Are epidemics on scale-free networks predictable?

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The scale-free topology has been widely described in many artificial and natural networks. It is characterized by a broad distribution of individual connectivities which can take values over several orders of magnitude.

In this work, we study how these large connectivity fluctuations affect the sensitivity to the noise of an epidemic scenario and consequently its predictability. We investigate this problem by inspecting thoroughly the time evolution of the number of infected at the beginning of the outbreak. We study numerically the variability of epidemic outbreaks spreading on scale-free networks and compare these results with simulations on random homogeneous networks, in which connectivities are normally distributed around their average value <k>. Propagation on random networks corresponds to the usual assumption of homogeneous mixing in classical epidemiology and provides a useful reference model to assess the effect of degree fluctuations.

We consider the usual compartmentalization of individuals into 3 categories: susceptible (S), infected (I) and immunized (R), and the time evolution of the system is described by the usual epidemiological schemes SI, SIS or SIR. In this work, we will focus on the temporal evolution of the prevalence (number of infected in the population). For a fixed set of the parameters of the model (infection scheme, infection rate, number of index cases), we simulate numerically a large number of outbreaks (up to 10^5), and we analyze different averages: average over a number e of outbreaks on the same network, average of a single outbreak on r different networks, and average of e outbreaks on r networks. We study quantities such as the coefficient of variation of the prevalence (CV_i), the time to peak of CV_i, and the distribution of the prevalence doubling time. In the light of the numerical results for these quantities, we discuss the influence of the different sources of noise on the variability of the epidemic scenario.

In particular, our results show that on scale-free networks, a peak of the CV_i is reached in the very first stages of the epidemic outbreaks, before its exponential growth. At this peak, the CV_i is of order 2-3 in contrast with a CV_i of order 1 (1.0 to 1.5) obtained for random homogeneous networks. These value are calculated when "dying" outbreaks are discarded (SIS and SIR models), and then may be larger if all outbreaks are considered. We also verified that the results are robust for large ranges of the models' parameters.

Our results suggest that in the situation of an emerging disease spreading on a scale-free network, the epidemic scenario is very sensitive to the topology of the network. Furthermore, these large fluctuations make the prediction of the disease time evolution -based solely on the topology of the network and on the first infected cases- almost impossible.