Mixed SI (R) epidemic dynamics in random graphs with general degree distributions

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A B S T R A C T

Analytical description of disease propagation on random networks has become one of the most productive fields in recent years, yet more complex contact patterns and dynamics have been resorted to numerical study. In this paper, an epidemic model is defined in which each individual, once infected, has chances to recover from infection at certain rate. The chance is represented by a parameter $q \in [0, 1]$. This model can be viewed as an interpolation between classical SI model ($q = 0$) and SIR model ($q = 1$). We develop a low-dimensional system of non-linear ordinary differential equations to model the mixed susceptible-infected (-recovered) SI (R) epidemics on random network with general degree distributions. Both the final size of epidemics and the time-dependent behaviors are derived within this simple framework. In addition, we present the exact transmissibility and the epidemic threshold for this model.

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1. Introduction

Many infectious diseases spread over networks by contacts between susceptible and infective individuals. Classical early work in mathematical epidemiology often assumed a homogeneously mixing community of individuals (also called the law of mass action [1,12]), each having the same susceptibility to disease and the same ability to transmit disease. However, this rarely reflects true populations, where the number of contacts is highly heterogeneous and each individual only has contact with a small fraction of the population.

Since the past two decades or so, there has been considerable interest in understanding disease propagation by using random networks [2,10,13,14,17,18,23,24,31], which allow for more realistic and accurate capture of heterogeneities compared with well-mixed models. Some quantities of interest such as epidemic probability and expected final size of epidemics have been precisely solved in random networks with general degree distributions (namely, configuration models) through bond percolation theory [6,14,17,19]. The heterogeneity introduced in the network framework, however, makes it rather difficult to describe the time-dependent properties of an epidemic analytically. Some efforts have been made by using high-dimensional pair-approximation methods (or moment closure methods) [9,11,26], which in principle ignore the correlations between the states of nodes (individuals) several steps apart. Alternatively, some researchers adopt approximate approaches that assume all nodes of the same degree having the same infection probability at any given time [4,20]. Others have conducted simulation-based studies of epidemic dynamics [8,21,27].

More recently, Volz [29] and Miller [15] introduce a low-dimensional system of non-linear ordinary differential equations to model susceptible-infected-recovered (SIR) epidemics on random networks assuming infection and recovery occur at constant rates. The calculations account for the effects induced by heterogeneous connectivity and finiteness of degree that are

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missed in standard well-mixed SIR equations. Besides the dynamical properties, the final size of an epidemic is also predicted in their frameworks. In contrast to the previous moment closure methods [11], the number of equations in the resulting system does not grow with the number of different degrees. Rigorous proof of the obtained equations is provided in [7] based on measure-valued processes.

In the present work, we move a further step beyond this framework by considering more complex susceptible-infected (-recovered) SI (R) epidemics in random networks, where an infected individual has chances to recover (but not necessarily certainly) at some rate. We use a parameter $q \in [0, 1]$ to represent the possibility of recovery. This model can be thought of as a mix or interpolation between the classical SI model, where no infected individuals can recover, and SIR model, where all infected ones are recovered eventually. A unique feature of our model is that the three exclusive states (susceptible, infected, and recovered) can coexist as time $t \to \infty$, which is more realistic than the pure SIR model.

By introducing a virtual recovered state, $\widetilde{R}$, we show that it is possible to analyze the dynamics of mixed SI (R) epidemics spread on configuration models [16,18] using a coupled system of only three ordinary differential equations. The epidemic growth at any given time as well as its final size are examined in this relatively simple framework, which is less computationally demanding and amenable to the analytical derivations. A derivation of the transmissibility for our model is provided. We demonstrate the theoretical results by concrete examples on configuration models including power-law networks and Poisson random graphs.

The rest of the paper is organized as follows. In Section 2, we present the theoretical framework and give some preliminaries. The network mixed SI (R) dynamics is then developed in Section 3. Section 4 is devoted to the transmissibility and the epidemic threshold. Finally, we conclude the paper in Section 5.

2. The model and notations

Consider a population consisting of n individuals. Each individual is represented by a node in the network modeled by the configuration model [16], in which the degree distribution is specified, but the graph is in other respects random.

To define a configuration model network, one specifies the degree distribution by giving the properly normalized probability p_k that a randomly chosen node has degree k. Assign an i.i.d. degree d_v drawn from the distribution p_k to each node v. If the sum of degrees is odd, all degrees are reassigned until the sum is even. We then create a set X consisting of d_v "stubs" of edges for each node v. There are $\sum_v d_v$ stubs in total. A pair of these stubs is then chosen uniformly at random and connected together to form a complete edge until X is used up. This procedure generates a uniform choice from the ensemble of all networks with the specified degree distribution. The resulting network has $\sum_v d_v / 2$ edges, and is locally tree-like in the limit of large size n. It has negligible self-loops and multiple edges in the limit of large network size n for degree distributions with finite mean [18].

We define the probability generating function [24,30] of the degree distribution p_k as

$$G(x) = \sum_{k=0}^{\infty} p_k x^k, \tag{1}$$

where the dummy variable x serves as a place-holder. The mean degree of the network is then given by $\langle k \rangle = G'(1)$.

Nodes in the network fall into one of three exclusive states: susceptible, infected or recovered. We denote the fraction of the population in each state at time t by $S = S(t)$, $I = I(t)$ and $R = R(t)$, respectively. The dynamics of the disease propagation can be described as follows. An infected node transmits infection to each of its neighbors independently at a constant rate β. Thus, a susceptible node becomes infected at rate $k\beta$ where k is the number of infected neighbors it has. Once infected, with probability q a node recovers at a constant rate γ, whereupon it will never infect any neighbors, and with probability $1 - q$, it will remain infected without recovery. Note that if $q = 0$ the model reduces to the SI model where only two states, susceptible and infected, are possible, while if $q = 1$ we readily reproduce the SIR model. At first glance, one might imagine that the above mixed SI (R) model is just a "slowdown" version of standard SIR model with recovery rate $q\gamma$. This, however, is not correct because in the pure SIR model with recovery rate $q\gamma$ $I(\infty) = 0$, namely, nobody will be in the infected state at the end of an epidemic, while in the mixed SI (R) model $I(\infty) > 0$ as long as $q < 1$.

Now here comes the trick: we modify the notations by introducing a state of "virtual recovered". The fraction of virtual recovered node at time t is denoted by $\widetilde{R} = \widetilde{R}(t)$. An infected node becomes virtual recovered with probability $1 - q$ at rate γ. Bearing in mind that virtual recovered nodes are still infectious, the fraction of infectious node altogether at time t now amounts to $I(t) + \widetilde{R}(t)$. By definition we have $S + I + \widetilde{R} + R = 1$. At the end of an epidemic, the fraction of infectious (i.e., "infected" + "virtual recovered") nodes is represented by $\widetilde{R}(\infty)$ since $I(\infty)$ is equal to zero (note that this is consistent with the last statement in the preceding paragraph, where I includes the present $\widetilde{R}$ state). In what follows, we will stick on this four-state epidemic model. A flow chart is shown in Fig. 1.

Similarly as in [15,24,29] we define an "infectious contact" from an infected node u to its neighbor v to be a contact that would cause infection of v if v were susceptible. Here comes a second trick: we choose a node v in the network uniformly at random and modify the spread of the disease by disallowing infectious contacts from v to its neighbors. Denote a (any) neighbor of v by u. Let $\theta = \theta(t)$ be the probability that there has not been infectious contact from u to v at time t. It is worth noting that, by doing so, disease transmission along different edges to node v is independent. Moreover, disallowing infection originated from v does not modify the probability that v has become infected, although it does affect the dynamics after v is