

Ph.D. course on Network Dynamics

Homework 4

To be discussed on Thursday, January 12, 2012

In class, we studied the SIR dynamics with transmission rate r and infection time τ . In particular, we analyzed the SIR dynamics on the branching process approximation of the configuration model with prescribed degree distribution $\{p_k\}$, starting with the root infected and every other node susceptible. We argued that, if τ is a deterministic constant, the problem reduces to studying an associated two-phases branching process with offspring distribution $\tilde{p}_k := \sum_{j \geq k} p_j \binom{j}{k} \gamma^k (1 - \gamma)^{j-k}$ in the first generation, and $\tilde{q}_k := \sum_{j \geq k} q_j \binom{j}{k} \gamma^k (1 - \gamma)^{j-k}$ in the following generations, where

$$\gamma = \gamma(\tau) := 1 - e^{-r\tau},$$

is the probability that a rate r exponential clock ticks before time τ , and we use the convention

$$q_k := \frac{p_{k+1}(k+1)}{\mu}, \quad \mu := \sum_k p_k k, \quad \nu := \frac{\mu_2}{\mu} - 1, \quad \mu_2 := \sum_k p_k k^2.$$

We proved that necessary and sufficient condition for spread of the epidemics in the original two-phases branching process (i.e., the one with offspring distributions $\{p_k\}$ in the first generation and $\{q_k\}$ in the following ones) is $\gamma\nu > 1$, or, equivalently, $\mu_2 > 2\mu$.

Exercise 1 (More on the SIR dynamics). *Let $\tilde{\Phi}_p(y) := \sum_k \tilde{p}_k y^k$, $\tilde{\Phi}_q(y) := \sum_k \tilde{q}_k y^k$ be the generating functions associated to the degree distributions of the associated two-phases branching process approximation of the SIR dynamics on the configuration model with degree distribution $\{p_k\}$.*

- (a) Prove that, if $\gamma\nu > 1$, then the probability of extinction of the associated two-phases branching process is $\bar{\rho} = \bar{\Phi}_p(\bar{\rho}_q)$, where $\bar{\rho}_q = \bar{\Phi}_q(\bar{\rho}_q)$ is the unique fixed point of $\bar{\Phi}_q(y)$ in the interval $[0, 1)$.

Exercise 2 (SIR dynamics with random infection time). *In class, we have focused on the SIR dynamics when the infection time τ (i.e., the time between the instant a node gets infected and when it recovers, during which the node infects its susceptible neighbors independently at rate r). In this exercise, we shall relax this assumption and let τ be an arbitrary nonnegative-valued random variable.*

- (a) Consider a graph with two nodes $\mathcal{V} = \{1, 2\}$ connected by one link; assume that, at time $t = 0$, one of the two nodes is infected, and the other one is susceptible, i.e., $X_1(0) = I$, $X_2(0) = S$. Prove that the final configuration will be $X_1(\infty) = R$, $X_2(\infty) = R$ with probability $\bar{\gamma} = 1 - \mathbb{E}[e^{-r\tau}]$, and $X_1(\infty) = R$, $X_2(\infty) = S$ with probability $1 - \bar{\gamma} = \mathbb{E}[e^{-r\tau}]$.
- (b) For $k \geq 1$, consider a star-shaped graph with node set $\mathcal{V} = \{0, 1, \dots, k\}$ where 0 is the center, i.e., such that the link set is $\mathcal{E} = \{\{0, j\} : 1 \leq j \leq k\}$. Prove that the probability that j of the k initially susceptible nodes are eventually infected is $\binom{k}{j} \mathbb{E}[e^{-(k-j)r\tau}(1 - e^{-r\tau})^j]$.

Now, consider the SIR process with random infection time τ on the two-phases branching process approximation of the configuration model with prescribed degree distribution $\{p_k\}$. Assume that the root node starts infected, while all the other nodes start susceptible. Prove that:

- (c) necessary and sufficient condition for spread of the epidemics to an infinite number of nodes is $\bar{\gamma}\nu > 1$;
- (d) if $\bar{\gamma}\nu > 1$, then the probability of extinction of the associated two-phases branching process is $\bar{\rho} = \bar{\Phi}_p(\bar{\rho}_q)$, where

$$\bar{\Phi}_p(y) := \mathbb{E}[\Phi_p(1 + (\bar{\gamma} - 1)(1 - e^{-r\tau}))],$$

and $\bar{\rho}_q = \bar{\Phi}_q(\bar{\rho}_q)$ is the unique fixed point of

$$\bar{\Phi}_q(y) := \mathbb{E}[\Phi_q(1 + (\bar{\gamma} - 1)(1 - e^{-r\tau}))]$$

in the interval $[0, 1)$.

Exercise 3 (Site percolation). *As we mentioned in class, the SIR model on a tree can be interpreted as a model for ‘bond’ percolation. Here, ‘bond’ stands for edge, or link, as a homage to the early literature on this subject, mainly focused on lattices rather than complex networks, see, e.g., [1]. In fact, in the SIR model on a tree, spread of a disease from the root corresponds to that node belonging to a large connected component of the graph obtained from the original one by removing each edge independently with probability $1 - \gamma$, and keeping it with probability γ .*

Similarly, one can consider ‘site’ (read as ‘node’, or ‘vertex’) percolation, whereby nodes are removed from the original graph: let us assume that every node $v \in \mathcal{V}$ is retained with some probability θ and removed (together with all its incident links) with probability $1 - \theta$, removal of the nodes being mutually independent events. Consider the configuration model with prescribed degree distribution $\{p_k\}$. According to the (two-phases) branching process approximation:

- (a) *what is the threshold θ^* , such that the largest connected component of the graph remaining upon removal of the nodes has size linear in n if and only if $\theta > \theta^*$?*
- (b) *provided that $\theta > \theta^*$ is above this threshold, what is the fraction of nodes in the connected component of the remaining graph?*
- (c) *argue that for power law degree distributions $p_k = K_\beta k^{-\beta}$ with $\beta \in (2, 3]$, a constant fraction of the nodes remains connected upon random removal of nodes provided that $\theta > 0$, i.e., the probability that a node is retained is strictly positive. (which has lead to the claim that “the Internet is robust to random damage”)*

References

- [1] G. Grimmett, *Percolation*, 2nd ed., Springer, 1999.