Influence of mobile agents on the spreading behavior of SIS model

Chengyi Xia\textsuperscript{a}, Shiwen Sun\textsuperscript{a}, Zhongxin Liu\textsuperscript{b} and Zengqiang Chen\textsuperscript{b}

\textsuperscript{a} School of Computer and Communication Engineering, Tianjin University of Technology, 300191 P.R.China
\textsuperscript{b} Department of Automation, Nankai University, 300071, P.R.China

Abstract

We propose an improved SIS (Susceptible-Infected-Susceptible) model with mobile agents to explore the effect of agents’ motion on the epidemic spreading. Under the random jumping situation, the analytic formula of critical threshold is derived by the mean field theory. Then a large number of numerical simulations are performed to verify the theoretic prediction, and the simulation results at the condition of different population density and infection radius agree well with the mean field analysis. In addition, we also find that the long range jump will also remarkably influence the dissemination behavior of epidemic spreading.

Keywords: epidemic spreading, individual motion, SIS model

1. Introduction

Real epidemics are influencing and threatening the global world, such as SARS, Bird Flu and H1N1 Flu. How to analyze and predict the spreading behavior of epidemics becomes an urgent task. Currently, the epidemic dynamics attract the interest of many researchers from medicine, biology, mathematics, physics [1]. Among them, mathematical modeling and computer simulation are often applied into the epidemic dynamics and great advances are made in this field [1]. For example, SIS and SIR (Susceptible-Infected-Refractory) epidemic models are two famous epidemiological models which can successfully describe the transmission processes of smallpox, measles, tuberculosis and so on [2].

However, the connection pattern among agents is often ignored in classical SIS and SIR models, and a great deal of data have proven that there exists the high heterogeneity among the connection pattern within many complex systems such as social, biological and engineering ones [3]. In addition, small world effect is also found in a number of systems [4]. Thus, it is necessary to combine the connection pattern and epidemiological modeling [5]. Especially,
Pastor-Satorras et al [6] find that the epidemic threshold approximates to 0 for Barabási and Albert scale-free network model [3] when the network size is infinite, this result changes many intrinsic conclusions on epidemiology and initiates large quantities of relevant researches [7, 8, 9, 10, 11, 12, 13, 14].

At present many researches mainly consider the spreading behavior on static networks, that is, to assume that the network structure keeps constant during the disease evolution. But for the real complex systems, the interaction pattern and strength between agents vary continually. For example, motion of agents in social networks and mobility of terminals in communication networks may lead to the modification of the topological network structure. Therefore, it is very important to study the epidemic spreading characteristics on dynamically changing networks. Based on two-dimensional lattice, Miramontes et al [15] propose a new SIS model which allows the agents to move locally within 8 neighbors or globally in the lattice, and the results show that global long jump can accelerate the epidemic outbreaks. Liu et al [16] present a model of mobile agents to study the epidemic spreading in communities with different densities of agents, and then they also study the influence of objective traveling on the epidemic spreading [17]. Frasca et al [18] present a novel model which allows the individuals to move randomly inside the neighborhood with a given radius, and also carries out the long-range motion with the specified probability, and they conclude that the long-range movement will remarkably affect the spreading behavior of SIR model. All these results largely enrich our knowledge of the epidemic spreading behavior on dynamical social networks.

In this paper we will extend the model of Frasca et al [18] into SIS model, then perform the mean-field analysis and give out the epidemic critical threshold of SIS which is also validated by the numerical simulations. In Section 2, an improved SIS model with agents’ motion are proposed to describe the influence of motion on the epidemic spreading, then this model is analyzed with the mean-field theory and the analytical formula of the critical threshold is derived. A large number of numerical simulations are made to verify the theoretical results in Section 3. At last some concluding remarks are summarized in Section 4.

2. SIS model with agents’ motion

2.1. The model of agents’ motion

The motion model can be shown as Fig.1. Initially, all $N$ agents are assigned into the two-dimensional(2D) planar region $(L \times L)$ which is satisfied with the periodic condition. Each agent can jump into any position (i.e. long-range motion) inside the plane with the probability $p$ or perform the local motion with the probability $1 - p$. Among them, the local motion can be described as follows,

\[
\begin{align*}
    x_i(t + \Delta t) &= x_i(t) + v_i(t)\Delta t \\
    \theta_i(t + \Delta t) &= \theta_i(t)
\end{align*}
\]  

(1)

where $x_i(t)$ is the position of the agent $i (i = 1, 2, ..., N)$ in the plane at time $t$, $v_i(t)$ and $\theta_i(t)$ are the moving velocity and direction of the agent $i$. $\Delta t$ is the time interval of the agent motion. $v_i(t)$ and $\theta_i(t)$ are $N$ independently and identically distributed random variables between the interval $[-\pi, \pi]$. In addition, each agent will keep the velocity modulus $v$ constant after the long jump, and perform the local motion according to Eq.(1) where $v_i(t) \equiv (\cos\theta_i(t), \sin\theta_i(t))$. Obviously, the agent can only move in the short range when $p = 0$, $p = 1$ stands for the random jumping in the plane and $0 < p << 1$ denotes the real situation of agents’ motion.
2.2. Improved SIS model with agents’ motion

SIS model is often used to investigate the threshold and critical behavior of epidemic spreading. In the model, all individuals are assumed to be in two discrete states: susceptible (S) and infected (I). The susceptible (healthy) individuals are infected with the probability $\beta$ if they contact the infective ones, and the infected ones will be cured with the probability $\gamma$ after they receive the medical care. In addition, the cured ones can be infected unlucky if they again keep in touch with infected ones. Traditionally, the SIS model can be described by the following equation,

$$
\begin{align*}
I(t + \Delta t) &= I(t) - \gamma I(t) + \beta S(t)I(t) \\
S(t) + I(t) &= 1
\end{align*}
$$

where $S(t)$ and $I(t)$ stands for the percentage of susceptible and infected agents over the total population, respectively.

However, the classical model can’t include the motion characteristics. Here we can consider all individuals in the system as the mobile agents in the 2D space, and combine the above-mentioned motion model into the SIS epidemic model to analyze the effect of mobile agents on the spreading behavior. At the same time, we assume that every agent can only interact with other agents from the neighborhood with the radius $r$.

If we allow the agents to randomly jump in the planar space (that is to say, $p = 1$), an improved SIS model can be derived from the classic SIS model based on the mean-field theory and described as follows,

$$
\begin{align*}
I(t + \Delta t) &= I(t) - \gamma I(t) + S(t)[1 - (1 - \beta)^{A\rho I(t)}] \\
S(t) + I(t) &= 1
\end{align*}
$$

where $\beta$ is the infection rate and $\gamma$ is the cure rate, $\rho = N/L^2$ denotes the density of mobile agents in the planar space, $\Delta t$ is the time step of infection and $A = \pi r^2$ stands for the infection range of each infected agent.

From Eq. (3), we can see that the infection density at time $t + \Delta t$ is equal to the infected ratio at time $t$ minus the cured ratio, and plus newly infected ones. Therefore, we can perform the Taylor expansion for the Eq. (3) in the vicinity of critical point($I(t) << 1$),

$$
I(t + \Delta t) \approx I(t) - \gamma I(t) + S(t)\beta \pi r^2 I(t)
$$

Insert the normalized condition $S(t) = 1 - I(t)$ into Eq.(4),

$$
I(t + \Delta t) \approx I(t) - \gamma I(t) + [1 - I(t)]\beta \pi r^2 I(t)
$$
Ignore the higher order term of $I(t)$ (i.e. $O(I(t^2))$), we can derive

$$I(t + \Delta t) \approx I(t) - \gamma I(t) + \beta \pi r^2 I(t)$$

(6)

So it can be seen that the following conditions must be fulfilled for the epidemics,

$$1 - \gamma + \beta \pi r^2 \rho > 1$$

(7)

Let $\lambda = \beta / \gamma$ be the effective infection rate, that is to say,

$$\lambda > \lambda_c$$

(8)

where $\lambda_c$ shows the critical threshold of the newly improved SIS model,

$$\lambda_c = \frac{1}{\pi r^2}$$

(9)

Therefore, the epidemics will be spreading when $\lambda > \lambda_c$, while the infection density will tend to zero and the infectious disease will not be epidemic when $\lambda < \lambda_c$. From Eq.(9), we can see that the infection threshold can only correlate with the density of mobile agents and infection radius of agents in the planar space:

- When the population density $\rho$ is given, the larger the infection radius, the smaller the infection threshold and the higher the steady infection density, and the epidemic will be more easily spread.

- When the infection radius $r$ is given, the larger the population density, the smaller the infection threshold and the higher the steady infection density, and the epidemic will also be more easily transmitted.

Furthermore, Eq.(9) is derived under the random mixing conditions and is not suitable for the realistic situations for mobile population. Thus, a large number of numerical simulations are needed to verify the theoretic analysis.

3. Numerical Results

In this section, we will perform large scale numerical simulations to validate the theoretical prediction in the pre-subsection. All simulations use an agent-based modeling strategy where the SIS dynamics is applied to each agent by considering the actual state of all agents within the given neighborhood at each time step. In all simulations we assume $N = 1600$, $I(0) = 0.05$, $v = 0.1$, $\rho$ and $L$ are selected to meet $\rho = N/L^2$.

Figure 2 describes the relationship between the steady state prevalence($I(\infty)$) and effective spreading rate ($\lambda$) when $\rho = 1$ and $\rho = 2$. In the simulation, we fix $\gamma = 1.0$ to make $\lambda = \beta$ and keep the infection radius $r = 1.0$. It shows that the infection critical value is 0.325 which is indicated by the reverse triangle symbol in Fig.2 when $\rho = 1$, while the analytical result is $\lambda_c = 1/(\pi r^2 \rho) = 0.318$ according to Eq.(9). When $\rho = 2$, the numerical result of $\lambda_c$ is 0.163 and analytical result is 0.159. Thus it can be seen that the simulation result agrees well with the mean-field analysis, and $I(\infty)$ increases as the effective spreading rate when $\lambda > \lambda_c$. Hence diminishing the infection rate and augmenting the cure rate is efficient for us to reduce the infection of epidemics. In addition, in the endemic state the steady state prevalence is higher for the denser population even if the infection rate($\lambda$) is same. This indicates that separating and evacuating the dense population is necessary to control the disease spreading.
The relationship between $I(\infty)$ and $\lambda$ is reported in Fig.3 when $r$ is set to be different values. Similarly, we fix $\gamma = 1.0$ to make $\lambda = \beta$ and keep the population density $\rho = 1.0$. We can see that $\lambda_C \approx 0.324$ when $r = 1.0$ and $\lambda_C \approx 0.165$ when $r = \sqrt{2}$, as indicated by the vertical arrows in Fig.3. While the analytical results are respectively 0.319 and 0.159 which are computed from Eq.(9), the numerical simulation is again consistent with the mean field result. As before, higher $\lambda$ means the larger infection density and prevalence in the endemic situation. At the same time the steady infection prevalence is higher for the larger interaction radius even if the infection parameter($\lambda$) is the same for different mobile populations.

In Fig.4 we give out the effect of the individuals’ motion on the critical value of infection under the same epidemic parameters. The rectangular symbol stands for $\lambda_C$ when $p = 0$, the triangular symbol denotes $\lambda_C$ when $p = 1$, and the broken line is the analytical result of Eq.(9). While the critical value of $0 < p < 1$ is usually between the previous simulation results. It is
obvious that the long range jump largely reduces the critical threshold of infection and facilitates the epidemic spreading behavior among mobile agents.

4. Conclusions

In this paper we put forward an improved SIS disease transmission model which integrates the individuals’ motion into the standard SIS epidemic model, to investigate the effect of individual motion on the epidemic spreading. Based on the mean-field theory, the critical threshold of infection spreading with random jump is derived. Then a great number of numerical simulations are carried out to validate the theoretical predictions, and we examine the relationship between the steady prevalence and the effective spreading rate under the given infection radius or the density of agents. We find that the simulation result is coincident with the mean field analysis, and the long jump also influences the spreading behavior. All these results show that the newly proposed model can characterize the spreading action of agents more really.

References