Chapter 4

Epidemics

4.1 SIR epidemics with fixed infection times

In the SIR model, individuals are in one of three states: $S$ = susceptible, $I$ = infected, $R$ = removed (cannot be infected). Often this epidemic takes place in a homogeneously mixing population. However, here, we have a graph that gives the social structure of the population; vertices represent individuals and edges a connection. $S-I$ edges become $I-I$ at rate $\lambda$, i.e., after a time $T$ with an exponential($\lambda$) distribution: $P(T > t) = e^{-\lambda t}$. The two versions of the model we consider differ in the length of time individuals remain infected. In the first, infections always last for time 1. In the second, infection times are nonconstant with an exponential(1) distribution being an important special case.

In this section we consider the dynamics in which each infection lasts for exactly one unit of time. This case is simple because each edge will be $S-I$ (or $I-S$) only once. When that happens the infection will be transferred to the other end with probability

$$\tau^f = P(T \leq 1) = 1 - e^{-\lambda}$$

(4.1.1)

and the transfers for different edges are independent. Here, superscript ‘$f$’ is for “fixed time.” Due to the last observation, we can delete edges with probability $e^{-\lambda}$ and the connected components of the resulting graph will give the epidemic sizes when one member of the cluster is infected. We can have a large epidemic if and only if the reduced graph has a giant component. In the physics literature this idea is attributed to Grassberger (1983), in math to Barbour and Mollison (1990), and in complex networks to Newman (2002).

Results for percolation on random graphs generated by the configuration model were given in Section 2.7. To keep the treatment here self-contained we will repeat a few of those results.

**Theorem 4.1.1.** If the original graph is Erdős-Renyi with mean degree $\mu$, then the reduced graph is Erdős-Renyi with mean degree $\mu \tau^f$. So, a large epidemic occurs with positive probability if $\mu \tau^f > 1$. If $z_0$ is the fixed point smaller than 1 of the generating function

$$G(z) = \exp(-\mu \tau^f (1 - z)),$$

(4.1.2)
then $1 - z_0$ gives both the limiting probability an infected individual will start a large epidemic, and the fraction of individuals who will become infected when a large epidemic occurs.

The formula for the probability of a large epidemic comes from the fact that, in its early stages, the growth of the epidemic is well approximated by a branching process. See Section 1.2. The probability of a large epidemic is the probability the branching process does not die out, which is $1 - z_0$. Theorem 1.3.2 shows that all starting points which lead to a large cluster are in the giant component, so $1 - z_0$ is also the fraction of individuals who will become infected when a large epidemic occurs.

### 4.2 SIR epidemics with general infection times

We now turn to the case in which the duration of the infection, $\sigma$, is random. By conditioning on the value of $\sigma$ we see that the probability an infected site fails to infect a given susceptible neighbor is

$$P(\sigma < T) = \int_0^\infty dt f_\sigma(t) e^{-\lambda t} = E e^{-\lambda \sigma}$$

This implies that the probability that the infection is transmitted in the model with random duration is

$$\tau^e = E(1 - e^{-\lambda \sigma})$$

where the superscript $e$ is a holdover from the time we only consider $\sigma$ with an exponential distribution. Using the reasoning for (4.2.1), the probability two neighbors both escape infection is

$$\int_0^\infty dt f_\sigma(t) e^{-2\lambda t} = E(e^{-2\lambda \sigma}) > (E e^{-\lambda \sigma})^2$$

where in the last step we have used $E(X^2) > (EX)^2$ for $X = e^{-\lambda \sigma}$.

To connect with percolation we turn each edge $\{x, y\}$ in the graph into two oriented edges $(x, y)$ and $(y, x)$. Let $\sigma_x$ be the duration of the infection at $x$ and let $T(x,y)$ be independent infection times that are exponential with rate $\lambda$. To define a graph we say that the oriented edge $(x, y)$ is present if $\sigma_x > T(x,y)$.

The presence of the edges out of $x$ are positively correlated events since they are more likely to be present if $\sigma_x$ is large. However, edges out of different vertices $x$ and $x'$ are independent.

Newman (2002) thought that the edge events were independent (see the discussion before his formula (13)). As a consequence his formula for the size of the giant component is not correct. However, his epidemic threshold is, since that requires only that the mean number of neighbors infected is $> 1$. Suppose for the moment, that we have a graph generated by the configuration model in which $p_k$ is the degree distribution, $q_k = (k + 1)p_{k+1}\mu$ is the size-biased distribution, and $\nu$ is the mean of the size biased distribution. Then the condition for a giant component is

$$\nu \tau^e > 1$$
Our next goal is to compute the probability of a large epidemic and the fraction of individuals that will be infected if one occurs. When the duration of the infection is constant these quantities are the same (see Theorem 4.1.1), but not if the duration is random. To simplify computations, we will consider an 

**Erdős-Rényi graph with mean degree** \( \mu \) rather than a graph generated by the configuration model, so that we have only have one degree distribution.

\[
p_k = e^{-\mu \mu^k / k!}
\]

with generating function \( G(z) = \exp(-\mu(1-z)) \).

If the epidemic starts with one infected individual then the generating function of the number of neighbors that will become infected is

\[
\hat{G}(z) = \int_0^\infty dt \sigma(t) \sum_{j=0}^\infty z^j \sum_{k=j}^\infty p_k \binom{k}{j} (1 - e^{-\lambda t})^j e^{-(k-j)\lambda t}
\]

Interchanging the order of summation, and using the binomial theorem, we have

\[
\hat{G}(z) = \int_0^\infty dt \sigma(t) \sum_{k=0}^\infty p_k (e^{-\lambda t} + z(1 - e^{-\lambda t}))^k
\]

\[
= \int_0^\infty dt \sigma(t) G(e^{-\lambda t} + z(1 - e^{-\lambda t}))
\]

\[
= \int_0^\infty dt \sigma(t) G(1 - 1 + e^{-\lambda t} + z(1 - e^{-\lambda t}))
\]

\[
= EG(1 + (z - 1)[1 - e^{-\lambda t}])
\]

**Theorem 4.2.1.** Suppose \( \mu \tau^e > 1 \). If \( z_0 \) is the fixed point of \( \hat{G}(z) = z \), less than 1 then \( 1 - z_0 \) gives the probability of a large epidemic.

To compute the final size we will use the random graph defined in (4.2.3). Following the oriented edges out from \( x \), the set of all sites that can be reached \( \mathcal{C}_x \) is the **outward cluster**. The size of the growing outward cluster is (when it is small) well approximated by a branching process in which the offspring distribution has generating function \( \hat{G}(z) \) which leads to the result in Theorem 4.2.1.

If we want to know whether \( y \) will be infected in the epidemic, we start at \( y \) and cross edges in the direction opposite their orientation. The set of points that can be reached (the **inward cluster**), \( \mathcal{D}_y \), is the set of starting points that will lead to an infection of \( y \). Since the sites that come in to a site \( y \) come from different sites, their states are independent and are occupied with probability \( \tau^e \). Since each vertex is connected to a Poisson(\( \mu \)) number of incoming edges at a vertex is Poisson(\( \mu \tau^e \)) and its generating Function is

\[
\bar{G}(z) = \exp(-\mu \tau^e(1 - z))
\]
**Theorem 4.2.2.** Suppose $\mu \tau^e > 1$. If $z_1$ is the fixed point of $\bar{G}(z) = z$, less than 1 then $1 - z_1$ gives the fraction of sites infected in a large epidemic.

The generation function of the Poisson $G$ is strictly convex, and $E[1 - e^{-\lambda S}] = \tau$ so

$$\bar{G}(z) = EG(1 + (z - 1)[1 - e^{-\lambda S}])$$

$$> G(1 + (z - 1)E[1 - e^{-\lambda S}]) = G(1 + (z - 1)\tau^e)$$

by (4.2.2). If we let $y = 1 + (z - 1)\tau^e$ then

$$G(1 + (z - 1)\tau^e) = \exp(-\mu(y - 1)) = \exp(-\mu(z - 1)\tau) = \bar{G}(z)$$

Thus in the case of exponential infection times, the final size of a large epidemic is not the same as the probability of a large epidemic. Since $\bar{G}(z) > G(z)$ the first point $z_0 > z_1$.

**Concrete Example.** To investigate the differences between $\hat{G}$ and $\bar{G}$, we will consider a concrete example. It is not easy to compute $\bar{G}(z)$ so, we will take a rather extreme infection time distribution $P(\tau = \infty) = p$ and $P(\tau = 0) = 1 - p$. In this case an infected node either infects no one with probability $1 - p$ or all of its neighbors with probability $1 - p$. so

$$\bar{G}(z) = (1 - p) + pG(z) = 1 - p + p\exp(-\mu(1 - z))$$

while $\check{G}(z) = \exp(-\mu p(1 - z))$. Intuitively this is like the difference between site percolation where an open site can reach all of its neighbors, and bond percolation where we flip independent coins for different edges. Note that $\bar{G}'(1) = \mu p = \check{G}'(1)$.

![Figure 4.1: $G(z)$ (solid line) versus $\bar{G}(z)$ (dashed line) for the concrete example with $\mu = 3.$](image)
This system is often referred to as the SIR in a homogeneously mixing population, referring to the fact that each individual interacts equally with all of the others. We will now make a small change to notation we have used. Let $\beta$ be the total rate at which an individual infects its neighbors so that $\lambda = \beta/N$ is the infection rate per edge (and we forget about the fact that there are only $N-1$ edges. We assume that an infected stays infected for an exponentially distributed time $T$ with mean $1/\gamma$, i.e., $P(T > t) = e^{-\gamma t}$. This is convenient so that when dealing with applications the process is on its natural time scale. Continuing to write $S =$ susceptible, $I =$infected, $R =$removed, the following differential equations hold when the population size is large:

\[
\begin{align*}
\frac{dS}{dt} &= -\beta \frac{SI}{N} \\
\frac{dI}{dt} &= \beta \frac{SI}{N} - \gamma I \\
\frac{dR}{dt} &= \gamma I 
\end{align*}
\]  

(4.3.1)

In the SIR epidemic an infected person creates new infecteds at rate $\beta$ and becomes healthy at rate $\gamma$. A basic fact about the exponential distribution is that if $S = \text{exponential}(\beta)$ and $T = \text{exponential}(\gamma)$ then

\[
P(S < T) = \frac{\beta}{\beta+\gamma} 
\]  

(4.3.2)

This implies that the number of individuals $\kappa$ infected by one infected in an otherwise susceptible population has distribution.

\[
P(\kappa = k) = \left(\frac{\beta}{\beta+\gamma}\right)^k \frac{\gamma}{\beta+\gamma} \quad \text{for} \ k = 0, 1, 2, \ldots 
\]  

(4.3.3)

This is the shifted geometric distribution with parameter $p = \gamma/(\beta+\gamma)$, which gives the distribution number of failures before the first success in a sequence of independent trials. The ordinary geometric distribution, which gives the number of trials to get the first success has mean $1/p$, so the shifted one has mean

\[
\frac{1}{p} - 1 = \frac{\beta + \gamma}{\gamma} - 1 = \frac{\beta}{\gamma}
\]

$\beta/\gamma$ is called the basic reproduction number and is usually denoted by $R$. It is the number of secondary infections caused by one infection in the initial phase of the epidemic when only a small fraction of the individuals are removed.
4.3.1. Asymptotic behavior

Suppose \( \beta > \gamma \) so that \( R > 1 \). Letting \( s = S/N, i = i/N, \) and \( r = R/N, \) the equations in (4.3.1) become

\[
\begin{align*}
\frac{ds}{dt} &= -\beta si \\
\frac{di}{dt} &= \beta si - \gamma i \\
\frac{dr}{dt} &= \gamma i
\end{align*}
\]  \hspace{1cm} (4.3.4) \hspace{1cm} \text{ode}

We cannot solve these equations explicitly, but we can extract some useful information about the limiting behavior. Using the first two equations

\[
\frac{di}{ds} = \frac{\beta si - \gamma i}{-\beta si} = -1 + \frac{\gamma}{\beta s}
\]

Solving we have

\[
i = -s + \frac{\gamma}{\beta} \ln s + C \quad \text{where} \quad C = i(0) + s(0) - (\gamma/\beta) \ln(s(0)). \hspace{1cm} (4.3.5) \hspace{1cm} \text{solode}
\]

For initial conditions, we choose \( i(0) = \epsilon, \, s(0) = 1 - \epsilon \). We have set \( I(0) = \epsilon N \) since the ODE is not accurate when the number of infecteds is small. For this initial condition

\[
C = 1 - (\gamma/\beta) \ln(1 - \epsilon),
\]

so using (4.3.5) we have

\[
i(t) + s(t) = 1 + \frac{\gamma}{\beta} \ln(s(t)/(1 - \epsilon)).
\]

As \( t \to \infty, i(t) \to 0, \, s(t) \to s(\infty). \) The limit of \( s(t) \) exists since \( s(t) \) is decreasing. If we let \( \epsilon \to 0 \) then

\[
s(\infty) = 1 + \frac{\gamma}{\beta} \ln(s(\infty)).
\]

Rearranging we have

\[
s(\infty) = \exp(- (\beta/\gamma) [1 - s(\infty)]). \hspace{1cm} (4.3.6) \hspace{1cm} \text{fpeq}
\]

4.3.2. Extinction probability

If we think of the people that an individual infects as their children then in the initial stages of the epidemic we have a branching process. As noted in (4.3.3) the probability of \( k \) children is

\[
p_k = \left( \frac{\beta}{\beta + \gamma} \right)^k \frac{\gamma}{\beta + \gamma}
\]
The generating function of this distribution is

\[ \phi(x) = \sum_{k=0}^{\infty} \left( \frac{\beta x}{\beta + \gamma} \right)^k \frac{\gamma}{\beta + \gamma} = \frac{\gamma}{\beta + \gamma} \left( 1 - \frac{\beta x}{\beta + \gamma} \right)^{-1} = \frac{\gamma}{\gamma + \beta (1-x)} \]

\( \phi(x) = x \) is a quadratic equation:

\[ 0 = -\gamma + \gamma x + \beta x - \beta x^2 = (\beta x - \gamma)(1 - x), \quad (4.3.7) \]

so if \( \beta > \gamma \) then the extinction probability

\[ \rho = \gamma/\beta \quad (4.3.8) \]

For a simpler proof, note that the first thing that happens is either the death of the ancestor with probability \( \gamma/(\gamma + \beta) \) or the birth of a second particle with probability \( \beta/(\beta + \gamma) \), so

\[ x = \frac{\gamma}{\gamma + \beta} \cdot 1 + \frac{\beta}{\gamma + \beta} \cdot x^2, \]

since when we have two particles the probability both of their families die out is \( x^2 \). Rearranging we have the quadratic in (4.3.7).

Note that as in the case of the epidemic with exponential infection times on the Erdös-Rényigraph, the probability that the epidemic dies out given in (4.3.8) is not the same as the limiting number of susceptibles since \( s(\infty) = \gamma/\beta \) does not solve the equation in (4.3.6).

The difference can be using the argument for the epidemic on an Erdös-Rényigraph with exponential infection times. If we draw oriented edges from \( x \) to the neighbors it infects then the probability of extinction is the probability the outgoing cluster containing \( x \) is finite, while to determine whether \( y \) becomes infected we start at \( y \) and follow the arrow in a direction opposite of their orientation, the incoming cluster.
4.4 Miller-Volz equations

In 2008 Erik Volz published a remarkable paper deriving differential equations for the spread of epidemics on random walks with specified degree distributions, generated by the configuration model. I think that at the time people viewed these as heuristic or approximate but it turns out that they are exact in the limit of large population size.

Although the networks he considered were undirected in the sense that any two neighbors can transmit the infection to the other, it is useful to keep track of who infects who, so for each undirected edge \( \{a, b\} \) we have two directed edges \((a, b)\) and \((b, a)\). To quote Volz, ”the first element in the ordered pair will be called the ego and the second the alter.” Let \( \mathcal{A}_{X,Y} \) be the set of arcs with ego in \( X \) and alter in \( Y \), \( \mathcal{A}_X \) be the set of arcs with ego in \( X \).

\[
M_{X,Y} = |\mathcal{A}_{X,Y}|/|\mathcal{A}_X|
\]

To describe the model we will use the notation of Miller rather than Volz since it is Miller’s proof that we will follow. Let \( \beta \) be the rate at which infected individuals infect susceptible neighbors, \( \gamma \) be the recovery rate \((I \rightarrow R \text{ transitions})\). Let \( S, I, \) and \( R \) be the fraction of susceptible, infected, and removed nodes at time \( t \). We let \( \psi(x) \) be the probability generating function of the degree distribution \( p_k \). Letting \( p_I = M_{S,I}/M_S, p_S = M_{S,I}/M_S, \) and \( \theta \) be the fraction of degree one vertices that remain susceptible at time \( t \) we have the following five equations

\[
\begin{align*}
S &= \psi(\theta) \\
\frac{d\theta}{dt} &= -\beta p_I \theta \\
\frac{dp_I}{dt} &= \beta p_S p_I \theta \frac{\psi''(\theta)}{\psi'(\theta)} - \beta p_I (1 - p_I) - \gamma p_I \\
\frac{dp_S}{dt} &= r p_S p_I \theta \left(1 - \frac{\psi''(\theta)}{\psi'(\theta)}\right) \\
\frac{dI}{dt} &= \beta p_I \theta \psi'(\theta) - \gamma I
\end{align*}
\]

Miller (2011) reduced Volz’s system of ODE to a single equation. To begin to develop his ideas we define an infectious contact from \( v \) to a neighbor \( u \) is a contact that would cause the infection of \( u \) if it was susceptible. Here \( v \) must be infected but \( u \) can be \( S, I, \) or \( R \). Let \( \theta(t) \) be the probability an edge has not transmitted an infectious contact. To compute this pick an edge at random, and then give it an orientation from \( v \) (the base) to \( u \) (the target). We disallow infectious contacts from \( u \) to \( v \). \( \theta(\infty) \) probability of no infectious contact from \( v \) to \( u \).

To calculate the size of an epidemic it suffices to calculate the probability that a vertex who is not allowed to infect its neighbors is infected, since a vertex cannot start a chain of infection that leads to its initial infection. The infections along the different edges incident
to such a vertex are independent so
\[ S(t) = \sum_{k=0}^{\infty} p_k \theta(t)^k = \psi(\theta(t)) \] (4.4.1) \thetatoS

Let \( \phi \) be the probability the base is infected but has not transmitted infection to the target.
\[ \theta'(t) = -\beta \phi(t) \] (4.4.2) \thde

An edge no longer satisfies the definition of \( \phi \) when the infection crosses the edge or when the base node recovers. The rate at which neighbors become infectious matches the rate at which neighbors stop being infections so
\[ \phi'(t) = -((\beta + \gamma)\phi(t) - h'(t)) \] (4.4.3) \phide

where \( h(t) \) be the probability that a neighbor is susceptible. Neighbors have the size-biased degree distribution. That is, if \( \mu = \sum_j j p_j \) then
\[ h(t) = \frac{\sum_{k=0}^{\infty} k p_k \theta(t)^{k-1}}{\mu} = \frac{\psi'(\theta(t))}{\psi'(1)} \] (4.4.4) \hfrompsi

Differentiating the last equation neighbors become infected at rate
\[ -h'(t) = -\frac{\psi''(\theta(t))\theta'(t)}{\psi'(1)} = \frac{\beta \phi(t) \psi''(\theta(t))}{\psi'(1)} \] (4.4.5) \2b

by (4.4.2). Using (4.4.3) and (4.4.5) we have
\[ \phi'(t) = \left[ -\beta + \gamma + \frac{\beta \psi''(\theta(t))}{\psi'(1)} \right] \phi(t) \] (4.4.6) \phide

so using (4.4.2) we have
\[ \phi'(t) = \left[ 1 - \frac{\gamma}{\beta} + \frac{\psi''(\theta(t))}{\psi'(1)} \right] \theta'(t) \]

Integrating gives
\[ \phi(t) = \theta - \frac{\gamma}{\beta} (1 - \theta) - \frac{\psi'(\theta)}{\psi'(1)} \]

where the constant of integration is found by taking \( \phi(-\infty) = 0 \), \( \theta(-\infty) = 1 \). Using (4.4.2) now we have
\[ \theta'(t) = -\beta \theta + \gamma (1 - \theta) + \frac{\beta \psi'(\theta)}{\psi'(1)} \] (4.4.7) \MillerDE

which is Miller’s differential equation. To find the values of \( S \), \( I \), and \( R \) we note that
\[
S = \psi(\theta) \\
I = 1 - R - S \\
R' = \gamma I 
\]
Final epidemic size. Letting $t \to \infty$ in (4.4.1) we have $S(\infty) = \psi(\theta(\infty))$. Let

$$T = \frac{\beta}{\beta + \gamma}$$

This is the probability that a randomly chosen neighbor of $u$, call it $v$, has an infectious contact with $u$ given that $v$ has become infected. If $h = h(\infty)$ is the probability the neighbor is never infected then the probability of an infectious contact is $T(1-h)$. Thus the probability of not transmitting the infection along the chosen edge is

$$\theta_\infty = 1 - T + Th$$

(4.4.4) tells us that $h(t) = \psi'(\theta(t))/\psi'(1)$ so

$$\theta_\infty = 1 - T + T \frac{\psi'(\theta(t))}{\psi'(1)}$$

Example. Erdős-Renyi graphs. $\psi(z) = \exp(-\mu(1-z))$, so $\psi'(z)/\psi'(1) = \exp(-\mu(1-z))$ and (4) becomes

$$\theta'(t) = \gamma - (\beta + \gamma)\theta(t) + \beta \exp(-\mu(1 - \theta(t)))$$
4.4. MILLER-VOLZ EQUATIONS

References


