

Epidemic Spread in Adaptive Social Networks with Community Structure

Leah B. Shaw¹ and Ilker Tunc²

¹ College of William and Mary, Williamsburg VA 23187, USA

lbshaw@wm.edu

<http://lbshaw.people.wm.edu/>

² College of William and Mary, Williamsburg VA 23187, USA

Abstract. When an epidemic spreads in a population, individuals may adaptively change the structure of their social contact network in response. We study the spread of epidemics in an adaptive network with community structure. Community structure is a characteristic of social networks that has been neglected in previous adaptive network epidemic models. We model the effect of heterogeneous communities on infection levels. We also show how an epidemic can alter the community structure.

Keywords: adaptive networks, community structure, epidemics.

1 Introduction

We consider an epidemic spreading in a social network in which nodes represent individuals and links their interactions. Node dynamics are assumed to be SIS (susceptible-infected-susceptible). People are assumed to change their social behaviors during an epidemic as in [1]. Avoidance of the disease is implemented by rewiring susceptible nodes away from infected nodes to other susceptible nodes. Previous models for epidemic spread in adaptive networks [1,2,3] have not included community structure. However, it is often thought that most social networks have community structure, in which groups of nodes have high connectivity within the group and relatively few connections to other groups [4].

2 Model and Results

Our model is that of [1] with the following alterations. We use two parameters d and f to generate an initial network with two communities A and B. The parameter d is the probability that when generating a link the link begins with a node in community A. f is the probability that the link connects communities A and B. We fix $d > 0.5$ so that we obtain two heterogeneous communities having different average degrees. By changing f , we change the strength of the community structure. We generally consider strong community structure (few cross connections). When rewiring links, we preserve the community structure by using two rewiring parameters (dependent on f and d) for the probability α

a susceptible node in community A rewires to another susceptible in the same community and likewise with β for B.

We performed Monte Carlo simulations for a system of $N = 10^4$ nodes and $K = 10^5$ links. Further, we derived mean field ordinary differential equations for both node and link dynamics using a moment closure approximation for three point terms as in [1,2,3].

We find that the extent of community structure affects the infection levels. When the communities are heterogeneous, for example if A has high average degree and B has low average degree, the infection level in the two communities can be either similar or drastically different depending on the extent of community structure and the infection rate p . If the communities are weakly connected (e.g., $f \sim 10^{-3}$), there can exist distinct threshold infection rates p_A, p_B in the two communities. For $p < p_A$, a stable endemic state does not exist. For $p_A < p < p_B$, the infection is endemic in A but appears only stochastically in B. Finally, for $p > p_B$, the infection is endemic in both communities. If on the other hand the two communities are more strongly connected (e.g., $f \sim 0.1$), the infection threshold and infection levels are similar in both communities.

We have also found changes in the community structure as a result of the epidemic spread. Our rewiring rules are chosen such that if SI links occurred randomly throughout the system, the original community structure would be preserved. However, if community A is above the epidemic threshold and community B is below, there are disproportionately more SI links in the A community and fewer in the B community. As a result, there is a net flux of links away from A and toward B until the system reaches a steady state with fewer AA links and more BB links than would be expected from the initial network structure dictated by the parameters d and f . Thus the epidemic spread alters the community structure and has a homogenizing effect.

We have studied both epidemic thresholds and alteration of community structure via both Monte Carlo simulations of the full system and our lower dimensional mean field model. We find both approaches to be in good agreement in their predictions of steady state infection levels and average numbers of links within and between the communities.

References

1. Gross, T., D'Lima, C.J.D., Blasius, B.: Epidemic Dynamics on an Adaptive Network. *Phys. Rev. Lett.* 96, 208701 (2006)
2. Shaw, L.B., Schwartz, I.B.: Fluctuating Epidemics on Adaptive Networks. *Phys. Rev. E* 77, 066101 (2008)
3. Shaw, L.B., Schwartz, I.B.: Enhanced Vaccine Control of Epidemics in Adaptive Networks. *Phys. Rev. E* 81, 046120 (2010)
4. Newman, M.E.J.: The Structure and Function of Complex Networks. *SIAM Review* 45, 167–256 (2003)