k\Sigma_{k'} P(k'|k)\frac{1}{k'}[S_k(t) + \mu I_{k'}(t) - \beta T_k - \alpha k' S_{k'}\Theta_i], \qquad i = 1, 2.
\end{aligned} \tag{23}$$

Similar to the above section, the stationary state for Eqs.(23) is

$$\begin{aligned}
I_k(t) &= k\Sigma_{k'} P(k'|k)\frac{1}{k'}[(1-\mu)I_{k'}(t) + \beta T_k + \alpha k' S_{k'}\Theta_i] = \frac{k}{\langle k\rangle}[(1-\mu)I + \beta T + \alpha T_1\Theta_i], \\
S_k(t) &= k\Sigma_{k'} P(k'|k)\frac{1}{k'}[S_k(t) + \mu I_{k'}(t) - \beta T_k - \alpha k' S_{k'}\Theta_i] = \frac{k}{\langle k\rangle}[\mu I + S - \beta T - \alpha T_1\Theta_i], \qquad i = 1, 2.
\end{aligned} \tag{24}$$

Manipulating the operator $\Sigma_k P(k)$ on both sides of Eqs.(24) gives

$$\begin{aligned}
I &= (1-\mu)I + \beta T + \alpha T_1\Theta_i, \\
S &= S + \mu I - \beta T - \alpha T_1\Theta_i, \qquad i = 1, 2,
\end{aligned} \tag{25}$$

that is,

$$\mu I = \beta T + \alpha T_1\Theta_i, \qquad i = 1, 2. \tag{26}$$

From Eqs.(22), (24) and (25),

$$\begin{aligned}
T &= \Sigma_k P(k) S_k I_k \\
&= \Sigma_k P(k)\frac{k^2}{\langle k\rangle^2}[(1-\mu)I + \beta T + \alpha T_1\Theta_i] \\
&\quad \times [\mu I + S - \beta T - \alpha T_1\Theta_i] \\
&= \frac{\langle k^2\rangle}{\langle k\rangle^2} SI.
\end{aligned} \tag{27}$$

For the case of Θ_1, from Eqs.(15), (16), (26) and (27), we have

$$\mu I = \beta\frac{\langle k^2\rangle}{\langle k\rangle^2} SI + \alpha\frac{I}{\langle k\rangle}\frac{\langle k^2\rangle}{\langle k\rangle} S. \tag{28}$$

So the threshold for the prevalence of epidemic is

$$n_{c_3} = \frac{\mu\langle k\rangle^2}{(\alpha+\beta)\langle k^2\rangle}. \tag{29}$$

For the case of Θ_2, from Eqs.(15), (20), (26) and (27),

$$\mu I = \beta\frac{\langle k^2\rangle}{\langle k\rangle^2} SI + \alpha\frac{\langle k^2\rangle}{\langle k\rangle} S\frac{\langle k^2\rangle}{\langle k\rangle^2} I. \tag{30}$$

So the threshold for the prevalence of epidemic disease is

$$n_{c_4} = \frac{\mu\langle k\rangle^3}{(\alpha\langle k^2\rangle + \beta\langle k\rangle)\langle k^2\rangle}. \tag{31}$$

If the parameter $\beta = 0$ in Eq.(29) and Eq.(31), the corresponding results are same as Eq.(20) and Eq.(21) respectively.

4.2. The epidemic rate is β/n_i inside the same cities

In this case, the number of infected individuals generated by the infection taking place in node of the degree class k is $\beta\dfrac{S_k I_k}{S_k + I_k}$, we also let $T_k = \dfrac{S_k I_k}{S_k + I_k}$.

According to Eqs.(24) and (25), we obtain

$$T = \Sigma_k P(k) T_k = \Sigma_k P(k)\frac{S_k I_k}{S_k + I_k} = \frac{IS}{n}. \tag{32}$$

By using the same method, we have the following results:

(1) For the Θ_1 case, we have

$$I = \frac{n[(\beta-\mu)\langle k\rangle^2 + \alpha n\langle k^2\rangle]}{\beta\langle k\rangle^2 + \alpha n\langle k^2\rangle}, \tag{33}$$

thus, the prevalence of epidemic disease takes place if $(\beta-\mu)\langle k\rangle^2 + \alpha n\langle k^2\rangle > 0$, i.e.,

$$n_{c_5} = \begin{cases} 0, & \beta/\mu > 1, \\ \dfrac{(\mu-\beta)\langle k\rangle^2}{\alpha\langle k^2\rangle}, & \beta/\mu < 1. \end{cases} \tag{34}$$

(2) For the Θ_2 case,

$$n_{c_6} = \begin{cases} 0, & \beta/\mu > 1, \\ \dfrac{(\mu-\beta)\langle k\rangle^3}{\alpha\langle k^2\rangle^2}, & \beta/\mu < 1. \end{cases} \tag{35}$$

From Eq.(34) and Eq.(35), we can find that the epidemic always happens, no matter the size of networks, when $\beta/\mu > 1$.

5. Numerical simulations

In this section, we present numerical simulations to support our results, which are based on the BA networks with $P(k) = k^{-\gamma}, \gamma = 3$, and $\langle k\rangle = 6$, if we set $N = 200$, then $\langle k^2\rangle = 75$; and if we set $N = 1000$, then $\langle k^2\rangle = 126$. In each figure we compare the effect of $\Theta_i, i = 1, 2$ and other parameters on the threshold.

In Fig.1(a) we show the effect of different μ, β, Θ_i on the threshold α. From the Eqs.(6) and (7), we have:

$$\begin{aligned} &\beta = 0.4, \mu = 0.5, \Theta_1 \Rightarrow \alpha = 0.1, \\ &\beta = 0.3, \mu = 0.5, \Theta_1 \Rightarrow \alpha = 0.2, \\ &\beta = 0.3, \mu = 0.5, \Theta_2 \Rightarrow \alpha = 0.0160, \\ &\beta = 0.4, \mu = 0.5, \Theta_2 \Rightarrow \alpha = 0.0320. \end{aligned} \tag{36}$$

In Fig.1(b) we compare the effect of the network's size on the threshold α, the effect of the network's size on other cases are similar, so we do not simulate it again. Let $\mu = 0.5, \beta = 0.3$ unchanged, we show the threshold α when the different value $\langle k\rangle$, $\langle k^2\rangle$ and Θ_i are considered.

From the Eqs.(6) and (7), we have:

$$\begin{aligned} &N = 200, \Theta_1 \Rightarrow \alpha = 0.2, \\ &N = 1000, \Theta_1 \Rightarrow \alpha = 0.2, \\ &N = 200, \Theta_2 \Rightarrow \alpha = 0.016, \\ &N = 1000, \Theta_2 \Rightarrow \alpha = 0.0095. \end{aligned} \tag{37}$$

From Fig.1 we can find that our simulations accord with the above values for threshold α.

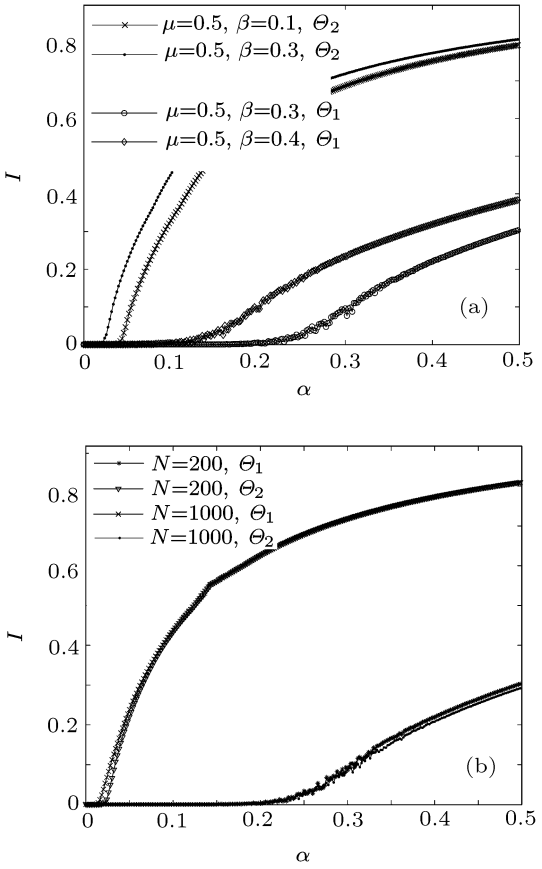

Fig.1. Simulations were conducted to verify Eqs.(6) and (7) by giving the different value N, μ, β, Θ_i, $i = 1, 2$. (a) with $N = 200$ unchanged, by changing μ, β, Θ_i, $i = 1, 2$ as in Eqs.(36), to check whether the threshold α is corresponding to Eqs.(36); (b) with $\mu = 0.5$, $\beta = 0.3$ unchanged, by changing the size of networks as in Eqs.(37), to show whether the threshold α is corresponding to Eqs.(37).

In Fig.2 we present the effect of different α, β, Θ_1, Θ_2 on the thresholds n_{c_1}, n_{c_2}. From the Eqs.(20) and (21), we have:

$$\begin{aligned} &\alpha = 0.1, \mu = 0.1, \Theta_1 \Rightarrow n_{c_1} = 0.480, \\ &\alpha = 0.1, \mu = 0.15, \Theta_1 \Rightarrow n_{c_1} = 0.720, \\ &\alpha = 0.1, \mu = 0.1, \Theta_2 \Rightarrow n_{c_2} = 0.0384, \\ &\alpha = 0.1, \mu = 0.15, \Theta_2 \Rightarrow n_{c_2} = 0.0576. \end{aligned} \tag{38}$$

Simulations in Fig.2 accord with the above values for threshold n.

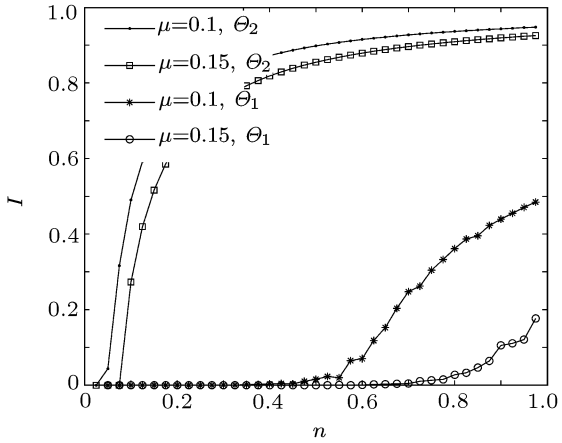

Fig.2. Simulations were conducted to verify the threshold n given in the Eqs.(20) and (21), by changing α, μ, Θ_i, $i = 1, 2$ as in Eqs.(38), to see whether the threshold n is corresponding to Eqs.(38). Threshold n is calculated with N=200, $\langle k\rangle$=6, $\langle k^2\rangle$=75, α=0.1.

In Fig.3 we simulate the effect of different α, β, μ, Θ_1, Θ_2 on thresholds n_{c_3}, n_{c_4}. With $\alpha = \beta = 0.1$ unchanged, from the Eqs.(29) and (31), we have:

$$\begin{aligned}
&\mu = 0.1, \Theta_1 \Rightarrow n_{c_3} = 0.24,\\
&\mu = 0.2, \Theta_1 \Rightarrow n_{c_3} = 0.48,\\
&\mu = 0.1, \Theta_2 \Rightarrow n_{c_4} = 0.0356,\\
&\mu = 0.2, \Theta_2 \Rightarrow n_{c_4} = 0.0712. \qquad (39)
\end{aligned}$$

Simulations in Fig.3 accord with the above values for threshold n.

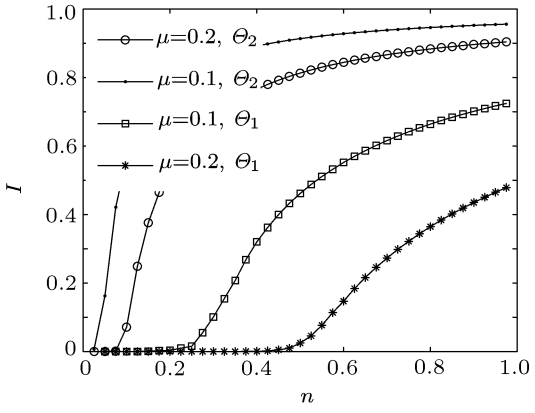

Fig.3. Simulations were conducted to verify the threshold n given in the Eqs.(29) and (31), by change $\alpha, \beta, \mu, \Theta_i$, $i = 1, 2$ as in Eqs.(39), to check whether the threshold n is corresponding to Eqs.(39). Threshold n is calculated with N=200, $\langle k\rangle$=6, $\langle k^2\rangle$=75, α=β=0.1.

In Fig.4, the effect of different α, β, μ, Θ_1 and Θ_2 on thresholds n_{c_5} and n_{c_6} are considered.

From the Eqs.(34), (35), we have:

$$\begin{aligned}
&\mu = 0.4, \alpha = 0.2, \beta = 0.2, \Theta_1 \Rightarrow n_{c_5} = 0.48,\\
&\mu = 0.2, \alpha = 0.2, \beta = 0.3, \Theta_1 \Rightarrow n_{c_5} = 0,\\
&\mu = 0.4, \alpha = 0.2, \beta = 0.2, \Theta_2 \Rightarrow n_{c_6} = 0.0384,\\
&\mu = 0.2, \alpha = 0,2, \beta = 0.3, \Theta_2 \Rightarrow n_{c_6} = 0. \qquad (40)
\end{aligned}$$

Simulations in Fig.4 accord with the above values for threshold n.

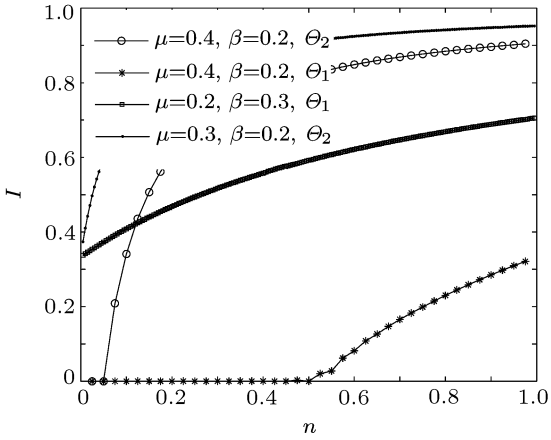

Fig.4. Simulations were conducted to verify the threshold n given in the Eqs.(34) and (35), by change $\alpha, \beta, \mu, \Theta_i$, $i = 1, 2$ as in Eqs.(40), to check whether the threshold n is corresponding to Eq.(40). Threshold n is claculated with N=200, $\langle k\rangle$=6, $\langle k^2\rangle$=75, α=0.2.

6. Conclusions

In this paper we discussed the epidemic thresholds for SIS models on heterogenous networks, including the cases without mobility of individuals among different cities, and with the mobility of individuals and epidemic spreading in different cities but the epidemic spreading taking place inside the city is neglected. The case with all of these three factors is also discussed. From the theoretical analysis and the simulations for the thresholds of epidemic spread, we can conclude that the prevalence of an epidemic disease is easier when the epidemic spreading happens among different cities, what's more, this effect for the case of Θ_2 is more obvious than the case of Θ_1.

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