Dynamics of Epidemics

M Marder
Center for Nonlinear Dynamics and Department of Physics
The University of Texas at Austin, 78712, USA

This article examines how diseases on random networks spread in time. The disease is described by a probability distribution function for the number of infected and recovered individuals, and the probability distribution is described by a generating function. The time development of the disease is obtained by iterating the generating function. In cases where the disease can expand to an epidemic, the probability distribution function is the sum of two parts; one which is static at long times, and another whose mean grows exponentially. The time development of the mean number of infected individuals is obtained analytically. When epidemics occur, the probability distributions are very broad, and the uncertainty in the number of infected individuals at any given time is typically larger than the mean number of infected individuals.

Introduction A series of papers by Strogatz, Watts [1], Vespignani [2, 3], Meyers [4, 5, 6], Newman [7, 8, 9, 10, 11], Stanley [12], Barabási [13] and collaborators applies methods from graph theory and percolation theory to the spread of disease on random networks. These papers mainly study the final state of a population once the disease has run its course, with all individuals susceptible but uninfected, or recovered. Here I show how to apply the same analytical techniques to dynamics of the epidemic and find how the number of infected individuals varies in time.

A starting point for this study was to clear up a technical point arising when an epidemic is possible, but not certain. Newman, Strogatz and Watts [14] find a probability distribution function $P_k$ that $k$ individuals have been infected, and they show that $u \equiv \sum_k P_k < 1$. They determine $u$ from a self-consistent equation, and interpret this distribution function as describing the probability of a finite outbreak that does not grow to system size. The remaining probability is contained in an outbreak that fills the whole system. This interpretation is puzzling. Since $k$ can have any size, why does $P_k$ describe only finite outbreaks? How does the self-consistent equations determining $u$ figure out how to find only these finite outbreaks, and discard the larger ones? The authors assert that the system-size outbreaks would contain loops that invalidate the formalism they are employing, but how does the formalism know this? These questions are resolved when one examines the probability distribution after $n$ times steps, $P_k^{(n)}$. One finds that the probability distribution is the sum of two pieces. The first piece $Q_k^{(n)}$ converges to a time-independent function $Q_k$ in the long-time limit, with $\sum_k Q_k < 1$. The second piece $R_k^{(n)}$ never stops evolving. Its mean and width grow exponentially. So long as the mean of $R_k^{(n)}$ is much smaller than the total system size, it can be described by standard generating function techniques, and this description is not invalidated by the presence of loops. Thus, the generating function formalism has been finding $Q_k$ and the reason this function emerges is that $P_k^{(n)}$ converges to $Q_k$ pointwise, although at any given time step $n$, a finite fraction of $P_k^{(n)}$ is contained in a very broad tail of the distribution that has formed out in front of $Q_k$. Techniques essentially identical to those used previously to describe $Q_k$ can be used to analyze $R_k^{(n)}$. In particular, one can find closed-form expressions for the mean number of people infected at time $n$. When an epidemic is possible, both the mean and width of $R_k^{(n)}$ grow exponentially in time. In general, one’s uncertainty about precisely how many people will be infected in the future grows as fast as or faster than the number of diseased individuals.

Dynamical Equations Consider a random network in which the probability distribution of nodes with $k$ edges is $P_k$. Following Newman, Strogatz, and Watts [14], the generating function for the distribution of nodes is

$$G_0(x) \equiv \sum_{k=0}^{\infty} P_k x^k. \quad (1)$$

Consider choosing a random edge in the system. The probability that the node reached by this edge will have $k$ new edges in addition to the one chosen to start with is generated by

$$G_1(x) \equiv \frac{G_0'(x)}{G_0'(1)}. \quad (2)$$

Consider conventional Susceptible-Infected-Recovered dynamics on this network [9]. At each time step, uninfected nodes connected by an edge to infected nodes become infected in turn. Let $P_k^{(n)}$ give the probability that a grand total of $k$ individuals has been infected after $n$ time steps, and let the generating function for $P_k^{(n)}$ be

$$H^{(n)}(x) \equiv \sum_{k=0}^{\infty} P_k^{(n)} x^k. \quad (3)$$

Imagine starting with a single infected individual. At step 0, one has $H^{(0)} = x$. At the next time step, the generating function for the total number of individuals infected is

$$H^{(1)}(x) = xG_0(x), \quad (4)$$

since $G_0(x)$ gives the probability that a given node has 0, 1, 2, ... edges, and one multiplies by $x$ because one began with one infected individual. Each of the edges departing the first

*Electronic address: marder@mail.utexas.edu
one reaches some other node. The probability it will have $k$ additional edges leaving it is given by $G_1(x)$. Using the powers property in Section IIA of Ref. 9, one has

$$H^{(2)}(x) = xG_0(xG_1(x)).$$  

(5)

Continuing in this fashion, one has

$$H^{(n)}(x) = H^{(n-1)}(xG_1(x)).$$  

(6)

This expression is inconvenient form for numerical work, so define instead

$$F^{(0)}(x) = 1$$  

(7a)

$$F^{(n)}(x) = G_1(xF^{(n-1)}(x))$$  

(7b)

$$H^{(n)}(x) = xG_0(xF^{(n-1)}(x)).$$  

(7c)

To extract the probability distribution function from a generating function $H(z)$, note that from Cauchy’s theorem

$$P_k = \frac{1}{2\pi i} \int_{z=1} dz H(z) = \int_0^1 d\theta e^{-2\pi ik\theta} H(e^{2\pi i\theta}).$$  

(8)

Suppose now that $H$ has been evaluated around the unit circle at $M$ points, with $\theta_l = l/M$, $l \in [0, M-1]$, and let

$$H_l = H(e^{2\pi i\theta_l}).$$  

(9)

Then one has

$$P_k = \frac{1}{M} \sum_{l=0}^{M-1} e^{-2\pi ikl/M} H_l = \frac{1}{M} \text{DFT}(H; -1)[k]$$  

(10)

where the last expression means that one takes the $k$’th element of the inverse discrete Fast Fourier Transform. Using Eq. (7c) and employing Eq. (10) to obtain probabilities $P_k$, one easily obtains hundreds of iterates of the map, for hundreds of thousands of values of $k$.

**Static and growing distributions** Some results of solving Eqs. (7c) appear in Figure 1. Figure 1(A) shows distributions resulting from the polynomial $G_0(x) = 7x + 2x^2 + .05x^3 + .04x^4 + .01x^5$. The threshold for an epidemic is determined by $z_2 > z_1$, where $z_1 = G_0(1)$ is the average number of neighbors of each node, and $z_2 = G_1(1)z_1$ is the average number of second neighbors. In the present case, $z_1 = 1.46$ and $z_2 = 1.38$, so the infection is contained, and the probability distribution converges to a definite limit enclosing unit probability. The upper curve shows the cumulative sum $S_k = \sum_{k'=1}^{k} P^{(100)}_{k'}$. The mean number of people infected after 100 iterations is 27, but the distribution is broad; for example, there is a 1% chance that more than 480 people will be infected. Figure 1(B) shows results from the polynomial $G_0(x) = 7x + .1x^2 + .05x^3 + .01x^4 + .14x^5$, which gives $z_1 = 1.79$, $z_2 = 3.42$. Since $z_2 > z_1$, an epidemic is possible. One can compute the probability of an epidemic spiraling out of control following 3; also see Eq. (12). There is a root of $G_1(u) = u$ at $u = .492$ and $G_0(u) = .3790$. This computation predicts a 37.9% chance that the disease will run its course without becoming an epidemic. The upper curve in Figure 1 (B) shows the cumulative sum $S_k = \sum_{k'=1}^{k} P^{(11)}_{k'}$ and there is a broad plateau where this sum has reached .38. The mean number of infected individuals after 11 iterations is 4650 but there is a 1% chance more than 26000 people will be infected. Figure 1 (C) uses the probability distribution $p_0 = 0$, $pk \propto k^{-\alpha}e^{-k/\kappa}$ with $\alpha = 2$ and $\kappa = 20$. Now $z_1 = 1.8$, $z_2 = 5.3$, and the epidemic grows even more rapidly. There is a 41% chance that the epidemic will be contained. The mean number of infected individuals after 7 steps is 5500, but there is a 1% chance that more than 50,000 will be infected.

Thus when there is the possibility of an epidemic, the probability distribution does indeed split into two components. The first component $Q_k$ is static in the long-time limit and describes the probability that spread of disease terminates with a number of infected individuals much smaller than the total population. The second component $R^{(n)}_k$ continues to evolve forever. From a formal point of view, the definition of $Q_k$ is

$$Q_k = \lim_{n \to \infty} \int d\theta e^{-2\pi ik\theta} H^{(n)}(e^{2\pi i\theta}).$$  

(11)

For any fixed $k$, this limit converges. Then $R^{(n)}_k$ can be
fixed as $R_k^{(n)} = P_k^{(n)} - Q_k$. One can similarly decompose the probability distribution resulting from $F^{(n)}$ into static and evolving components. To see now how the probability of not participating in the epidemic emerges from self-consistent equations, define $F^{\infty}(x) = \lim_{n \to \infty} F^{(n)}(x)$. This limit exists for any $x < 1$, since large powers of $x < 1$ in the power series for $F^{(n)}$ suppress the parts of $F^{(n)}$ that are continuing to evolve. Return to (7b), and write

\[
\lim_{x \to 1} \lim_{n \to \infty} F^{(n)}(x) - G_1(xF^{(n-1)}) = 0
\]

\[
\Rightarrow \lim_{x \to 1} F^{\infty}(x) - G_1(xF^{\infty}) = 0
\]

\[
\Rightarrow u = G_1(u) \quad \text{with} \quad u = \lim_{x \to 1} F^{\infty}(x). \quad (12)
\]

Finally $G_0(u) = \lim_{x \to 1} \lim_{n \to \infty} H^{(n)}(x)$ gives the probability that the disease does not spiral into an epidemic.

Figure 2 shows an explicit decomposition of the data in Figure 1(B) into components $Q$ and $R$. The task is carried out by taking the final curve in Figure 1(B) and noticing that it has converged to a static value up to around $k = 32$ (the precise cut point does not matter much) and is continuing to evolve for larger $k$. For $k > 32$, $Q_k$ is estimated by a power-law fit. The area under $Q_k$ found this way is .3791 which compares well with the predicted value of .3790.

**Size of infected cluster** One can work out analytically the average size of the infected/covered cluster as a function of time. Note that $F^{(n)}(1) = 1$ and let

\[
M_n = \frac{d}{dx} F^{(n)}(x) \big|_{x=1}.
\]

Using $M_0 = 0$, one can solve this iterated map exactly as a power series, which has the compact final expression

\[
M_n = \frac{z_2}{z_1} \sum_{l=0}^{n-1} \left( \frac{z_2}{z_1} \right)^l = \frac{z_2}{z_1} \left[ 1 - (z_2/z_1)^n \right]. \quad (14)
\]

Then the average number of individuals in the cluster is

\[
\langle k \rangle_n = \frac{d}{dx} H^{(n)}(x) \big|_{x=1} = 1 + z_1 \left[ 1 + \frac{z_2}{z_1} \left( 1 - (z_2/z_1)^n \right) \right]. \quad (15)
\]

If $z_2 < z_1$, one obtains the expected result \[8, 14, 15\] for large $n$ that

\[
\langle k \rangle_n = 1 + z_1 \left( 1 + \frac{z_2}{z_1 - z_2} \right) = 1 + \frac{z_1^2}{z_1 - z_2}. \quad (16)
\]

In the opposite case, $z_2 > z_1$, Eq. (14) becomes $M_n \approx (z_2/z_1)^n/(1 - z_2/z_1)$ and for large $n$ the average size of the infected population is

\[
\langle k \rangle_n \approx \frac{z_1(z_2/z_1)^n}{z_2/z_1 - 1}. \quad (17)
\]

The width of the distribution is proportional to the mean. The dominant contribution to $\langle k^2 \rangle_n$ at large $n$ is

\[
\sqrt{\langle k^2 \rangle_n - \langle k \rangle_n^2} \approx \frac{z_2(z_2/z_1)^n}{z_2/z_1 - 1} \sqrt{\frac{z_2 - z_1^2 + z_2G''_1(1)}{(z_2/z_1 - 1)}}. \quad (18)
\]

*When infection is not certain across an edge* Newman\[8, 14, 15\] describes the case where infection is not certain across an edge connecting two nodes, but occurs with probability $T$. In this case, the probability of infecting neighbors starting with a randomly chosen node is generated by

\[
G_0(1 + T(x - 1)), \quad (19)
\]

the probability of infecting neighbors starting with a randomly chosen edge, excluding the incoming edge is generated by

\[
G_1(1 + T(x - 1)), \quad (20)
\]

and employing these two generating functions, the evolution equations\[8\] are unchanged, and \[15\] for the average degree of infection generalizes to

\[
\langle k \rangle_{n+1} = \frac{d}{dx} H^{(n+1)}(x) \big|_{x=1} = 1 + \frac{z_2^2 T - z_2T(z_2/z_1)^n}{z_1 - z_2 T}. \quad (21)
\]

Essentially $z_2$ is replaced by $Tz_2$.

**Individuals added at each time step** Another interesting quantity to track is the probability of adding individuals of varying degree number $k$ at each time step. This can be done by adding a subscript to the variable $x$ that tracks the time step at which an individual has entered the cluster. Doing so one has

\[
H^{(0)}(x_0) = x_0.
\]
As shown in Figure 3, this scaling form does appear to describe the growing part of the probability distribution \( R_k \) to adopt a scaling form at long times. To capture the growing part of the distribution, one computes

\[
R_k^{(n)} \approx \frac{1}{\langle k \rangle_n} R(\kappa) \quad \text{where} \quad \kappa = k/\langle k \rangle_n.
\]  

As shown in Figure 3, this scaling form does appear to describe \( R \) after sufficiently many iterations. On a log scale the tail of \( R \) for small \( \kappa = k/\langle k \rangle_n \) converges pointwise, but on a linear scale convergence is uniform.

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