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Anomalous epidemic spreading in heterogeneous networks

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Epidemic spreading in heterogeneous networks has attracted great interest in recent years. To capture the significant effect of residence of individuals on epidemic spreading, we consider herein a simple susceptible-infected-susceptible model with random waiting time in heterogeneous networks. We provide the analytical dynamical expressions for the time evolution for infected individuals and find a fractional memory effect of power-law waiting time on anomalous epidemic spreading. This work provides new quantitative insights in describing contagion processes and could help model other spreading phenomena in social and technological networks.

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I. INTRODUCTION

The spread of epidemic is a vital question for human survival and social development, and how to model the epidemic process has attracted widespread and lasting attention [1–3]. The spreading of a disease generally depends on the biological properties of the disease, fighting the disease and medical treatments, interactions and contact of individuals, transport fluxes and human movements, the residence duration of travel, and so on [3–5]. Classical models of epidemic spreading, such as the susceptible-infected-susceptible (SIS) and susceptible-infected-recovered (SIR) models, etc., which take into account the impact of transition and reaction processes in a homogeneous mixing approximation, provide a basic modeling approach to the spreading of epidemic processes [6].

In further consideration of the effects of the migrations and diffusion of individuals and the contact pattern structure, Vespignani *et al.* [4,7,8] study the behavior of epidemic spreading and diffusion defined on networks with heterogeneous topology and propose the particle-network framework and the generalized reaction-diffusion processes and metapopulation models in heterogeneous networks under the assumption that the diffusion of particles (or individuals) does not depend on their random residence times in nodes.

As we all know, the residence duration has a crucial influence on the infection of individuals in the spreading of a disease, and it should also be considered in epidemic spreading. However, until now few works have approached this factor in modeling contagion phenomena [9–15]. Without considering the transition and reaction processes, Fedotov and Stage [5,16] have studied the anomalous cumulative inertia in human behavior and found an anomalous effect of random residence time on the diffusion in scale-free networks. Motivated by their research, we shall herein consider the effect of the random residence time on reaction-diffusion processes in heterogeneous networks and introduce a fairly general and suited method to describe the dynamical epidemic processes that integrate the migration and residence of individuals, the reaction activity, and the complex features and heterogeneities of networks. Moreover, we show the coupling relations between reaction and diffusion terms and find the strong memory effect of the power-law waiting time on anomalous epidemic spreading in complex networks. This epidemiological framework can also help model the spreading of information, cultural norms, and pollution control in complex networks.

II. ANOMALOUS DIFFUSION DYNAMICS IN THE PARTICLE-NETWORK FRAMEWORK

We start by recalling the heterogeneous networks using the particle-network framework in which each particle (or individual) can diffuse along the edges, connecting notes with a diffusion coefficient [3,7]. A representation of the system is provided by quantities defined in terms of degree k:

$$N_k(t) = \frac{1}{V_k}\sum_i \rho_{i,k}(t), \tag{1}$$

where V_k is the number of nodes with degree k, $\rho_{i,k}(t)$ is the nonnegative integer number of particles in the node i with degree k, and the sums run over the set of nodes having degree equal to k. The degree-block variable $N_k(t)$ represents the average number of particles in nodes with degree k. It is assumed that the particles with similar degree are statistically equivalent.

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In order to gain further insight into the spreading properties of the heterogeneous networks in the particle-network framework we assume that when the particle enters into a node i with degree k of the network it need some waiting time t, drawn from $\psi(t)$, before it moves out the node i [14,16]. Let $N_k^-(t) = \frac{1}{V_k}\sum_i \rho_{i,k}^-(t)$ represent the mean loss flux diffusing away the node with degree k at time t and $N_k^+(t) = \frac{1}{V_k}\sum_i \rho_{i,k}^+(t)$ be the mean gain flux diffusing into the node of degree k at t. Here the symbols $\rho_{i,k}^-(t)$ and $\rho_{i,k}^+(t)$ respectively denote the integer numbers of particles leaving and arriving at the node i with degree k at time t. Then the variation in time of the particle subpopulation $N_k(t)$ in each degree block k can be written as

$$\frac{dN_k}{dt} = N_k^+(t) - N_k^-(t). \tag{2}$$

Note that the gain flux of degree k comes from each neighbor and equals the average over all possible degrees k' of the flux out of the node on the edge, according to the conditional probability $P(k'|k)$ that an edge belonging to a node of degree k is connecting to a node of degree k' [3,17]. So $N_k^+(t)$ can be read as

$$N_k^+(t) = k\sum_{k'} N_{k'}^-(t)\frac{1}{k'}P(k'|k). \tag{3}$$

Furthermore, considering that the loss flux of the node with degree k is from those particles that were originally at this node at $t = 0$ and wait until time t to leave and those particles that arrived this node at an earlier time t' and wait until time t to leave, one can write the loss flux $N_k^-(t)$ as

$$N_k^-(t) = N_k(0)\psi(t) + \int_0^t N_k^+(t')\psi(t-t')\,dt', \tag{4}$$

where $N_k(0)$ is initial average number of nodes with degree k. From Eq. (2), we have

$$N_k^+(t) = \frac{dN_k}{dt} + N_k^-(t). \tag{5}$$

Substituting (5) into (4) yields

$$N_k^-(t) = N_k(0)\psi(t) + \int_0^t \left[\frac{dN_k(t')}{dt'} + N_k^-(t')\right]\psi(t-t')\,dt'. \tag{6}$$

Taking the Laplace transform $t \to s$ of Eq. (6), we find

$$N_k^-(s) = N_k(s)\Phi(s). \tag{7}$$

Here $N_k^-(s)$ and $N_k(s)$ are respectively the Laplace transforms of $N_k^-(t)$ and $N_k(t)$, and $\Phi(s) = \frac{s\psi(s)}{1-\psi(s)} = \frac{\psi(s)}{\Psi(s)}$, where $\psi(s)$ and $\Psi(s)$ are respectively the Laplace transforms of the probability density function (PDF) of the waiting time $\psi(t)$ and the survival function $\Psi(t) = 1 - \int_0^t \psi(t')\,dt'$. Equation (7) is in agreement with the result by using a different way in Ref. [16]. We invert (7) into time space and obtain $N_k^-(t) = \int_0^t N_k(t')\Phi(t-t')\,dt'$. Substituting this into (3), we finally derive the equation describing the time evolution of $N_k(t)$ for each class of degree k as

$$\frac{dN_k(t)}{dt} = k\sum_{k'}\int_0^t N_{k'}(t')\Phi(t-t')\,dt'\frac{1}{k'}P(k'|k) - \int_0^t N_k(t')\Phi(t-t')\,dt'. \tag{8}$$

Here $\Phi(t)$ denotes the inverse Laplace $s \to t$ transform of $\Phi(s)$. Equation (8) explicitly brings the waiting time of particles in modeling diffusion processes in heterogeneous networks.

If the waiting time PDF is a power law given by $\psi(t) = \frac{\alpha}{t+\tau_0}(\frac{\tau_0}{t+\tau_0})^\alpha$, where $0 < \tau_0, 0 < \alpha$, then in Laplace space one has $\psi(s) \sim 1 - \Gamma(1-\alpha)\tau_0^\alpha s^\alpha$ for small τ_0, and thus $\Phi(s) \sim \frac{1}{\Gamma(1-\alpha)\tau_0^\alpha}s^{1-\alpha}$ [16,18]. Hence, in this case Eq. (8) reduces to

$$\frac{dN_k(t)}{dt} = \frac{k}{\Gamma(1-\alpha)\tau_0^\alpha}\sum_{k'}\frac{{}_0D_t^{1-\alpha}N_{k'}(t)}{k'}P(k'|k) - \frac{{}_0D_t^{1-\alpha}N_k(t)}{\Gamma(1-\alpha)\tau_0^\alpha}. \tag{9}$$

where ${}_0D_t^{1-\alpha}f(t)$ is the Riemann-Liouville fractional derivative operator, equaling in Laplace $t \to s$ space to $s^{1-\alpha}L[f(t)]$ [19]. Note that because of the effect of the fractional kinetics operator [5], the average number of particles with degree k at time t in heterogeneous networks has a strong memory dependence on the previous spreading. This anomalous cumulative property has also been found in the transport of particles on scale-free networks containing some nodes with heavy-tailed residence times in Ref. [16]. If the heterogeneous networks are uncorrelated networks obeying $P(k'|k) = \frac{k'P(k')}{\langle k\rangle}$, where $P(k)$ is a degree distribution and $\langle k\rangle$ is the average degree [3], then Eq. (9) becomes

$$\frac{dN_k(t)}{dt} = k\frac{{}_0D_t^{1-\alpha}N(t)}{\Gamma(1-\alpha)\tau_0^\alpha\langle k\rangle} - \frac{{}_0D_t^{1-\alpha}N_k(t)}{\Gamma(1-\alpha)\tau_0^\alpha}. \tag{10}$$

Here $N(t) = \sum_k N_k(t)P(k)$ is the average number of particles in all nodes in the network, and in nonreactive diffusion system $N(t)$ is a constant, that is, $N(t) = N(0)$ with $N(0)$ being the initial average number. Taking the Laplace transform $t \to s$ of Eq. (10), we find in nonreactive system

$$N_k(s) = \frac{N_k(0) + \frac{k}{\Gamma(1-\alpha)\tau_0^\alpha\langle k\rangle}\frac{1}{s^\alpha}N(0)}{s + \frac{1}{\Gamma(1-\alpha)\tau_0^\alpha}s^{1-\alpha}}. \tag{11}$$

In the above expression $N_k(s)$ represents the Laplace transform of $N_k(t)$. Inverting Eq. (11) to the time domain $s \to t$, we then get the solution of Eq. (10) in terms of one-parameter and two-parameter Mittag-Leffker functions [20]

$$E_\alpha(z) = \sum_{n=0}^{+\infty}\frac{z^n}{\Gamma(1+\alpha n)}, \tag{12}$$

and

$$E_{\alpha,\beta}(z) = \sum_{n=0}^{+\infty}\frac{z^n}{\Gamma(\beta+\alpha n)}, \tag{13}$$

through

$$N_k(t) = N_k(0)E_\alpha\left[-\frac{1}{\Gamma(1-\alpha)\tau_0^\alpha}t^\alpha\right] + \frac{kN(0)t^\alpha}{\Gamma(1-\alpha)\tau_0^\alpha\langle k\rangle}E_{\alpha,\alpha+1}\left[-\frac{1}{\Gamma(1-\alpha)\tau_0^\alpha}t^\alpha\right]. \quad (14)$$

Equation (14) shows that the average number of particles in nodes with degree k in the nonreactive diffusion system with random waiting time in the heterogeneous networks in particle-network framework depends not only on the degree k but also on the anomalous exponent α of the random waiting time. When $\alpha = 1$, the solution reduces to

$$N_k(t) = \left[N_k(0) - \frac{k}{\langle k\rangle}N(0)\right]e^{-\frac{1}{\tau_0}t} + \frac{k}{\langle k\rangle}N(0), \quad (15)$$

which depends only on the degree k. In the limit of long time $t \to +\infty$, we recover the usual result [4,16],

$$N_k(t) \sim \frac{k}{\langle k\rangle}N(0), \quad (16)$$

which is in proportion to the degree k.

III. ANOMALOUS EPIDEMIC SPREADING WITH RANDOM WAITING TIME

A. The time evolution of the average number of infectious individuals in nodes with degree *k*

Furthermore, to address the effect of the waiting times spent by individuals in epidemic spreading in heterogeneous networks, we shall study a basic epidemic SIS model governed by the following set of reactions:

$$I \xrightarrow{\mu} S, \quad (17)$$

$$S + I \xrightarrow{\beta} 2I, \quad (18)$$

where μ and β are transition rates for recovery and infection, respectively. We assume $\rho(t)$ individuals diffusing in a heterogeneous network with V nodes, and each node i with degree k of the network has a number $\rho_{i,k,I}(t)$ of infectious and $\rho_{i,k,S}(t)$ of susceptible individuals at time t. One can see that $\rho(t) = \rho(0)$ is a constant in SIS reactive system where $\rho(0)$ is the initial total number of individuals. We introduce the average numbers of infectious and susceptible individuals in nodes with degree k at time t, that is, $I_k(t) = \frac{1}{V_k}\sum_i \rho_{i,k,I}(t)$, $S_k = \frac{1}{V_k}\sum_i \rho_{i,k,S}(t)$, where the sums are performed over nodes of degree k and V_k is the number of nodes with degree k. It is clear that $N_k(t) = I_k(t) + S_k(t)$ is the total average number of individuals in nodes with degree k [3]. Denote the average numbers of infectious and susceptible individuals in all nodes by $I(t) = \sum_k I_k(t)P(k)$ and $S(t) = \sum_k S_k(t)P(k)$, respectively. Then the sum $N(t) = I(t) + S(t) = \sum_k N_k(t)P(k) = \frac{\sum_k N_k(t)V_k}{V} = \frac{\rho(t)}{V}$, which is the average number of individuals in all nodes is invariable under reactions (17) and (18). We assume that the PDFs of the residence time at any node are respectively the same for infectious and susceptible individuals, and the reaction processes take place only inside the nodes for simplicity (see Fig. 1). To explicitly describe the time evolution for infectious individuals, we write a balance description as:

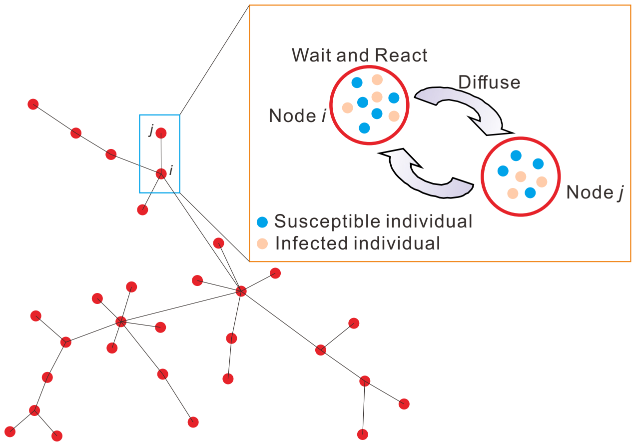

FIG. 1. Epidemic SIS model with random waiting time in heterogeneous networks. An infected or susceptible individual waits at the node i with degree k_1 for some time τ when it may react according to Eqs. (17) and (18), and then it moves away to one of neighbor node j with degree k_2 along an edge, after which the process is renewed.

$$\frac{dI_k(t)}{dt} = I_k^+(t) - I_k^-(t) - \mu I_k(t) + \beta\Gamma_k(t), \quad (19)$$

where $I_k^+(t)$ represents the average number of new arriving infections at the node of degree k from elsewhere at time t, and $I_k^-(t)$ is the loss flux of infections diffusing away from the node of degree k at t. The term $\mu I_k(t)$ denotes the number of the infectious individuals in nodes with degree k which recovers from the disease and returns to the pool of susceptible individuals. The last term on the right-hand side denotes the added infected individuals by the interaction kernel $\Gamma_k(t)$ which is a function of $I_k(t)$ and $S_k(t)$. In the usual case of a mass-action law for the force of infection, one has $\Gamma_k(t) = \frac{I_k(t)S_k(t)}{N_k(t)}$. And if each susceptible individual may react with all of the infectious individuals in the same node, then $\Gamma_k(t) = I_k(t)S_k(t)$ [3,4]. Here the diffusing gain flux of infected individuals of degree k can also be written by the lost flux of other nodes with degree k' as:

$$I_k^+(t) = k\sum_{k'} I_{k'}^-(t)\frac{1}{k'}P(k'|k). \quad (20)$$

We note that the individuals siting on a node with degree k may keep infected for a waiting time before it diffuses into a neighboring node [3]. We assume that the reactive and new infected individuals will have new waiting time [for example, the infected individual may have new plan of stagnation after the reaction (18)]. This yields

$$I_k^-(t) = I_k(0)\Psi_k^{R_1}(t,0)\psi_I(t) + \int_0^t [I_k^+(t') + 2\beta\Gamma_k(t')]\Psi_k^{R_1}(t,t')\psi_I(t-t')\,dt', \quad (21)$$

where $\Psi_k^{R_1}(t,t') = e^{-\int_{t'}^{t}[\mu+\beta\frac{\Gamma_k(\tau)}{I_k(\tau)}]d\tau}$ denotes the probability for the infected individuals to keep infected without defeating disease or infecting new infections in the time interval $[t', t]$ for $t' \geqslant 0$, and the symbol $\psi_I(t)$ represents the waiting time PDF for the infected individual staying at a node for time t and then moving out to the other node. The right-hand side is a sum of outgoing infected individuals that were originally at the nodes with degree k at $t = 0$ being sustained and without infecting other susceptible individuals until time t to leave, those infected individuals that arrived from their neighbors of any degree k' and produced after the infecting process $S + I \rightarrow 2I$ in their nodes of degree k at an earlier time $t' > 0$ wait without reacting until time t to leave. The first term on the right-hand side is the influence of the initial state.

Note that Eq. (21) can be rewritten as

$$\frac{I_k^-(t)}{\Psi_k^{R_1}(t,0)} = I_k(0)\psi(t) + \int_0^t [I_k^+(t') + 2\beta\Gamma_k(t')]\frac{1}{\Psi_k^{R_1}(t',0)}\psi(t-t')\,dt', \quad (22)$$

where we used the relation $\Psi_k^{R_1}(t,0) = \Psi_k^{R_1}(t',0)\Psi_k^{R_1}(t,t')$ [21]. Combining Eqs. (19) and (22) yields

$$\frac{I_k^-(t)}{\Psi_k^{R_1}(t,0)} = I_k(0)\psi_I(t) + \int_0^t \left[\frac{dI_k(t')}{dt'} + I_k^-(t') + \mu I_k(t') + \beta\Gamma_k(t')\right]\frac{1}{\Psi_k^{R_1}(t',0)}\psi_I(t-t')\,dt'. \quad (23)$$

By taking the Laplace transform and using the property $L(\frac{df(t)}{dt}) = sL[f(t)] - f(0)$, we find

$$L\left[\frac{I_k^-(t)}{\Psi_k^{R_1}(t,0)}\right] = \frac{s\psi_I(s)}{1-\psi_I(s)}L\left[\frac{I_k(t)}{\Psi_k^{R_1}(t,0)}\right] = \Phi_I(s)L\left[\frac{I_k(t)}{\Psi_k^{R_1}R(t,0)}\right], \quad (24)$$

Here $\psi_I(s)$ is the Laplace $t \rightarrow s$ transform of $\psi_I(t)$, and $\Phi_I(s) = \frac{s\psi_I(s)}{1-\psi_I(s)} = \frac{\psi_I(s)}{\Psi_I(s)}$, where $\Psi_I(s)$ is the Laplace transform of the survival function $\Psi_I(t) = 1 - \int_0^t \psi_I(t')\,dt'$. We invert the above Eq. (24) to time space and obtain

$$I_k^-(t) = \int_0^t \Phi_I(t-t')I_k(t')\Psi_k^{R_1}(t,t')\,dt', \quad (25)$$

where $\Phi_I(t)$ denotes the inverse Laplace $s \rightarrow t$ transform of $\Phi_I(s)$. From Eqs. (19) and (20), one gets

$$\frac{dI_k(t)}{dt} = k\sum_{k'} I_{k'}^-(t)\frac{1}{k'}P(k'|k) - I_k^-(t) - \mu I_k(t) + \beta\Gamma_k(t). \quad (26)$$

Inserting Eq. (25) into Eq. (26), we finally obtain the time evolution of $I_k(t)$ for infected individuals in any given degree as

$$\frac{dI_k(t)}{dt} = k\sum_{k'}\int_0^t \Phi_I(t-t')I_{k'}(t')\Psi_{k'}^{R_1}(t,t')\,dt'\frac{1}{k'}P(k'|k) - \int_0^t \Phi_I(t-t')I_k(t')\Psi_k^{R_1}(t,t')\,dt' - \mu I_k(t) + \beta\Gamma_k(t). \quad (27)$$

This master equation shows the complex dependence of epidemic spreading on the heterogeneous networks, the spent time for each individual and chemical reactions in the location. Note that in nonreactive system, i.e., $\mu = \beta = 0$, the Eq. (27) becomes Eq. (8) for the simple anomalous diffusion process in heterogeneous networks. In the case of uncorrelated networks obeying $P(k'|k) = \frac{k'P(k')}{<k>}$, Eq. (27) becomes

$$\frac{dI_k(t)}{dt} = \frac{k}{\langle k\rangle}\int_0^t \Phi(t-t')\left[\sum_{k'} I_{k'}(t')\Psi_{k'}^{R_1}(t,t')P(k')\right]dt' - \int_0^t \Phi_I(t-t')I_k(t')\Psi_k^{R_1}(t,t')\,dt' - \mu I_k(t) + \beta\Gamma_k(t). \quad (28)$$

We now consider the epidemic spreading under the assumption that the infections on a node of degree k first react and then diffuse away with a unitary diffusion rate. We find that in this case the PDF of the waiting time is $\psi_I(t) = \delta(t)$, and the infections for each class of degree k at time $t > 0$ are all from the contribution of arriving infections, i.e., $I_k(t) = I_k^+(t)$. Thus, in Eq. (21) $\int_0^t I_k^+(t')\Psi_k^{R_1}(t-t')\psi(t-t')\,dt'$, which are the arriving infections without reacting, and diffusing away at the later time t is $I_k(t)[1 - \mu - \frac{\beta\Gamma_k(t)}{I_k(t)}]$. Besides, the nonreactive initial infections $I_k(0)$ at the nodes with degree k have been moved away before time t, so we have $I_k(0)\Psi_k^{R_1}(t,0)\psi(t) = 0$. Finally, since the produced infections $2\beta\Gamma_k(t)$ in the reactive dynamics waits for time 0 and leave the node of degree k, one gets $\int_0^t 2\beta\Gamma_k(t)\Psi_k^{R_1}(t-t')\psi(t-t')\,dt' = 2\beta\Gamma_k(t)$. Therefore, Eq. (21) in this case reduces to $I_k^-(t) = I_k(t)[1 - \mu + \frac{\beta\Gamma_k(t)}{I_k(t)}]$. Substituting it into Eq. (19) and combining Eq. (20) we find

$$\frac{dI_k(t)}{dt} = -I_k(t) + k\sum_{k'}[I_{k'}(t)(1-\mu) + \beta\Gamma_{k'}(t)]\frac{1}{k'}P(k'|k), \quad (29)$$

which is in agreement with the result in Ref. [4].

We then analyze the special epidemic spreading with exponential waiting time $\psi_I(t) = \lambda e^{-\lambda t}$ under the assumption that reaction and diffusion process take place simultaneously. In this case one has $\Phi_I(s) = \lambda$, and thus $\Phi_I(t) = \lambda\delta(t)$ [21,22], which implies $I_k^-(t) = \lambda I_k(t)$. Then Eq. (27) reduces to

$$\frac{dI_k(t)}{dt} = k\lambda\sum_{k'} I_{k'}(t)\frac{1}{k'}P(k'|k) - \lambda I_k(t) - \mu I_k(t) + \beta\Gamma_k(t), \quad (30)$$

which is the continuous-time equation for the spread of the infection on heterogeneous metapopulations in Ref. [23].

We now turn to investigate the epidemic spreading for the waiting time PDF $\psi_I(t) = \frac{\alpha}{t+\tau_0}(\frac{\tau_0}{t+\tau_0})^\alpha$ for $0 < \tau_0, 0 < \alpha$ [16,18]. In this case $\Phi_I(s) \sim \frac{1}{\Gamma(1-\alpha)\tau_0^\alpha} s^{1-\alpha}$ for small τ_0. Inserting it into Eq. (24) and taking the inverse Laplace transform, we obtain $I_k^-(t) = \frac{1}{\Gamma(1-\alpha)\tau_0^\alpha}\Psi_k^{R_1}(t,0)\,{}_0D_t^{1-\alpha}[\frac{I_k(t)}{\Psi_k^{R_1}(t,0)}]$, so that the reaction-diffusion equation describing the time evolution for $I_k(t)$ in heterogeneous networks can be written as

$$\frac{dI_k(t)}{dt} = \frac{k}{\Gamma(1-\alpha)\tau_0^\alpha}\sum_{k'}\Psi_{k'}^{R_1}(t,0)\,{}_0D_t^{1-\alpha}\left[\frac{I_{k'}(t)}{\Psi_{k'}^{R_1}(t,0)}\right]\cdot\frac{1}{k'}P(k'|k) - \frac{1}{\Gamma(1-\alpha)\tau_0^\alpha}\Psi_k^{R_1}(t,0)\,{}_0D_t^{1-\alpha}\left[\frac{I_k(t)}{\Psi_k^{R_1}(t,0)}\right] - \mu I_k(t) + \beta\Gamma_k(t). \tag{31}$$

Notice that because of the memory effect of the fractional kinetics operator with the anomalous exponent α [5] the epidemic spreading with power-law waiting time in heterogeneous networks has a strong memory dependence on the SIS reactions and the average number of infected individuals at previous times. We call it anomalous epidemic spreading. Note also that in Eq. (31) the reaction effect $\Psi_k^{R_1}(t,0)$ which includes the quantity $S_k(t)$ for susceptible individuals is not simply adding to the diffusion term but enters into the diffusion operator in the form of $\Psi_k^{R_1}(t,0)\,{}_0D_t^{1-\alpha}[\frac{I_k(t)}{\Psi_k^{R_1}(t,0)}]$. This leads to a complex coupling relation between diffusion and reaction processes and then a dependence of $I_k(t)$ on the average number of susceptible individuals at previous times. For uncorrelated networks, Eq. (31) reduces to

$$\frac{dI_k(t)}{dt} = -\frac{1}{\Gamma(1-\alpha)\tau_0^\alpha}\Psi_k^{R_1}(t,0)\,{}_0D_t^{1-\alpha}\left[\frac{I_k(t)}{\Psi_k^{R_1}(t,0)}\right] + \frac{k}{\Gamma(1-\alpha)\tau_0^\alpha\langle k\rangle}\sum_{k'}\Psi_{k'}^{R_1}(t,0)\,{}_0D_t^{1-\alpha}\left[\frac{I_{k'}(t)}{\Psi_{k'}^{R_1}(t,0)}\right]P(k') - \mu I_k(t) + \beta\Gamma_k(t). \tag{32}$$

It should be mentioned that in Eq. (31) there still exists the complex relation between fractional diffusion operator ${}_0D_t^{1-\alpha}$ and reactive survival probability $\Psi_k^{R_1}(t,0)$. But by averaging both terms over of Eq. (31) over $P(k)$, we find $\frac{dI(t)}{dt} = -\mu I(t) + \beta\Gamma(t)$, which is independent of the diffusion. Here $\Gamma(t) = \sum_k \Gamma_k(t)P(k)$. It is an expected result since when we ignore the difference of degrees, the related diffusion between different degrees is also ignored, and then the variation of the average number of infected individuals of all nodes only comes from the reactions.

B. The time evolution of the average number of susceptible individuals in nodes with degree *k*

Analogously, we can describe the time evolution for the average number of susceptible individuals in nodes with degree k. Let $S_k^+(t)$ and $S_k^-(t)$ be the gain flux and the loss flux of susceptible individuals at the nodes of degree k at x at time t, $\Psi_k^{R_2}(t,t') = e^{-\beta\int_{t'}^{t}\frac{\Gamma_k(\tau)}{S_k(\tau)}d\tau}$ denote the probability for the susceptible individuals to keep healthy without being infected in the time interval $[t',t]$, and $\psi_S(t)$ represent the waiting time PDF for the susceptible individual staying at the node with degree k for time t and then moving out to the other node. We can now write the following balance equations for the time evolution of $S_k(t)$:

$$\frac{dS_k(t)}{dt} = S_k^+(t) - S_k^-(t) + \mu I_k(t) - \beta\Gamma_k(t), \tag{33}$$

$$S_k^+(t) = k\sum_{k'} S_{k'}^-(t)\frac{1}{k'}P(k'|k), \tag{34}$$

$$S_k^-(t) = S_k(0)\Psi_k^{R_2}(t,0)\psi_S(t) + \int_0^t [S_k^+(t') + \mu I_k(t')]\Psi_k^{R_2}(t,t')\psi_S(t-t')\,dt'. \tag{35}$$

Similarly to the derivation approach of Eq. (27), from above three equations the dynamical equation for the time evolution of $S_k(t)$ can be obtained as follows:

$$\frac{dS_k(t)}{dt} = k\sum_{k'}\int_0^t \Phi_S(t-t')S_{k'}(t')\Psi_{k'}^{R_2}(t,t')\,dt'\frac{1}{k'}P(k'|k) - \int_0^t \Phi_S(t-t')S_k(t')\Psi_k^{R_2}(t,t')\,dt' + \mu I_k(t) - \beta\Gamma_k(t). \tag{36}$$

Here $\Phi_S(t)$ is the inverse Laplace $s \to t$ transform of $\Phi_S(s) = \frac{s\psi_S(s)}{1-\psi_S(s)} = \frac{\psi_S(s)}{\Psi_S(s)}$, where $\psi_S(s)$ and $\Psi_S(s)$ are the Laplace $t \to s$ transforms of the waiting time PDF $\psi_S(t)$ and the survival function $\Psi_S(t) = 1 - \int_0^t \psi_S(t')\,dt'$ for susceptible individuals, respectively. The above dynamical equation (36) shows the complex coupling relation among epidemic process, random waiting time, and topological fluctuations of network.

By combining Eqs. (27) and (36), we find that

$$\frac{dN_k(t)}{dt} = k\sum_{k'}\int_0^t \left[\Phi_I(t-t')I_{k'}(t')\Psi_{k'}^{R_1}(t,t')\,dt' + \Phi_S(t-t')S_{k'}(t')\Psi_{k'}^{R_2}(t,t')\,dt'\right]\frac{1}{k'}P(k'|k) - \int_0^t \Phi_I(t-t')I_k(t')\Psi_k^{R_1}(t,t')\,dt' - \int_0^t \Phi_S(t-t')S_k(t')\Psi_k^{R_2}(t,t')\,dt'. \tag{37}$$

Note that this equation is not in agreement with Eq. (8), which describes the time evolution of the sum of the average numbers of infectious and susceptible individuals for each class of degree k, even in the case $\psi_I(t) = \psi_S(t)$. This is because of the assumption that the reactive and produced infected and susceptible individuals have new residence times no matter how long they have stayed there before. For example, they may be treated at hospitals in isolation at some later time.

When we substitute power-law waiting time $\psi_S(t) = \frac{\alpha}{t+\tau_0}(\frac{\tau_0}{t+\tau_0})^\alpha$ with $0 < \tau_0$, $0 < \alpha$ into Eq. (36), we then get the fractional dynamical equation for $S_k(t)$ in heterogeneous networks:

$$\begin{aligned}\frac{dS_k(t)}{dt} &= \frac{k}{\Gamma(1-\alpha)\tau_0^\alpha}\sum_{k'}\Psi_{k'}^{R_2}(t,0)\,{}_0D_t^{1-\alpha}\left[\frac{S_{k'}(t)}{\Psi_{k'}^{R_2}(t,0)}\right]\cdot\frac{1}{k'}P(k'|k)\\ &\quad - \frac{1}{\Gamma(1-\alpha)\tau_0^\alpha}\Psi_k^{R_2}(t,0)\,{}_0D_t^{1-\alpha}\left[\frac{S_k(t)}{\Psi_k^{R_2}(t,0)}\right] + \mu I_k(t) - \beta\Gamma_k(t).\end{aligned} \tag{38}$$

One can see that in this case $S_k(t)$ depends on the previous memories of infected reactions and the mean numbers of susceptible individuals for all degrees before.

IV. EPIDEMIC THRESHOLDS FOR ANOMALOUS EPIDEMIC SPREADING IN UNCORRELATED NETWORKS

A. Epidemic thresholds for type I

We now consider some possibilities of the epidemic threshold in anomalous epidemic spreading in uncorrelated networks regarding the waiting time PDFs $\psi_I(t)$ and $\psi_S(t)$ and the interaction kernel $\Gamma_k(t)$. We first consider type I, where each susceptible individual may react with all of the infectious individuals in the same node, namely, $\Gamma_k(t) = I_k(t)S_k(t)$. For $\psi_I(t) = \delta(t)$ and $\psi_S(t) = \frac{\tau_0}{(t+\tau_0)^2}$, which means the infections on a node of degree k first react and then diffuse away with a diffusion rate $D_I = 1$, and the waiting time for susceptible individual has power-law behavior with the exponent $\alpha = 1$, one has in the stationary state $I_k(t) = \frac{k}{<k>}I(t)$ [4]. And when $\alpha = 1$, under the assumption of no correlations, the dynamical equation (38) reduces to

$$\frac{dS_k(t)}{dt} = \frac{k}{\tau_0\langle k\rangle}S(t) - \frac{1}{\tau_0}S_k(t) + \mu I_k(t) - \beta I_k(t)S_k(t). \tag{39}$$

In the stationary state Eq. (39) becomes

$$0 = -\frac{1}{\tau_0}S_k(t) + \frac{k}{\tau_0\langle k\rangle}S(t) + \mu I_k(t) - \beta I_k(t)S_k(t). \tag{40}$$

Substituting the value of $I_k(t) = \frac{k}{\langle k\rangle}I(t)$ and $S(t) = N(t) - I(t)$ into Eq. (40), we obtain

$$S_k(t) = \frac{\frac{k}{\tau_0\langle k\rangle}[N(t) - I(t)] + \mu\frac{k}{\langle k\rangle}I(t)}{\frac{1}{\tau_0} + \beta\frac{k}{\langle k\rangle}I(t)}. \tag{41}$$

Thus,

$$\begin{aligned}I(t) &= N(t) - \sum_k S_k(t)P(k)\\ &= N(t) - \sum_k \frac{\frac{k}{\tau_0\langle k\rangle}[N(t) - I(t)] + \mu\frac{k}{\langle k\rangle}I(t)}{\frac{1}{\tau_0} + \beta\frac{k}{\langle k\rangle I(t)}}\cdot P(k).\end{aligned} \tag{42}$$

We can write this equation in the form $I(t) = f[I(t)]$, and the solution exists if the first derivative of $f[I(t)]$ greater than 1 when $I(t) = 0$ [4]. Then we find

$$f'[I(t)]|_{I(t)=0} = 1 - \mu\tau_0 + \frac{\langle k^2\rangle}{\langle k\rangle^2}\cdot N(t)\beta\tau_0, \tag{43}$$

so the condition for the presence of an active phase is

$$N(t) > \frac{\mu}{\beta}\frac{\langle k^2\rangle}{\langle k\rangle^2}, \tag{44}$$

in agreement with the condition for epidemic spreading without considering the waiting time for $D_I = 1$ and $0 < D_S \leqslant 1$, where D_s is the constant diffusion coefficient for susceptible individuals (see Ref. [4]). This is an expected result since in the epidemic normal spreading with power-law waiting time with the exponent $\alpha = 1$, the susceptible individual may diffuse or wait at each time step, and the corresponding mean diffusion probability D_s satisfies $0 < D_S \leqslant 1$. In the limit $V \to \infty$, the condition (44) becomes $N(t) > 0$ [4].

If the waiting time PDFs for infected individuals is also a power-law distribution with $\alpha = 1$, then the dynamical equation (32) becomes

$$\frac{dI_k(t)}{dt} = -\frac{1}{\tau_0}I_k(t) + \frac{k}{\tau_0\langle k\rangle}I(t) - \mu I_k(t) + \beta I_k(t)S_k(t). \tag{45}$$

In the stationary state Eq. (45) becomes

$$0 = -\frac{1}{\tau_0}I_k(t) + \frac{k}{\tau_0\langle k\rangle}I(t) - \mu I_k(t) + \beta I_k(t)S_k(t). \tag{46}$$

Multiplying this equation by $P(k)$ and summing over k yields

$$I(t) = \frac{\beta}{\mu}\Gamma(t) = \frac{\beta}{\mu}\sum_k I_k(t)S_k(t)P(k). \tag{47}$$

From Eqs. (40) and (46), we get

$$N(t) = \frac{\langle k\rangle}{k}N_k(t). \tag{48}$$

Substituting Eq. (48) into Eq. (40), we find

$$S_k(t)=\frac{\mu+\frac{1}{\tau_0}+\beta\frac{k}{\langle k\rangle}N(t)-\sqrt{[\mu+\frac{1}{\tau_0}-\beta\frac{k}{\langle k\rangle}N(t)]^2+4\beta\frac{k}{\langle k\rangle\tau_0}I(t)}}{2\beta},\tag{49}$$

for $u+\frac{1}{\tau_0}-\beta\frac{k}{\langle k\rangle}N(t)>0$, and

$$S_k(t)=\frac{\mu+\frac{1}{\tau_0}+\beta\frac{k}{\langle k\rangle}N(t)+\sqrt{[\mu+\frac{1}{\tau_0}-\beta\frac{k}{\langle k\rangle}N(t)]^2+4\beta\frac{k}{\langle k\rangle\tau_0}I(t)}}{2\beta},\tag{50}$$

for $\mu+\frac{1}{\tau_0}-\beta\frac{k}{\langle k\rangle}N(t)<0$, such that when $I(t)=0$ one has $S(t)=N(t)$. Taking the similar technology as before, in the limit of $\tau_0\rightarrow 0$, we obtain

$$\begin{aligned}f'[I(t)]|_{I(t)=0}&=\frac{\partial[N(t)-\sum_k S_k(t)P(k)]}{\partial I(t)}|_{I(t)=0}\\&\sim 1+\beta\frac{\langle k^2\rangle}{\langle k\rangle^2}N(t)\tau_0-\mu\tau_0,\end{aligned}\tag{51}$$

for the above two cases. The condition for the presence of an active phase is then given by

$$N(t)>\frac{\mu}{\beta}\frac{\langle k^2\rangle}{\langle k\rangle^2}.\tag{52}$$

B. Epidemic thresholds for type II

We now consider the type II that each individual only has a finite number of contacts with others where $\Gamma_k(t)=\frac{I_k(t)S_k(t)}{N_k(t)}$. For $\psi_I(t)=\delta(t)$ and $\psi_S(t)=\frac{\tau_0}{(t+\tau_0)^2}$, we find that in the stationary state $I_k(t)=\frac{k}{\langle k\rangle}I(t)$ [4] and

$$0=-\frac{1}{\tau_0}S_k(t)+\frac{k}{\tau_0\langle k\rangle}S(t)+\mu I_k(t)-\beta I_k(t)S_k(t)/N_k(t)\tag{53}$$

hold. From Eq. (53), we get $I(t)=\frac{\beta}{\mu}\Gamma(t)=\frac{\beta}{\mu}\sum_k I_k(t)\frac{S_k(t)}{I_k(t)+S_k(t)}P(k)$. Substituting it into Eq. (53), one can find a solution $S_k(t)=\frac{k}{\langle k\rangle}S(t)$. Inserting this expression into $I(t)=\frac{\beta}{\mu}\Gamma(t)$, we have $S(t)=\frac{\mu}{\beta}N(t)$, and then $I(t)=(1-\frac{\mu}{\beta})N(t)$. Therefore, the threshold value in this case is the general result $\frac{\beta}{\mu}>1$,which is in agreement with the result for epidemic spreading in uncorrelated networks for $D_I=1$ and $0<D_S\leqslant 1$ without considering the waiting time of individuals in Ref. [4].

If the waiting time distribution for infected individuals is also power law with $\alpha=1$, namely, $\psi_I(t)=\frac{\tau_0}{(t+\tau_0)^2}$, then one has

$$0=-\frac{1}{\tau_0}I_k(t)+\frac{k}{\tau_0\langle k\rangle}I(t)-\mu I_k(t)+\beta I_k(t)\frac{S_k(t)}{N_k(t)},\tag{54}$$

in the stationary state. Combing Eqs. (53) and (54), we find that Eq. (48) still holds. Substituting Eq. (48) into Eq. (53) yields

$$S_k(t)=\frac{\mu+\frac{1}{\tau_0}+\beta-\sqrt{(\mu+\frac{1}{\tau_0}-\beta)^2+\frac{4\beta}{\tau_0 N(t)}I(t)}}{\frac{2\beta k}{\langle k\rangle N(t)}},\tag{55}$$

for $\mu+\frac{1}{\tau_0}-\beta>0$, and

$$S_k(t)=\frac{\mu+\frac{1}{\tau_0}+\beta+\sqrt{\left(\mu+\frac{1}{\tau_0}-\beta\right)^2+\frac{4\beta}{\tau_0 N(t)}I(t)}}{\frac{2\beta k}{\langle k\rangle N(t)}},\tag{56}$$

for $\mu+\frac{1}{\tau_0}-\beta<0$, such that when $I(t)=0$ we get $S(t)=N(t)$. From $I(t)=N(t)-\sum_k S_k(t)P(k)=f[I(t)]$, and Eqs. (55) and (56), we get $f'[I(t)]|_{I(t)=0}=\frac{1}{1+(\mu-\beta)\tau_0}$. Thus, we find the usual epidemic threshold $\frac{\beta}{\mu}>1$ satisfying $f'[I(t)]|_{I(t)=0}>1$ for $\tau_0>0$ in this case.

From these results one can see that the power-law residence time with $\alpha=1$ does not change the thresholds for epidemic spreading in uncorrelated networks without considering the effect of waiting time. Note that for power-law waiting time with the exponent $\alpha=1$ the fractional derivative operator in Eqs. (32) and (39) disappears, and then the average numbers $I_k(t)$ and $S_k(t)$ have no memory of the previous evolution and only depend on the average waiting time τ_0. Such epidemic spreading with random waiting time for anomalous exponent $\alpha=1$ can be seen as epidemic normal spreading.

V. MONTE CARLO SIMULATIONS

Finally, we implement Monte Carlo simulations to verify the dynamics for anomalous epidemic spreading with power-law waiting time on scale-free networks. We first generate a scale-free network using NetworkX 2.1. The algorithm is defined as follows. (i) A random zipf sequence with the size of $V=100$ nodes for the degree distribution $P(k)=k^{-\gamma}$ with the exponent $\gamma=2.5$ (see Fig. 2) is created. (ii) A random graph of networks is drawn shown in Fig. 3 using a configuration model where links are randomly assigned to match the given degree sequence [4].

We then simulate the anomalous epidemic spreading process in this scale-free network. In our algorithm we take the reaction time step size $\Delta t=2\times 10^{-3}$ and ignore small transport fluctuation of the average number of individuals at each node [24]. The internal clock of every individual at each node is set to measure the time elapsed since his or her last movement or reaction. The detailed anomalous diffusion and reaction processes for the individuals are modeled as follows.

(i) In the initial state $\rho(0)-1$ susceptible individuals are randomly placed at the nodes by uniform distribution, and one infectious individual is placed at one center node. The random waiting time t as the internal clock to make next jump for each individual is chosen from a series of values distributed according to $\psi(t)=\frac{\alpha}{t+\tau_0}(\frac{\tau_0}{t+\tau_0})^\alpha$ with $0<\tau_0, 0<\alpha$ [14,25].

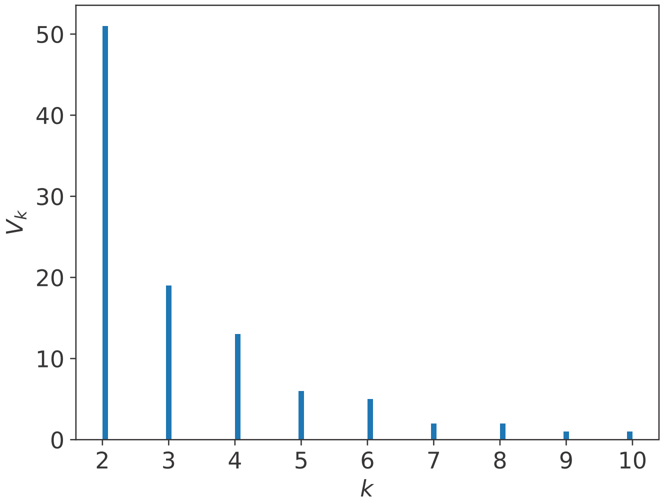

FIG. 2. A random zipf sequence with $V = 100$ nodes obeying the power-law degree distribution $P(k) = k^{-2.5}$.

(ii) At the clock time each individual located in a node with degree k diffuses into one of the neighboring nodes with the probability $\frac{1}{k}$, after which the internal clock for this individual is reset by the distribution as before [14].

(iii) For type I each susceptible individual sitting on the node i turns into an infectious individual with the probability of $1-(1-\beta\Delta t)^{\rho_i}$, where ρ_i is the number of infectious individuals at node i at each reaction time step [4]. Meanwhile, each infectious individual at node i except the new infected ones becomes susceptible individual with the probability $\mu\Delta t$. After these reactions the internal clocks for the new infected and susceptible individuals and the infectious individuals energizing others at the node i are all renewed.

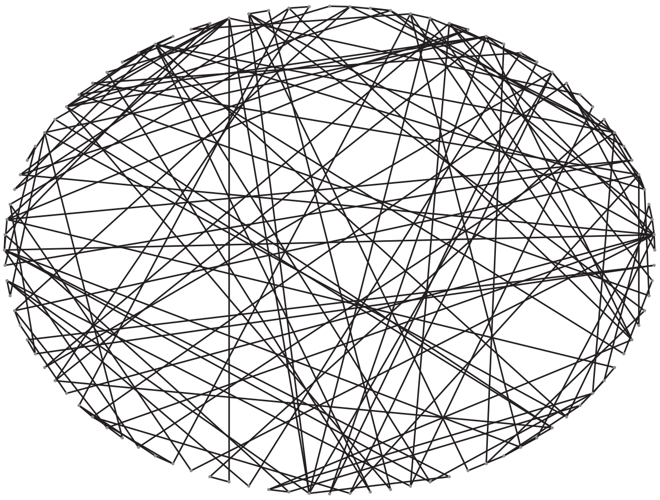

FIG. 3. A scale-free network respecting the degree sequence in Fig. 2.

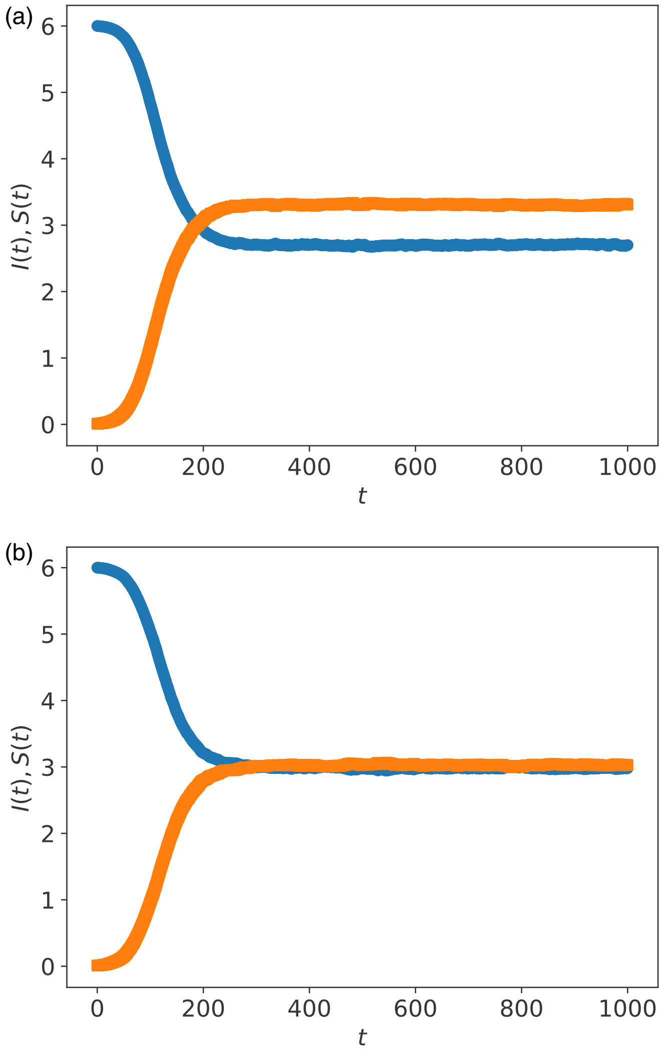

FIG. 4. The time evolution of the average numbers $I(t)$ [orange (light gray)] and $S(t)$ [blue (dark gray)] in the time interval [0, 1000] for anomalous epidemic spreading with power-law waiting time $\psi(t) = \frac{\alpha}{t+\tau_0}(\frac{\tau_0}{t+\tau_0})^{\alpha}$ with $\alpha = 1$ (a) and $\alpha = 0.55$ (b) in heterogeneous network of size $V = 100$. Here $\tau_0 = 0.22$, $\mu = 0.02$, and $\beta = 0.01$; the initial total number $\rho(0) = 601$; and thus the average number $N(t) = 6.01$. One can see that the stationary number for infectious individuals reduces with small anomalous exponent α of random waiting time, and the starting time when $I(t)$ becomes more than $S(t)$ in (b) is also retardant.

Figure 4 shows the time evolution of the average numbers of infectious and susceptible individuals in all nodes in the time interval [0, 1000] for $\alpha = 1$ and $\alpha = 0.55$. One can see that the average numbers of infected and susceptible individuals have been stable for a long time, the epidemic prevalence is lower with a smaller exponent for the power-law waiting time, and the starting time when $I(t)$ becomes larger than $S(t)$ is also retardant for $\alpha = 0.55$. Figure 5 shows that the stationary average number $I(t)$ of infectious individuals in all nodes is a monotonous increasing function of the total average number $N(t)$, and in both cases if the condition that the total average number $N(t) > \frac{\mu}{\beta}\frac{<k^2>}{<k>^2}$ for individuals is satisfied, then the stationary average number $I(t) > 0$. The result recovers the analytical epidemic threshold condition (52) for the power-law residence time with $\alpha = 1$ for individuals in uncorrelated networks. Besides, by comparing Figs. 5(a) and 5(b), we also find that the spreading of infectious diseases is slowed down when α reduces, and the point of intersection where

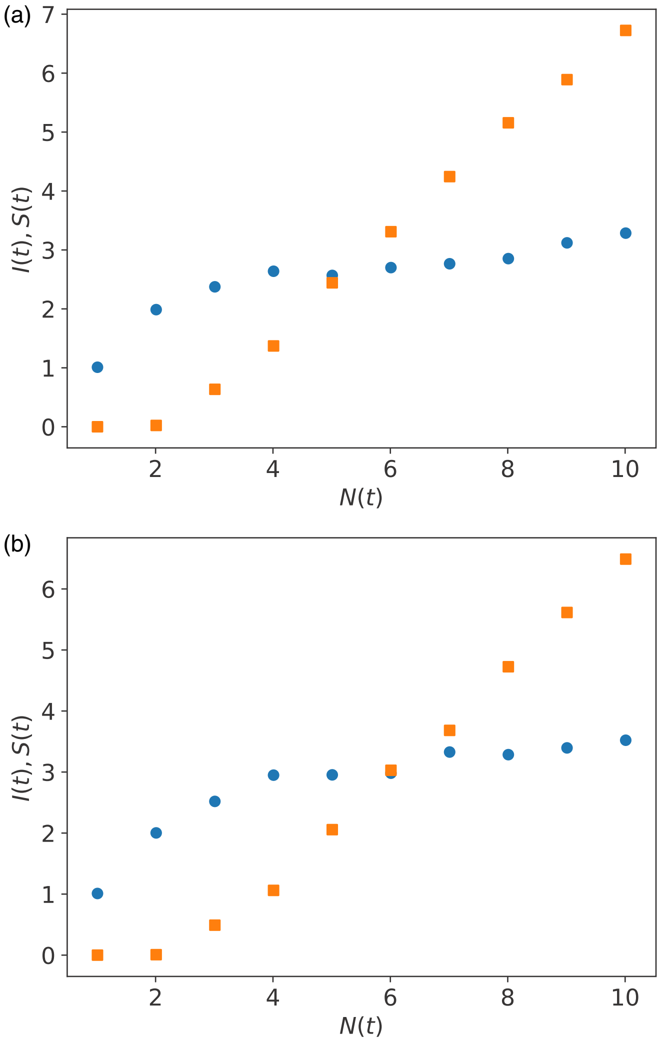

FIG. 5. The stationary average numbers $I(t)$ (orange square) and $S(t)$ (blue circle) for anomalous epidemic spreading in heterogeneous network of size $V = 100$ with power-law waiting time $\psi(t) = \frac{\alpha}{t+\tau_0}(\frac{\tau_0}{t+\tau_0})^\alpha$ with $\alpha = 1$ (a) and $\alpha = 0.55$ (b) with respect to the total average number $N(t)$ for $t = 1000$, $\tau_0 = 0.22$, $\mu = 0.02$, $\beta = 0.01$, and $\rho(0) = 101, 201, 301, 401, 501, 601, 701, 801, 901,$ and 1001. One can see that $I(t)$ is monotonous increasing, and in both cases $I(t) = 0$ when $N(t) = 1.01$ and $I(t) > 0$ [$I(t) = 0.0227$ for $\alpha = 1$ and $I(t) = 0.0074$ for $\alpha = 0.55$] when $N(t) = 2.01$. The simulation for $\alpha = 1$ verifies the analytical solution for the epidemic threshold for type I that if $N(t) > \frac{\mu}{\beta}\frac{\langle k^2\rangle}{\langle k\rangle^2} \approx 1.55$, then $I(t) > 0$. Notice also that the epidemic spreading is slowed down when α reduces, and the abscissa value for the intersection point of two discrete curves becomes larger with the decrease of exponent.

the average number for infection individuals in all nodes exceeds that for susceptible individuals delays for smaller anomalous exponent. These results imply that when $\alpha = 0.55$ the epidemic spreading in heterogeneous networks is undergoing anomalous delayed spreading. This is an expectable result since when $0 < \alpha < 1$, the average residence time for individuals $\langle T\rangle = \int_0^{+\infty} t\psi(t)\,dt$ diverges, leading to long-tailed trapping events [5,16,26], which delays the epidemic spreading. In Fig. 6 the linear dependent relation between the average numbers and the degree k for large time is shown.

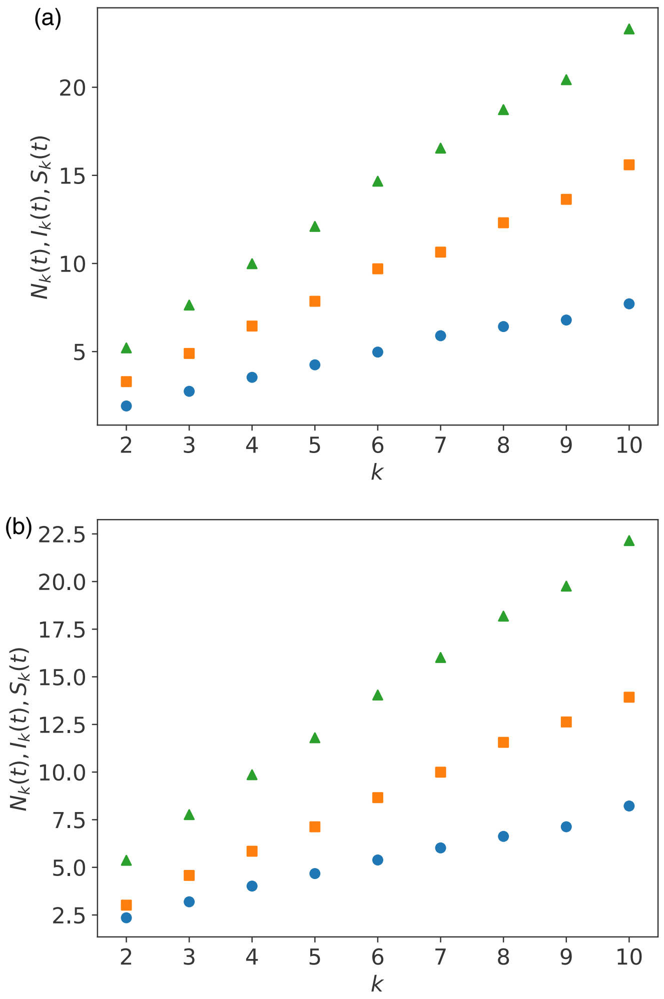

FIG. 6. The stationary average numbers $N_k(t)$ (green triangle), $I_k(t)$ (orange square), and $S_k(t)$ (blue circle) with respect to degree k for anomalous epidemic spreading in heterogeneous network of size $V = 100$ with power-law waiting time for $\alpha = 1$ (a) and $\alpha = 0.55$ (b) when $t = 1000$. Here $\rho(0) = 801$, $\tau_0 = 0.22$, and the reaction rates $\mu = 0.02$ and $\beta = 0.01$. It is shown that they are all linear-like in k. Note that such linear relation has also been found in epidemic spreading in heterogeneous networks without considering the effect of random waiting time (see Ref. [4]). The linear dependence of the stationary average number $N_k(t)$ on the degree k for $\alpha = 1$ is in agreement with the analytical result presented in Eq. (48).

VI. CONCLUSION

In summary, we introduce the random waiting time in standard epidemic SIS model in heterogeneous networks to capture the effect of detention period of individuals on the spread of an emerging disease and derive the generalized dynamical equations (27) and (36) for the time evolution of the mean numbers of infected and susceptible individuals. As examples, for the power-law waiting time, Eqs. (27) and (36), respectively, reduce to Eqs. (31) and (38), which include the coupled relation between fractional diffusion operator and reaction survival probability. This implies that the epidemic spreading in this case is anomalous and has a strong memory on the previous epidemic behaviors. These quantitative results will have a significant impact on the studying of epidemiology and also provide a suited theoretical approach for modeling other spreading phenomena in heterogeneous networks in biology, sociology, and technology.

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Correction: Equations (6) and (23) and the inline equation appearing before Eq. (24) contained errors and have been fixed.