Phase Transition of Epidemic Dynamics on Adaptive Networks

Condensed Matter Theory I   02110902   Yuta MURAKAMI

1 Introduction

Mathematical models of disease propagation have been studied for a long time, and various models have been proposed. In the last decade, much attention has been paid to the epidemic dynamics on a network, and those researches have revealed that the network structure affects the epidemic dynamics on the network. Similarly, the spreading of an infectious disease on the network can have a strong effect on the dynamics of the network structure. For example, people tend to avoid contact with infectious individuals in real networks. Therefore, an epidemic model on an adaptive network has been introduced as a model that takes into account the interaction between the dynamics of networks and the dynamics on networks [1, 2]. The study of these models develops our understanding of the epidemic spreading on networks.

In the previous study [2], the moment-closure approximation (MCA) and the degree-based mean-field (DBMF) theory have been used to analyze the epidemic dynamics and the network dynamics. These are common analytical approaches for dynamics on networks, however, these are often inaccurate due to the following assumptions. The DBMF theory is based on the assumption that there is no dynamical correlation. The MCA includes dynamical correlations at a pairwise level only.

In order to improve accuracy, the approximate master equation (AME) approach, which is the extension of the DBMF theory, has been proposed [3, 4]. The variables of the AME have full information of those neighbors, namely, the dynamical correlation is taken into account. The AME approach provides a good prediction of the time evolution and good estimates of critical values for binary-state dynamics on a network.

In this study, we extend the AME approach to three-state dynamics and analyze the adaptive SIRS (susceptible-infected-recovered-susceptible) model of Shaw *et al.* [2].

2 SIRS Model on an Adaptive Network

We consider a network with N nodes and K undirected links. The nodes correspond to individuals, and the links represent relationships between them. We assume that the networks have no degree correlation. The degree distribution of the network is p_k, and the mean degree of the network is $\langle k \rangle = \sum_k k p_k = 2K/N$. Self-loops and multiple links are not allowed.

At any time, each node is in a specific state, either susceptible (S), infected (I) or recovered (R). A susceptible node which has l infectious neighbors becomes infected with rate (probability per unit time) λl. An infected node becomes recovered with rate μ. A recovered node becomes susceptible again with rate ν. In addition, for every link between a noninfected node (S or R) and an infected node (I), the noninfected node cuts the link with rate ω and forms a new link with another randomly selected noninfected node. These rules guarantee that N and K remain constant over time.

3 Simulations and Results

Let $S_{klm}(t)$ ($I_{klm}(t)$, $R_{klm}(t)$) be the fractions of susceptible (infected, recovered) nodes that have degree k, l infectious neighbors and m recovered neighbors at time t. We derive the AMEs for these variables, and obtain time evolution of the system by numerical integration. Similarly, we obtain solutions of the MCA and the DBMF theory. In addition, We performed Monte Carlo simulations.

First, we examined the time evolution of infection, defined as the fraction of infected individuals $I(t)$. The AME solution agrees with the result of the simulation (Fig. 1).

Next, we studied the epidemic threshold λ_c. The SIRS model exhibits a phase transition between the healthy state and the endemic state. These states are characterized by a parameter λ and an order parameter I_∞ that expresses the fraction of infected nodes at steady state. If $\lambda < \lambda_c$, the system stays healthy and I_∞ is zero. In contrast, the endemic phase appears and $I_\infty > 0$ at $\lambda > \lambda_c$. The threshold obtained from AME approach is different from that obtained from MCA or DBMF theory, and match the result of simulations.

4 Summary

We have studied the adaptive SIRS model using the AME approach. By integrating AMEs numerically, the AMEs reproduce the time evolution of the model with good accuracy. Moreover, the epidemic threshold obtained from the AME approach is in good agreement with that found by the simulations.

References

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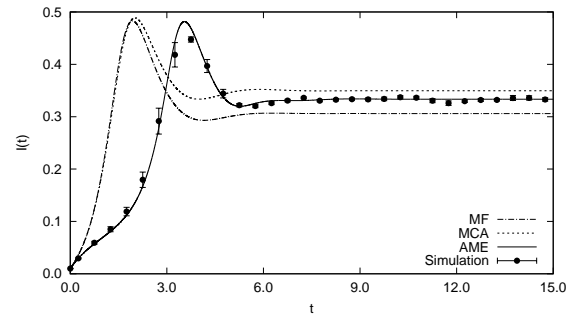[4] J. P. Gleeson, Phys. Rev. X **3**, 021004 (2013).

Fig. 1 Time evolution of the fraction of infected nodes $I(t)$. The initial degree distribution is regular-random network with $\langle k \rangle = 5$, and parameters are $N = 10^4$, $\lambda = 2.0$, $\mu = 1.0$, $\nu = 1.0$, $\omega = 5.0$.