Variability of the infection time in scale-free networks

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Abstract

Recent studies suggest that a large number of natural and artificial networks are characterized by very large degree fluctuations. This result means that a non-negligible number of nodes are extremely well connected while the majority just have a few links. The effect of such large fluctuations can be dramatic as illustrated by the fact that infectious agents can spread on these networks even for a very small value of the transmission probability.

Another consequence is that random immunization is inefficient for this kind of networks. Consequently, containment protocols and vaccination of traced contacts become our only defense but are unfortunately difficult to use at a large scale and in this context, an efficient method for detecting epidemics during their early stage becomes imperative. These efforts, now broadly labeled as "syndromic surveillance" are the centers of attention of public health agencies concerned with bioterrorism-related diseases. More precisely, an important point is to be able to determine and characterize specific nodes in the network which display interesting features in regards of an early detection system. In the present work, we focus on two specific features: (i) a small average infection time t_{inf} and (ii) low fluctuations around that time t_{inf}.

We analyze and compare the behaviors of the infection time obtained for the usual random Erdos-Renyi graph and the Barabasi-Albert scale-free network. We first compare the patterns obtained on both kind of networks and we then describe the variations of the infection time with the degree and with the topological distance to the initially infected node.

Keywords: scale-free networks;epidemic spreading;variability

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I. INTRODUCTION

Numerous studies have shown that many natural and artificial networks (e.g. air transportation, sexual contact, coauthorship, ...) have a distribution of their degree k which follows a power law ($P_k \sim k^{-\gamma}$) [1–5]. This implies the absence of a characteristic scale of their degree distribution, hence their name "scale-free network" (SFN) [6, 7].

Classically, epidemic modelisation is based on the homogeneous mixing paradigm. All individuals have the same probability to become infected and no heterogeneity in the contact network is taken into account.

However, superspreading events like the ones that appeared in the onset of the recent SARS outbreak [8], cannot be explained by using the previous paradigm. Consequently, they make very difficult the realistic estimation from initial data of the outbreak behavior [8, 9]. A solution to this issue could lie on the particular degree distribution of SFN which renders some features of social networks by bringing on a non-negligible number of highly connected nodes, called hubs or superspreaders. Therefore, from a public health point of view, studying the spreading of epidemics on SFN is all the more appropriate.

This issue, whose applications extend to new emergent diseases and bioterrorist threats, justify detailed studies of the incidence of the connectivity distribution at the initial stage of the epidemics. In particular, given the stochastic nature of epidemic processes, we focus our study on the characterization and the understanding of their variability. The variability plays an important role in the accuracy of models. Thus, it has to be quantified to assess the meaningfulness of simulations with respect to real outbreaks.

Concerning the epidemiological modeling, the simplest approach is to consider that infected individuals (I) may infect susceptible (S) ones with probability λ, which will then remain infected (SI model). This approach, in spite of its simplicity, allows to easily outline the initial growth of epidemic outbreaks.

Using a numerical approach, we analyzed the evolution of epidemics generated by different sets of initial parameters. Hence, we compared epidemic variability on a SFN (Barabási-Albert (BA) [10]) to an homogeneous network model (Erdös-Renyi (ER) [11]) in order to highlight the singularities due to the connectivity distribution.

II. INFECTION TIME FLUCTUATIONS

We consider that a good picture of the predictability of epidemic path is given by the variation of t_{inf} on each node. This information tells us how systematically nodes will be infected at regular moments during the outbreak. In this study, we characterize it by computing the t_{inf} coefficient of variation, $CV(t_{inf}) = \frac{\sqrt{\langle (t_{inf} - \langle t_{inf} \rangle)^2 \rangle}}{\langle t_{inf} \rangle}$, on a set of a thousand of outbreaks simulated on the same network.

In Fig. 1, we show nodes $\langle t_{inf} \rangle$ (left panel) and $CV(t_{inf})$ (right panel) for an ER and a BA network. In those plots, symbols aligned vertically represent nodes with a given degree k. By comparing Fig. 1 panels, we clearly notice that while the averaged t_{inf} on BA is lower than on ER network, its corresponding $CV(t_{inf})$ is larger. From a practical point of view, it means that, on one hand, BA nodes are infected more quickly (smaller t_{inf} values), but on the other hand, the moment t_{inf} will vary more from an epidemic to another (greater $CV(t_{inf})$), and consequently will be less predictable.

Figure 1 also reveals the tendency of $CV(t_{inf})$ to increase with the nodes degree, and the high values reached by high degree nodes on BA network.

On BA networks, low degree nodes are large majority. Their wide range of $CV(t_{inf})$ values tells us that the degree may not be the most relevant discriminant and that values computed over the same degree (lighter symbols) are not representative when dealing with small degree nodes. Consequently, variations of t_{inf} can be less easily predicted for low degree nodes. On the contrary, higher degrees nodes have values following a more clearly drawn slope, giving $CV(t_{inf})$ as a function of their degree more meaning.

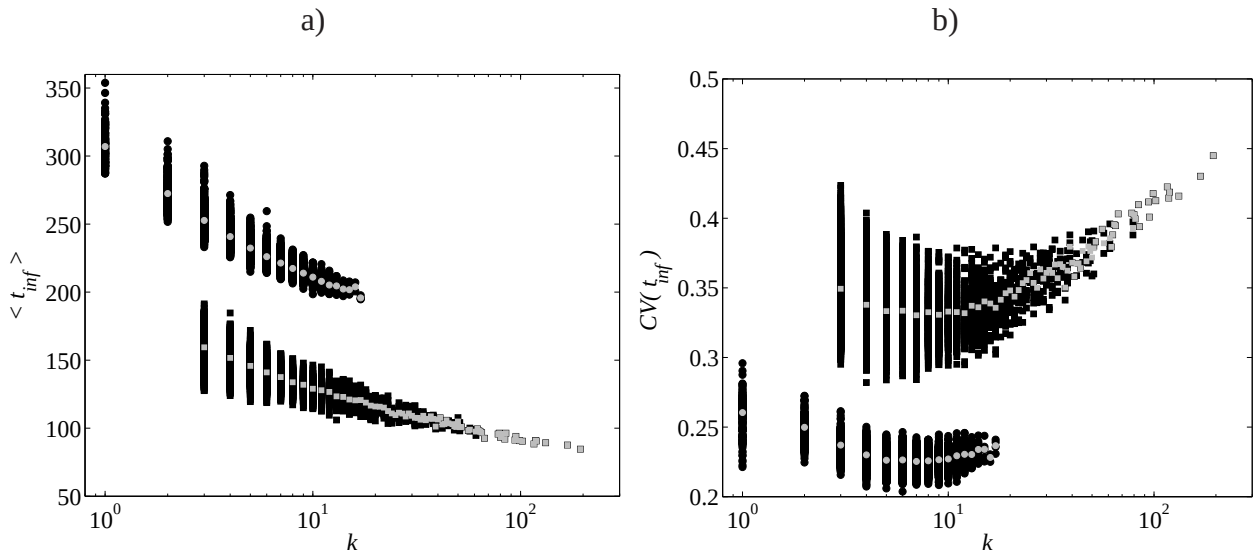

Figure 1: Infection time of network nodes as a function of their degree. **(a)** Averaged infection time: Each black symbol represents t_{inf} for a single node averaged over 10^3 outbreaks. Gray symbols show t_{inf} averaged over nodes with the same degree. **(b)** Infection time coefficient of variation: each black symbol stands for $CV(t_{inf})$ computed over 10^3 outbreaks. Gray symbols show $CV(t_{inf})$ computed over nodes with the same degree. For both panels, ■ are values on BA network, and • are values on ER network; results are computed on a single network ($N = 10^4$, $\langle k \rangle = 6$); initially infected node degree $k_0 = 6$; $\lambda = 0.01$.

III. CONCLUSIONS

In this short paper, we address the concern about the reliability and the efficiency of detection sites. A good site candidate has to be on the outbreak path as soon and as surely as possible. Here, we point out that, despite their low delay before infection (t_{inf}), superspreading nodes exhibit high variations of their moment of infection. In other words, we may not be able to predict an accurate and reliable time of infection for them. As a consequence, high degree nodes should be used with caution in the set-up of an early epidemic detection system.

We also draw attention to the differences between ER and BA networks concerning variability. As depicted on Fig. 1b, the homogeneous nature of ER networks seems to prevent singularities in the spreading, and thus tend to lower the $CV(t_{inf})$ of their nodes. Infection velocities, which can be deduced from Fig. 1a, also differ and are in concordance with previous studies [12]. These spreading disparities confirm that outbreaks on the two topologies behave distinctly in many points and ignoring their differences may cause problems.

In particular, our results stress that the epidemic variability is amplified on scale-free BA network compared to homogeneous ER network. This phenomenon has a practical importance for the modeling of epidemic control strategies, especially during the beginning of the spreading process which is a highly unstable period due to high degree nodes. In particular, this study suggest that this high variability should be taken into account in planning and designing control and containment strategies.

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