Spreading law in a highly interconnected world

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ABSTRACT

Infectious diseases and computer malwares spread among humans and computers through the network of contacts among them. These networks are characterized by wide connectivity fluctuations, connectivity correlations and the small world property. I show that these network properties lead to a novel spreading law which exhibits an initial power law growth, with an exponent determined by the average node distance on the network. This behavior is furthermore diminished or enhanced by disassortative or assortative connectivity correlations, respectively. Based on our current knowledge of several networks underlying the spreading of infectious diseases and computer malwares I predict that this law should characterize modern epidemic outbreaks. Finally I discuss the impact of these results on intervention strategies to halt epidemic outbreaks.

Categories and Subject Descriptors

G.2.2 [**Graph theory**]: Network problems; J.4 [**Life and medical sciences**]: Biology and genetics

General Terms

Theory

Keywords

Infectious diseases, computer viruses

1. INTRODUCTION AND CONCLUSIONS

Determining the spreading dynamics of infectious diseases is fundamental to design successful intervention strategies to halt epidemic outbreaks. Current mathematical models predict that the number of new infections grows exponentially during the initial phase of an epidemic outbreak [1, 2]. Within the exponential growth scenario infectious diseases are characterized by the average reproductive number, giving the number of secondary infections generated by a primary case, and the average generation time, giving the average time elapse between the infection of a primary and its secondary cases. In turn, vaccination strategies have been designed in order to modify the reproductive number and the generation time [1].

I have recently shown, however, that this picture dramatically changes if the graph structure underlying the spreading dynamics exhibits a power law degree distribution [3, 4], where the degree of a node is defined as the number of its connections. The significant abundance of high degree nodes (hubs) carry as a consequence that most nodes are infected in a time scale of the order of the disease generation time. Furthermore, the initial epidemic growth is no longer exponential, instead follows a power law growth $n(t) \sim t^D$ where D is the characteristic distance between nodes on the graph. Yet, these predictions are limited to uncorrelated graphs and the susceptible-infected (SI) model.

In this work I extend the theory of age-dependent branching processes to consider the topological properties of real networks. First, I generalize my previous study [3, 4] to include degree correlations. This is a fundamental advance since real networks are characterized by degree correlations that may significantly affect the system's behavior. Second, I consider the susceptible-infected-removed (SIR) model that provides a more realistic description of real epidemic outbreaks, allowing us to obtain conclusions about the impact of patient isolation and immunization strategies on the final size of the epidemics. Based on this mathematical framework, I survey our current knowledge about different networks underlying the spreading of infectious diseases and computer malwares. I discuss the impact of these network topologies on the spreading dynamics and intervention strategies to halt epidemic outbreaks.

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