Spread of Epidemics and Rumours with Mobile Agents

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Summary. We propose a simple model of infection that enables to study the coincidence time of two random walkers on an arbitrary graph. By studying the coincidence time of a susceptible and an infected individual both moving in the graph we obtain estimates of the infection probability. The main result of this paper is to pinpoint the impact of the network topology on the infection probability.

1 Introduction

In much of the literature on mathematical epidemiology, the members of the population are assumed to occupy fixed locations and the probability of infection passing between a pair of them in a fixed time interval is taken to be some function of the distance between them. Mean-field models are a special case in which this function is a constant [5]. In this work, we consider a different model in which the agents are mobile and can only infect each other if they are in sufficiently close proximity. The model is motivated both by certain kinds of biological epidemics, whose transmission may be dominated by sites at which individuals gather in close proximity (e.g. workplaces or public transport for a disease like SARS, cattle markets for foot-and-mouth disease, etc.) and by malware spreading between wireless devices via Bluetooth connections, for example.

To our knowledge the first attempts to model virus spreading in mobile networks relies on the use of a non-rigorous mean-field approximations that incorporate the mobility patterns of users. In [10], the authors derive a threshold for the persistence of the epidemic by computing the average number of neighbours of a given node. Using a similar approach but with different mobility patterns, Nekovee et al. [11, 13] explore the evolution of the number of devices that are infected in terms of the contact rate between users. A related line of work studying the dissemination of information in opportunistic networks [3] focuses on the following analogous problem: Suppose that all

individuals are interested in a piece of information that is initially held by one user. The information is transmitted between users who happen to be close to each other. As in the case of static networks [12], one may be interested in the time it takes for the rumour to be known to all users. To this end we need to understand how information is transmitted between an informed and an ignorant user. Our work gives some insight on the impact of the network structure on the likelihood of successfully transmitting the rumour.

2 Models and Results

We consider a simple mathematical model of the spread of infection as follows. There is a finite, connected, undirected graph $G = (V, E)$ on which the individuals perform independent random walks: they stay at each vertex for an exponentially distributed time with unit mean, and then move to a neighbour of that vertex chosen uniformly at random. The infection can pass from an infected to a susceptible individual only if they are both at the same vertex, and the probability of its being passed over a time interval of length τ is $1 - \exp(-\beta\tau)$, where $\beta > 0$ is a parameter called the infection rate. We shall consider a single infected and a single susceptible individual and ask what the probability is that the susceptible individual becomes infected by time t. This probability has been studied in the case of a complete graph in [6]. Here, we extend their results to a much wider class of graphs.

It is simplistic to consider just a single infective and a single susceptible individual. Nevertheless, insights gained from this setting are relevant in the "sparse" case, where the number of both infected and susceptible individuals is small and inter-contact times are fairly large.

We now describe the model precisely. Let $X_t, Y_t \in V$ denote the positions of the susceptible and infected individuals respectively at time t. We model $(X_t, t \geq 0)$ and $(Y_t, t \geq 0)$ as independent continuous-time Markov chains (CTMCs) on the finite state space V, with the same transition rate. We define the coincidence time up to time t, denoted $\tau(t)$, as the total time up to t during which both walkers are at the same vertex, i.e.,

$$\tau(t) = \int_0^t \mathbf{1}_{(X_s = Y_s)} ds. \tag{1}$$

Let $\gamma(t)$ denote the probability that the initial susceptible becomes infected by time t. Then, conditional on $\tau(t)$, we have

$$\gamma(t) = 1 - \exp(-\beta\tau(t)), \tag{2}$$

where $\beta > 0$ is the infection rate. We are interested in estimating the coincidence time $\tau(t)$ and the infection probability $\gamma(t)$ for different families of graphs. Observe that the Markov chains X_t, Y_t have invariant distribution π given by

$$\pi_x = \frac{\text{degree}(x)}{\sum_{v \in V} \text{degree}(v)} \tag{3}$$

and that they are reversible, i.e., $\pi_x q_{xy} = \pi_y q_{yx}$ for all $x, y \in V$. We consider the case when these chains are started independently in the stationary distribution and provide estimates on the coincidence time and the infection probability, for arbitrary graphs. A direct computation yields

Theorem 1. *Suppose X_0 and Y_0 are chosen independently according to the invariant distribution π. Then, we have*

$$\mathbb{E}[\tau(t)] = \sum_{v \in V} \pi_v^2 t, \quad and \quad \mathbb{E}[\gamma(t)] \leq 1 - \exp\left(-\beta t \sum_{v \in V} \pi_v^2\right).$$

3 Examples of Graphs

We present models of networks of interest to which we are going to apply the result of Theorem 1.

3.1 Complete Graphs

Consider the complete graph on n nodes, namely the graph in which there is an edge between every pair of nodes, $\text{degree}(v) = n - 1$ and $\pi_v = 1/n$ for all $v \in V$, so we have by Theorem 1 that $\mathbb{E}[\tau(t)] = t/n$. This result should be intuitive by symmetry. Theorem 1 also gives us an upper bound on the infection probability, $\mathbb{E}[\gamma(t)] \leq 1 - \exp(-\beta t/n)$. Roughly speaking, this says that it takes time of order n/β for the susceptible individual to become infected; for $t \ll n/\beta$, the probability of being infected is vanishingly small.

3.2 Regular Graphs

A graph $G = (V, E)$ is said to be r-regular if $\text{degree}(v) = r$ for all $v \in V$, so that $\pi_v = 1/n$ for all $v \in V$ if G is for any $r \geq 2$. Hence, if G is connected, we have the same estimates for $\tau(t)$ and $\gamma(t)$ as for the complete graph, which is a special case corresponding to $r = n - 1$.

The next examples we consider will be families of random graphs widely used in practice to model networks.

3.3 Erdős-Rényi Random Graphs

The Erdős-Rényi graph $G(n, p)$ is defined as a random graph on n nodes, wherein each edge is present with probability p, independent of all other edges. Let p to be a function of n chosen so that $np > c \log n$ for some constant $c > 1$ ensuring that the graph is almost surely connected. In this model, the node degrees concentrate around the mean value np, and have exponentially decaying tails away from this value. Thus, while Erdős-Rényi graphs are not exactly regular, they exhibit considerable homogeneity in node degrees.

3.4 Power Law Random Graphs

In contrast to the above graph models, many real-world networks exhibit considerable heterogeneity in node degrees, and have empirical degree distributions whose tails decay polynomially; see, e.g., [1, 8]. This observation has led to the development of generative models for graphs with power-law tails [1, 2] as well as random-graph models possessing this property [4]. For definiteness, we work with the model proposed in [4], but we believe that similar results will hold for the other models as well.

In the model of [4], each node v is associated with a positive weight w_v, and edges are present independently with probabilities related to the weights by

$$\mathbb{P}((u,v) \in E) = \frac{w_u w_v}{W} \text{ where } W = \sum_{x \in V} w_x. \tag{4}$$

We assume that $W \geq w_{\max}^2$, so that the above defines a probability. It can be verified that $\mathbb{E}[\text{degree}(v)] = w_v$ and so this model is also referred to as the expected degree model. If the weights are chosen to have a power-law distribution, then so will the node degrees. The following 3-parameter model for the ordered weight sequence is proposed in [4], parametrised by the mean degree d, the maximum degree m, and the exponent $\gamma > 2$ of the weight distribution:

$$w_i = m\left(1 + \frac{i}{i_0}\right)^{-\frac{1}{\gamma - 1}}, \quad i = 0, 1, \ldots, n-1, \tag{5}$$

where

$$i_0 = n\left(\frac{d(\gamma - 2)}{m(\gamma - 1)}\right)^{\gamma - 1}. \tag{6}$$

Note that $W = \sum_{i=0}^{n-1} w_i \sim nd$, for n large.

We consider a sequence of such graphs indexed by n. The maximum expected degree m and the average expected degree d may, and indeed typically will, depend on n. In models of real networks, we can typically expect d to remain bounded or to grow slowly with n, say logarithmically, while m grows more quickly, say as some fractional power of n. In this paper, we only assume the following:

$$d \geq \delta > 0, \quad d = o(m), \quad m \leq \sqrt{nd}, \quad \frac{m}{d} = o\left(n^{\frac{1}{\gamma - 1}}\right). \tag{7}$$

Here, δ is a constant that does not depend on n. In other words, the average expected degree is uniformly bounded away from zero. The third assumption simply restates the requirement that $w_0^2 \leq W$, so that (4) defines valid probabilities. The last assumption ensures that i_0, defined in (6), tends to infinity. We now describe our results about these models.

Theorem 2. *Consider a sequence of graphs $G = (V, E)$ indexed by $n = |V|$. On each graph, consider two independent random walks with initial condition*

X_0, Y_0 *chosen independently from the invariant distribution π for the random walk on that graph.*

We have $\mathbb{E}[\tau(t)] = t/n$ for regular graphs, including the complete graph, on n nodes.

For Erdős-Rényi random graphs $G(n,p)$ conditioned to be connected, and having $np \geq c \log n$ for some $c > 1$, we have $\mathbb{E}[\tau(t)] \sim t/n$, as n tends to infinity.

Finally, consider a sequence of power law random graphs defined via (4) and (5), and satisfying the assumptions in (7). Then, we have the following:

$$\frac{n\mathbb{E}[\tau(t)]}{t} \sim \begin{cases} c_1, & \text{if } \gamma > 3, \\ c_2(\log m), & \text{if } \gamma = 3, \\ c_3(m.d)^{3-\gamma}, & \text{if } 2 < \gamma < 3, \end{cases}$$

where $c_1, c_2, c_3 > 0$ are constants that do not depend on n, m or d.

The proof is rather long involving the computation of moments of the degree distributions and using concentration results. For lack of space it is omitted (see [7]).

4 Conclusion and Further Work

In this work we have presented a simple model for the spread of epidemics where individuals are mobile. In this framework we were interested in the setting where there are two individuals one infected and one healthy both performing random walks on the network. Our preliminary investigation highlights the effect of the topology on the spread of an epidemic, motivated by networking phenomena such as worms and viruses, failures, and dissemination of information. Under this natural model, we provided an explicit relationship between the structure over which the walks are performed and the coincidence time of the two walkers. To this end we analysed both homogeneous (regular, complete and Erdös-Rényi graphs) and heterogeneous (power-law graphs) networks. We pinpointed the existence of a phase transition for the coincidence time in the case of power-law networks depending on the parameter of the power-law degree distribution. We also derived bounds on the probability of infection.

As a final remark, we propose some several interesting directions to pursue the work presented here. In our present model individuals are supposed to start their walks in stationary regime. This can be relaxed since the networks we study are expanders and thus random walks on such networks have nice mixing properties as illustrated in [9] through the computation of the isoperimetric constant of the underlying graphs. We also anticipate that similar results can be derived when considering k walkers as long as k is small with respect to n the number of sites in the network.

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