JOURNAL OF THE ROYAL SOCIETY Interface

FirstCite® e-publishing

J. R. Soc. Interface
doi:10.1098/rsif.2008.0218
Published online

Epidemic thresholds in dynamic contact networks

Erik Volz[1,*] and Lauren Ancel Meyers[1,2]

[1]*Integrative Biology, University of Texas at Austin, Austin, TX 78712, USA*
[2]*Santa Fe Institute, Santa Fe, NM 87501, USA*

The reproductive ratio, R_0, is a fundamental quantity in epidemiology, which determines the initial increase in an infectious disease in a susceptible host population. In most epidemic models, there is a specific value of R_0, the epidemic threshold, above which epidemics are possible, but below which epidemics cannot occur. As the complexity of an epidemic model increases, so too does the difficulty of calculating epidemic thresholds. Here we derive the reproductive ratio and epidemic thresholds for susceptible–infected–recovered (SIR) epidemics in a simple class of dynamic random networks. As in most epidemiological models, R_0 depends on two basic epidemic parameters, the transmission and recovery rates. We find that R_0 also depends on social parameters, namely the degree distribution that describes heterogeneity in the numbers of concurrent contacts and the mixing parameter that gives the rate at which contacts are initiated and terminated. We show that social mixing fundamentally changes the epidemiological landscape and, consequently, that static network approximations of dynamic networks can be inadequate.

Keywords: concurrency; complex networks; susceptible–infected–recovered

1. INTRODUCTION

The reproductive ratio, R_0, is defined as the expected number of secondary infections of an initial infectious individual in a completely susceptible host population, and is related to the likelihood and extent of an epidemic (Anderson & May 1991). The *epidemic threshold* is a critical value of R_0, at which epidemics become possible. This value has been shown to depend on the transmission and recovery rates of a disease, as well as the structure of the host population through which it spreads (Diekmann & Heesterbeek 2000; Serrano & Boguñá 2006; Trapman 2007). A primary goal of public health is to bring diseases under their epidemic thresholds by lowering transmission rates, increasing recovery rates, disrupting contacts that can lead to disease transmission, or immunizing susceptible hosts (Meyers *et al.* 2005).

For most diseases, field epidemiologists go to great lengths to estimate R_0; and mathematical epidemiologists often derive results of their models in terms of R_0. This value thus serves as a cornerstone for disease forecasting and intervention and allows straightforward comparisons of not only different diseases and strains but also diverse mathematical models. For some complex epidemiological models, however, we do not yet know how to calculate R_0 (Anderson & May 1991; Altmann 1995, 1998).

Semi-random networks have been proposed as a realistic model for host-to-host contact patterns (Gupta *et al.* 1989; Andersson 1998; Callaway *et al.* 2000; Liljeros *et al.* 2001; Strogatz 2001; Newman 2002; Newman *et al.* 2002). Epidemiologists have used network models to study susceptible–infected–recovered (SIR) epidemics through heterogeneous contact networks and have shown that the reproductive ratio critically depends on host population structure. The mean number of contacts alone is often not sufficient for predicting disease dynamics (Andersson 1999; Eames & Keeling 2002; Meyers *et al.* 2005, 2006; Bansal *et al.* 2007; Volz 2008*a*).

A critical assumption of these network models is that contacts remain fixed throughout the epidemic period. This will not be true for many diseases, particularly those causing long-lasting outbreaks. Thus, researchers have turned their attention to modelling disease transmission through networks with transitory contacts (Altmann 1995, 1998; Ferguson & Garnett 2000; Bauch 2002; Eames & Keeling 2004; Gross *et al.* 2006; Volz & Meyers 2007). We recently introduced a simple model in which each individual has a constant number of concurrent contacts, but the identities of those contacts change stochastically through instantaneous neighbour exchanges (NEs). In a NE, two randomly chosen pairs of contacts are broken and then swapped (e.g. A–B and C–D become A–C and B–D). This class of network dynamics has already been well studied outside of epidemiology (Watts & Strogatz 1998; Maslov & Sneppen 2002; Evans & Plato 2007; Holme & Zhao 2007).

Here, we derive the epidemic thresholds for this simple class of dynamic random networks. Our model is made mathematically tractable by making certain

*Author for correspondence (erik.volz@gmail.com).

Received 20 May 2008
Accepted 3 July 2008

simplifying assumptions, such as that the number of concurrent partnerships of a given node is fixed, and that NEs happen instantaneously as a Poisson process. We refer to the process of NE as 'random mixing', and the rate of NE as the 'mixing rate'. In simple models, as the transmission rate increases, an epidemic is initially impossible but becomes possible above the epidemic threshold. In this model, as transmission rate increases, diseases cross through three states: initially epidemics are impossible, then epidemics become possible, but only when there is a critical level of random mixing, and, finally, epidemics are always possible regardless of the mixing rate.

Mathematical models of disease transmission through dynamic networks are relatively new and difficult, and thus epidemiologists previously have approximated dynamic contact patterns using static network models (Newman 2002; Meyers *et al.* 2005, 2006). These models allow easy calculation of important epidemiological quantities through bond percolation (BP) methods (Callaway *et al.* 2000; Newman 2002; Meyers *et al.* 2005, 2006). Using the reproductive ratio derived below for dynamic networks, we systematically evaluate the adequacy of these simple approximations. Under modest mixing rates, dynamic networks are almost fixed and can be adequately modelled as static networks. As the mixing rate increases, these approximations worsen. When the mixing rate is very high, however, the population becomes well mixed and can be effectively modelled using another simple framework introduced in Volz & Meyers (2007) and Volz (2008*b*).

Below, we begin by summarizing the epidemic model introduced in Volz & Meyers (2007). We then derive the reproductive ratio and epidemic thresholds for this model, and use these quantities to evaluate static network approximations of fluid host populations.

2. SIR EPIDEMICS IN DYNAMIC RANDOM NETWORKS

There is extensive theory describing static random networks with arbitrary degree distributions (Callaway *et al.* 2001; Newman *et al.* 2001, 2002; Chung & Lu 2002; Catanzaro *et al.* 2005), particularly networks generated by the *configuration model* (CM; Molloy & Reed 1995, 1998). We consider a network with degree distribution with density $\{p_k\}$; that is, $K(ego)$ is a random variable giving the degree of node *ego* and has density p_k for all nodes *ego*. $K(ego)$ is the number of simultaneous contacts experienced by a node and is referred to as the *concurrent degree*. In the limit of large network size, CM networks have the property that given an edge from node *ego* to node x, the probability that $x = alter$ is proportional to the degree of node alter (k_{alter}). Below, we use $\{ego, alter\}$ to denote the edge connecting nodes *ego* and *alter* to each other and $(ego, alter)$ to denote the contact from *ego* to *alter*. We consider only undirected networks in which every edge $\{ego, alter\}$ consists of two contacts $(ego, alter)$ and $(alter, ego)$.

In Volz & Meyers (2007), we introduced a class of dynamic networks that are a generalization of CM networks. These networks evolve by a *NE* process whereby the pairs of edges are selected uniformly at random and instantaneously interchanged. An edge swap can be represented by the following pseudo-chemical equation:

$$\{ego, alter\} + \{ego', alter'\} \rightarrow \{ego, alter'\} + \{ego', alter\}. \tag{2.1}$$

From the perspective of a given contact $(ego, alter)$, an edge swap will take place at a constant rate ρ, that is, at a rate ρ, the contact $(ego, alter)$ will be transformed to $(ego, alter')$, where $alter'$ is a node selected with probability proportional to the degree of $alter'$. This process conveniently preserves the degree sequence of the network. We will refer to a specific contact $(ego, alter)$ as a *transitory contact*, and the number of such contacts experienced over an individual's infectious period will be called the *transitory degree*.

We briefly review the model presented in Volz & Meyers (2007), which describes the co-dynamics of these evolving networks and a simple SIR-type epidemic. Let nodes fall in three mutually exclusive states: susceptible; infectious; and recovered. Given the difficulty of modelling both dynamic processes simultaneously, we considered only the simplest type of SIR dynamics. An infectious node transmits disease along each its edges at a constant rate r, causing susceptible neighbours to enter the infectious state; and, it enters the recovered state at a constant rate μ. Following the convention introduced in Volz & Meyers (2007), we refer to the combined network and disease dynamics as the NE model.

3. R_0 AND THE EPIDEMIC THRESHOLD

R_0 traditionally indicates the expected number of secondary infections following the introduction of an initial infected into a completely susceptible population. In network models, however, this definition does not always lead to threshold behaviour at $R_0 = 1$ (Newman 2002; Trapman 2007). For example, suppose a *static* network has degree distribution p_k (§2) and a uniform transmission probability τ' *per edge*. If we assume that the initially infected node is selected uniformly at random from the population, then the expected number of transmissions by that node will be $\tau' \sum kp_k$. As usual, when this value (the mean number of transmissions) exceeds unity, the growth in the number of cases is supercritical, and epidemics can occur. But in a CM network, an individual infected early in an outbreak (other than the very first individual infected) would not have degree described by distribution p_k, but rather would be selected with probability proportional to degree. Then, the number of secondary cases from such an individual would be $\tau' \sum (k-1)kp_k / \sum kp_k$. This latter quantity can be larger than the former, implying that epidemics can spread among high-degree nodes even when the mean degree appears inadequate to sustain transmission.

Therefore, we define the quantity R_* to be the expected number of secondary infections from an individual who is infected early in an epidemic but is not the very first case in the population (patient zero). Similar quantities were described in Andersson (1997) and Aparicio *et al.* (2000). Unfortunately, notation is

not consistent within the literature on epidemic thresholds. Not all authors differentiate between R_* and the definition of R_0 above (e.g. Andersson 1998).

For CM networks, R_* represents the expected number of transmissions events from an infected node chosen with probability proportional to degree, assuming that all of the node's contacts are susceptible except for the one that transmitted disease to it. When $R_*>1$, there is positive probability that epidemics will occur (Trapman 2007).

R_* depends on both the random number of transitory contacts experienced by a node over its infectious period and on the transmissibility τ of the disease (the probability that an infectious node will transmit disease to one of its transitory contacts). M will be a random variable denoting the number of transitory contacts, and Θ_0 will denote the infectious period. A node with a number k concurrent contacts will experience a number $m \geq k$ transitory contacts over its infectious period t. This quantity m, which depends on k, t and $\Pr[M=m|K=k,\Theta_0=t]$, results from the stochastic exchange of neighbours. An infected individual transmits disease to each transitory contact with a probability τ that depends on the other epidemic and social parameters. Thus, given m transitory contacts, the number of transmission events will also be a random variable.

3.1. Derivation of transmissibility

Suppose that a node *ego* becomes infected and that *ego* has a transitory contact with *alter* that overlaps with *ego*'s infectious period. The duration of *ego*'s infectious period will be denoted $\Theta_0(ego)$, which has distribution $\exp(\mu)$. We will use the term *infectious contact period* to mean the overlap between *ego*'s infectious period and the *ego–alter* transitory contact, and use the symbol $\Theta(ego, alter)$ to denote the duration of this period. Subscripts will be dropped when the context is obvious. We next define τ to be the probability of transmission from *ego* to *alter* during their infectious contact period. τ is easily derived using the theory of Markov processes, but here we provide a detailed calculation.

Our model assumes that recovery and edge swapping are two independent Poisson processes with rates μ and ρ, respectively. The termination of the infectious contact period between *ego* and *alter* will thus also be a Poisson process with rate $\mu+\rho$.

Then τ is given by

$$\begin{aligned}\tau &= E(1-\exp(-r\Theta(ego, alter))) \\ &= \int_{t=0}^{\infty} \Pr[ego \text{ transmits to } alter|\Theta(ego, alter)=t] \\ &\quad \times \Pr[\Theta(ego, alter)=t]\mathrm{d}t. \end{aligned} \tag{3.1}$$

Since the timing of both transmission and the infectious contact period are exponentially distributed with parameters r and $\mu+\rho$, respectively, we have

$$\Pr[\Theta(ego, alter)=t] = (\mu+\rho)\mathrm{e}^{-(\mu+\rho)t}, \tag{3.2}$$

$$\Pr[ego \text{ transmits to } alter|\Theta(ego, alter)=t] = 1-\mathrm{e}^{-rt}. \tag{3.3}$$

Substituting these expressions into the integral in equation (3.1) and solving yields

$$\tau = \frac{r}{r+\mu+\rho}. \tag{3.4}$$

Owing to the memoryless property of Poisson processes, every transitory contact corresponding to a given concurrent contact has uniform probability τ of resulting in transmission. Consider the history of a single concurrent contact. The individual becomes infected at time t_0, and the concurrent contact is exchanged at times $t_1, t_2, \ldots, t_{M-1}$. Recovery occurs at t_M. The total number of potential transmissions, M, is a random variable whose distribution is calculated in §3.2. Our goal is to find the transmission probability in each interval $(t_0, t_1), \ldots, (t_{M-1}, t_M)$ corresponding to the duration of a single contact. If we know that the interval begins and ends at times t_i and t_{i+1}, respectively, then the probability of transmission is $1-\exp(-r(t_{i+1}-t_i))$. If instead we assume only that the ith exchange occurs at time t_i, and that the individual has not yet recovered, then we have $t_M \sim t_i+\exp(\mu)$, and $t_{i+1} \sim t_i+\exp(\rho)$, by the memoryless property of Poisson processes. The probability of transmission during the interval beginning at t_i can be found by repeating the calculation given in equation (3.1), but shifting all time intervals by t_i. Once again we find

$$\begin{aligned}\tau_i = \int_{t=t_i}^{\infty} &(1-\exp(-r(t-t_i)))(\mu+\rho) \\ &\times\exp(-(\mu+\rho)(t-t_i))\,\mathrm{d}t = r/(r+\mu+\rho) = \tau,\end{aligned}$$

which says that each transitory contact has uniform probability of resulting in transmission. Consequently, given a total m transitory contacts along a single edge, the distribution of the number of transmissions along that edge has distribution Binomial(m, τ).

It is possible that many individuals will have more than one concurrent contact ($K(ego)>1$). Once infected, the number of transmission events along each of an individual's edges will be correlated since each edge is constrained by the length of the individual's infectious period. Owing to this correlation among edges emanating from the same individual, the number of transmission events per edge is not iid random variables across all edges in the network (Durrett 2006; Kenah & Robins 2007). Therefore, our calculation above does not hold in the case of $K(ego)>1$, and we can only say that the distribution of transmissions is approximately binomial in this case.

3.2. Derivation of R_*

In the following derivations, we will use probability generating functions (pgf's; Wilf 1994) to manipulate discrete distributions such as the random number of contacts or transmissions over an infectious period. We will use the pgf $H_1(x)$ to generate the random number of transmissions made by an infected individual, *ego*, such that

(i) *ego* was selected with probability proportional to concurrent degree, and

(ii) all of *ego*'s contacts are susceptible, except the one by which *ego* became infected.

The rest of this section will concern the derivation of $H_1(x)$. R_* will formally be defined as the mean of the distribution generated by $H_1(x)$.

First consider the distribution of M. The minimum number of transitory contacts during an infectious period is $M=K$, corresponding to no NEs. If a contact (*ego*, *alter*) is exchanged for another contact (*ego*, *alter'*) at rate ρ, then the time between exchanges is exponentially distributed with parameter ρ, and the number of such exchanges during an infectious period of length $\Theta_0=t$ will have a Poisson distribution with parameter ρt. Supposing $K=1$, the distribution for the number of transitory contacts will thus be given by

$$\Pr[M=m|\Theta_0=t]=\Pr[m-1 \text{ exchanges}|\Theta_0=t]$$
$$=\frac{(\rho t)^{m-1}\mathrm{e}^{-\rho t}}{(m-1)!}. \tag{3.5}$$

It follows that the pgf for the number of transitory contacts minus one $(M-1)$ given $K=1$ and $\Theta_0=t$ has a Poisson density and is generated by

$$f_t(x)=\sum_m \frac{(\rho t)^{m-1}\mathrm{e}^{-\rho t}}{(m-1)!}x^{m-1}=\mathrm{e}^{\rho t(x-1)}. \tag{3.6}$$

Because this is offset by one transitory contact (the original contact), the total number of transitory contacts, M, is generated by $xf_t(x)$. If an individual has k concurrent contacts, the total number of transitory contacts will be generated by the product of generating functions, $(xf_t(x))^k$.

The degree distribution p_k introduced in §2 will be generated by $g(x)=\sum_k p_k x^k$. The hazard of infection is proportional to the number of concurrent contacts at that time (Volz & Meyers 2007), so if a node is infected at time t, the probability of it having concurrent degree k will be proportional to k. Denote the probability density $q_k=kp_k/\langle K\rangle$, and let $g_1(x)$ generate the concurrent degree distribution for nodes selected with probability proportional to K discounting one concurrent contact. This is called the *excess* degree distribution (Newman 2003) and is generated by

$$g_1(x)=\sum_k q_k x^{k-1}=\frac{\sum_k kp_k x^{k-1}}{\sum_k kp_k}=\frac{g'(x)}{g'(1)}. \tag{3.7}$$

By analogy with equation (3.7), we will also define $\tilde{H}_1$, which generates transitory contacts selecting nodes proportional to the concurrent degree, but subtracting one transitory contact. The mean of the distribution generated by $\tilde{H}_1$ will give the expected number of potential transmissions of a second generation infected. Constructing this generating function involves several steps as follows:

— Integrating over all infectious periods, Θ_0, and weighting by the density $\Pr[\Theta_0=t]=\mu\mathrm{e}^{-\mu t}$.
— Summing over possible concurrent degree K, while weighting by the probability q_k.
— Adding a term $f_t(x)$ to account for the concurrent partnership by which *ego* was infected excluding the specific transitory contact that infected *ego*.

Therefore, we have

$$\tilde{H}_1(x)=\int \Pr[\Theta_0=t]\left(f_t(x)+\sum_k q_k(xf_t(x))^{k-1}\right)\mathrm{d}t$$
$$=\mu\int \exp(t(\rho(x-1)-\mu))\mathrm{d}t+\mu\sum_k q_k x^{k-1}$$
$$\times\int \exp(t((k-1)\rho(x-1)-\mu))\mathrm{d}t. \tag{3.8}$$

Provided $x\leq 1$, the integrals in equation (3.8) can be solved analytically, yielding a somewhat unusual generating function.

$$\tilde{H}_1(x)=\frac{\mu}{\mu-\rho(x-1)}+\sum_k q_k x^{k-1}\frac{\mu}{\mu-(k-1)\rho(x-1)}. \tag{3.9}$$

Differentiating with respect to x and evaluating at $x=1$ yields the mean number of potential transmissions for a second generation infected.

$$\tilde{H}_1'(1)=\left[\frac{\mu\rho}{(\mu-\rho(x-1))^2}+\sum_k\left((k-1)q_k x^{k-2}\right.\right.$$
$$\left.\left.+\frac{\mu\rho}{(\mu-(k-1)\rho(x-1))^2}(k-1)q_k x^{k-1}\right)\right]_{x=1}$$
$$=\frac{\rho}{\mu}+\frac{\mu+\rho}{\mu}\frac{g''(1)}{g'(1)}, \tag{3.10}$$

where we have used the definition of $g_1(x)$ in equation (3.7).

Now that we have derived the number of possible transmissions from an infected node, we next consider the distribution of actual transmissions given the number of potential transmissions. In §3.1, we saw that given m transitory contacts corresponding to a single concurrent contact, the number of transmissions would be distributed as binomial(m,τ), which is generated by $(1-\tau+\tau x)^m$. But we also saw that this breaks down when m corresponds to multiple $(k>1)$ concurrent contacts. Nevertheless, we will make the approximation that the distribution is binomial when $k>1$. This will provide only an approximate generating function for the number of transmissions from a second generation infected, but, most importantly, it will still give the correct epidemic threshold. This is because the first moment of the distributions will coincide. In other words, we will use the fact that the mean value of the sum of k correlated identically distributed random variables will be the same as the mean value of the sum of k iid random variables. Using the composition property of pgf's, we have $H_1(x)=\tilde{H}_1(1-\tau+\tau x)$, and the solution for the reproductive ratio is given by

$$R_*=\left[\frac{\mathrm{d}}{\mathrm{d}x}H_1(x)\right]_{x=1}=\left[\frac{\mathrm{d}}{\mathrm{d}x}\tilde{H}_1(1-\tau+\tau x)\right]_{x=1}$$
$$=\tau\tilde{H}_1'(1)=\frac{\tau\rho}{\mu}+\tau\frac{\mu+\rho}{\mu}\frac{g''(1)}{g'(1)}. \tag{3.11}$$

Depending on the degree distribution, solving for explicit values of R_* can be very simple. We use three

common degree distributions to demonstrate this and other quantities derived below:

— Poisson with mean z: $p_k = z^k e^{-z}/k!$, $k \geq 0$, generated by

$$g(x) = e^{z(x-1)}. \tag{3.12}$$

— Power law with exponent α and cut-off κ: $p_k = k^{-\alpha}/\sum_{k=1}^{\kappa} k^{-\alpha}$, $k \geq 1$, $k \leq \kappa$, generated by

$$g(x) = \frac{\sum_{k<\kappa} k^{-\alpha} x^k}{\sum_{k<\kappa} k^{-\alpha}}. \tag{3.13}$$

— A constant: $p_k = \{1 \text{ if } k = \kappa, 0 \text{ otherwise}\}$, generated by

$$g(x) = x^{\kappa}. \tag{3.14}$$

When $\kappa = 1$, this is called the *monogamous* network.

Constant networks have $R_* = \rho\tau/\mu + (\kappa - 1)\tau(\mu + \rho)/\mu$, and thus a monogamous network ($\kappa = 1$) has just $R_* = \rho\tau/\mu$; Poisson networks have $R_* = \rho\tau/\mu + z\tau(\mu + \rho)/\mu$; and power law network have $R_* = \rho\tau/\mu + ((\sum_{k<\kappa} k^{2-\alpha} - k^{1-\alpha})/\sum_{k<\kappa} k^{1-\alpha})\tau(\mu + \rho)/\mu$. Consider the special case of a static network with $\rho = 0$. Intuitively, monogamous static networks never experience epidemics ($R_* = 0$), whereas Poisson networks have $R_* = z\tau$ as shown previously (Andersson 1998; Diekmann & Heesterbeek 2000; Newman 2002).

3.3. Epidemic thresholds

Epidemic thresholds are found by solving for parameters with the condition $R_* = 1$. The result is a set of critical functions of the parameters r, μ, ρ and parameters controlling the degree distribution. When parameters exceed their epidemic threshold, epidemics have positive probability. Solving for the critical transmissibility $\tau = r/(r + \mu + \rho)$ gives

$$\tau^* = \frac{r}{r + \mu + \rho} = \frac{\mu g'(1)}{g''(1)(\mu + \rho) + \rho g'(1)}. \tag{3.15}$$

Solving for the critical transmission rate, we have

$$r^* = \frac{\mu(\mu + \rho) g'(1)}{g''(1)(\mu + \rho) + (\rho - \mu) g'(1)}. \tag{3.16}$$

And, solving for the critical mixing rate, we have

$$\rho^* = \frac{\mu(r + \mu) g'(1) - r\mu g''(1)}{r g''(1) + g'(1)(r - \mu)}. \tag{3.17}$$

For the special case of a *monogamous* network in which all nodes have concurrent degree $k = 1$, this becomes

$$\rho^* = \frac{\mu(\mu + r)}{r - \mu}. \tag{3.18}$$

The critical mixing rate ρ^* does not exist for some values of transmission rate r and recovery rate μ. In particular, the mixing rate must always be positive and finite. As the denominator in equation (3.17) goes to zero, ρ^* diverges to infinity. So, the condition of $r g''(1) + g'(1)(r - \mu) = 0$ defines a lower bound on the ratio of r to μ below which epidemics are impossible even in the limit of large mixing rate.

$$(r/\mu)^*_{\text{lb}} = g'(1)/(g''(1) + g'(1)). \tag{3.19}$$

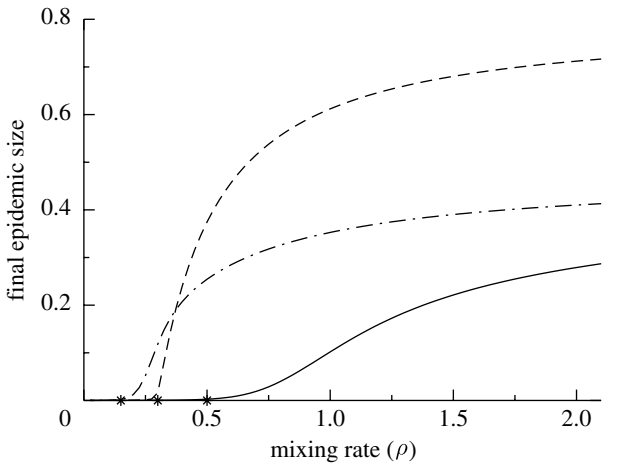

Figure 1. The final epidemic size as predicted by the NE model (Volz & Meyers 2007) versus the mixing rate ρ. The * symbols along the x-axis indicate the predicted critical value ρ^* (equation (3.17)) at which epidemics become possible. The power law (solid line) has parameters $\alpha = 4$, $\kappa = 75$ with $\mu = 0.17$, $r = 0.2$ and $\rho^* = 0.50$. The Poisson (dot-dashed line) has $z = 1.5$ with $\mu = 0.25$, $r = 0.2$ and $\rho^* = 0.15$. The monogamous (dashed line) network has $k = 1$ for all nodes, with $\mu = 0.1$, $r = 0.1$ and $\rho^* = 0.3$.

Similarly, it may be possible for epidemics to occur even if $\rho = 0$. This occurs when the numerator of equation (3.17) is zero, which is exactly the epidemic threshold for static networks (also derived using pgf's in Newman 2002).

$$(r/\mu)^*_{\text{ub}} = g'(1)/(g''(1) - g'(1)). \tag{3.20}$$

Figure 1 gives several examples of the final size (attack rate) and epidemic threshold given by equation (3.17) for three degree distributions: Poisson; power law; and a constant degree (equations (3.12)–(3.14)). The $*$ on the ρ-axis indicates the predicted epidemic threshold in terms of ρ. The final size in this figure is predicted by the NE model, introduced in Volz & Meyers (2007). As predicted, the final size takes off at the epidemic threshold derived above. As the mixing rate increases, so does the number of transitory contacts a typical infectious node has during its infectious period. Thus, intuitively, the size of the epidemic grows with the mixing rate, though it may or may not asymptotically approach 100 per cent. Figure 1 also provides an important check on our derivations. The dynamic NE model has already been tested against detailed simulations (Volz & Meyers 2007), so that the correct thresholds observed here also agree with the simulated NE model.

Figure 2 shows that, depending on r, μ and ρ, there are three qualitatively different epidemiological possibilities for a Poisson degree distribution ($z = 1.5$). Below the threshold $(r/\mu)^*_{\text{lb}}$ (equation (3.19)), no epidemics are possible; and above the threshold $(r/\mu)^*_{\text{ub}}$ (equation (3.19)), epidemics can occur regardless of the mixing rate ρ. Between the two thresholds, epidemics are possible, but only if the mixing rate exceeds its threshold ρ^* (equation (3.17)). Figure 2 also shows how the critical mixing rate diverges within the interval between $(r/\mu)^*_{\text{lb}}$ and $(r/\mu)^*_{\text{ub}}$.

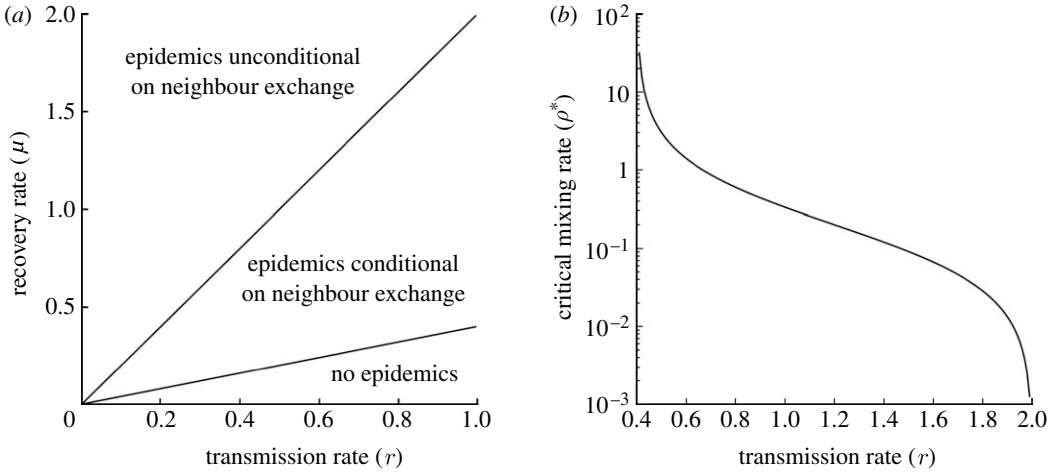

Figure 2. (*a*) Dynamics fall into three qualitatively different classes depending on the ratio r/μ. In the range where epidemics are conditional on NE dynamics, the critical mixing rate ρ^* (equation (3.17)) is well defined. (*b*) The critical mixing rate versus the transmission rate r for $\mu=1$. This assumes a Poisson degree distribution ($z=1.5$).

4. STATIC NETWORK APPROXIMATIONS AND BP

When applying BP methods to dynamic network data, it is common to approximate the dynamic contact network with a static network, such that each transitory contact is considered fixed (Meyers & Newman 2003; Jones 2005). A randomly chosen node *ego* will have a random number m transitory contacts generated by $F(x)$ during a hypothetical infectious period. To determine the form of $F(x)$, first consider the distribution for the number of transitory contacts, integrating over all infectious periods. $p_{m,k=1}$ will denote the probability of m transitory contacts per one concurrent contact during an individual's infectious period. We integrate over all possible infectious periods

$$p_{m,k=1} = \int_{t=0}^{\infty} \Pr[\Theta_0 = t] \times \Pr[m|\Theta_0 = t] \mathrm{d}t. \qquad (4.1)$$

Substituting equation (3.5) from §3 into the integral in equation (4.1) and solving yields the following geometric density:

$$p_{m,k=1} = \left(\frac{\mu}{\mu+\rho}\right)\left(\frac{\rho}{\mu+\rho}\right)^{m-1}. \qquad (4.2)$$

Using equation (4.2), it follows that the density $p_{m,k=1}$ is generated by

$$h(x) = \sum_{m=1}^{\infty} \left(\frac{\mu}{\mu+\rho}\right)\left(\frac{\rho}{\mu+\rho}\right)^{m-1} x^m = \frac{\mu x}{\mu+\rho-\rho x}. \qquad (4.3)$$

By approximation, we will suppose that each concurrent contact will realize an independent random number of transitory contacts such that, for a degree k node, M will be generated by $h(x)^k$. This approximation neglects correlations between the infectious period and the number of transitory contacts as in equation (3.8), and would be exact only in a scenario where the infectious period had zero variance (Trapman 2007). Making these approximations, we find $F(x) = g(h(x))$.

The *excess transitory degree distribution* is analogous to the excess degree distribution defined in §3. It gives the degree discounted by one contact of a node that is selected with probability proportional to its transitory degree and is generated by

$$F_1(x) = \frac{\left[\frac{\mathrm{d}}{\mathrm{d}x} g(h(x))\right]}{\left[\frac{\mathrm{d}}{\mathrm{d}x} g(h(x))\right]_{x=1}} = g'(h(x))h'(x)/(g'(1)h'(1)), \qquad (4.4)$$

where each term in the pgf is weighted by the transitory degree.

Assuming a static network, BP methods (Newman 2002) can be used to predict final epidemic size (FS) by solving[1] the following self-consistent equations:

$$u = F_1(1-\tau+\tau u) \qquad \mathrm{FS} = 1 - F(1-\tau+\tau u). \qquad (4.5)$$

This solution is only an approximation, as it does not take into account the dynamic nature of the underlying contact network and is based on an approximate generating function for the number of transitory contacts.

We can now evaluate the performance of the static network approximation. Figure 3 is a fixed point diagram that compares the FS calculated from the NE equations (Volz & Meyers 2007) with that calculated from solving equation (4.5). The true FS is found by integrating a system of ODEs known to reproduce epidemic prevalence that matches stochastic simulations (Volz & Meyers 2007). We have assumed a power law concurrent degree distribution ($\alpha=2.1$, $\kappa=75$), a recovery rate of $\mu=0.1$, a transmission rate of $r=\mu$ or $r=2\mu$ and mixing rates varying from $\rho=0$ to 0.5. The static network approach offers a reasonable approximation for relatively static populations (low ρ),

[1]A solution to these equations can be found by a very simple root-finding algorithm, which works because F_1 is convex: select a small number $u_0 \ll 1$. Then, solve $u_{i+1}=F_1(1-\tau+\tau u_1)$ for many iterations.

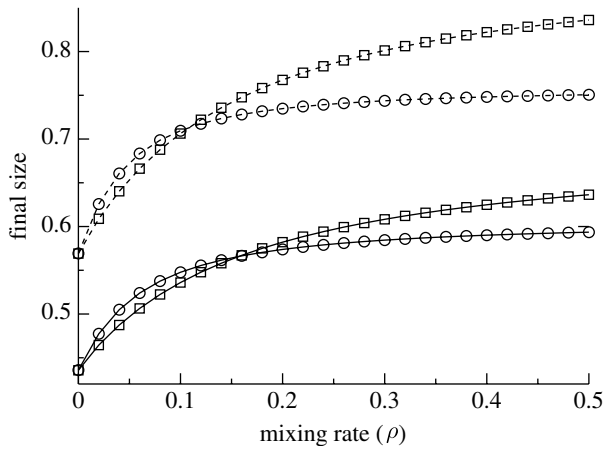

Figure 3. Predicted final epidemic size for the NE model (squares with solid line, $r=0.1$; with dashed line, $r=0.2$; Volz & Meyers 2007) and BP model (circles with solid line, $r=0.1$; with dashed line, $r=0.2$; equation (4.4)) over a range of mixing rates. The degree distribution is a power law ($\alpha=2.1$, $\kappa=75$), the recovery rate is $\mu=0.1$ and the transmission parameter is $r=\mu$ or $r=2\mu$.

but not for populations with high mixing rates. As expected, the BP and NE solutions coincide when $\rho=0$.

To provide some intuition for the divergence between the two models, we compare their reproductive ratios. Recall that equation (3.11) gives the reproductive ratio for the NE model, now denoted R_*^{NE}. For the static network model, BP calculations yield

$$R_*^{\mathrm{BP}} = \left[\frac{\mathrm{d}}{\mathrm{d}x}F_1(1-\tau+\tau x)\right]_{x=1} = \tau\frac{\mu+\rho}{\mu}\frac{g''(1)}{g'(1)} + 2\tau\left(\frac{\rho}{\mu}\right)^2. \tag{4.6}$$

Comparing these equations, we see that R_*^{NE} differs from R_*^{BP} by

$$\tau\rho\frac{\mu-2\rho}{\mu^2}.$$

$R_*^{\mathrm{NE}} = R_*^{\mathrm{BP}}$, when $\rho=0$ or $\rho=\mu/2$, which explains the two intersection points in figure 3. The second intersection does not in general occur when $\rho=\mu/2$. There is a one-to-one correspondence between R_* and final size; however, this correspondence differs for the NE model and BP approximation. Therefore, $R_*^{\mathrm{NE}} = R_*^{\mathrm{BP}}$ does not imply that final size will be the same for both models.

In the limit of large mixing rate, we have

$$\lim_{\rho\to\infty} R_*^{\mathrm{NE}} = \frac{r}{\mu}\left(\frac{g''(1)}{g'(1)}+1\right), \quad \lim_{\rho\to\infty} R_*^{\mathrm{BP}} = \infty.$$

This implies that the final size of an epidemic in the BP model approaches 1 as the mixing rate increases. By contrast, the dynamic NE model converges to a mass-action model in this limit, which in general will not have final size = 1 (Volz & Meyers 2007).

5. DISCUSSION

We have derived the conditions under which epidemics can spread through populations with heterogeneous contact patterns characterized by multiple concurrent, yet transitory contacts. The fate of an outbreak depends on the contagiousness of the disease, the recovery rate, the underlying heterogeneity in the numbers of concurrent contacts and the fluidity of social contacts. These equations provide insight into the impacts of population structure and disease characteristics on disease transmission through dynamic contact networks and offer a computationally tractable framework for forecasting and the evaluation control strategies.

There are three qualitatively different regimes for the epidemic threshold in terms of the parameter that controls random mixing via exchange of contacts: epidemics may be possible independent of random mixing; epidemics may be possible conditional on the rate of random mixing; or epidemics may be impossible even if mixing rates are very high. From a public health perspective, this suggests that freezing all current contacts will not necessarily prevent an epidemic and, conversely, rapid turnover in contacts will not necessarily make epidemics inevitable.

We also used the new equations to evaluate the performance of simpler static network models previously used to approximate dynamic networks. We present an intuitive static network approximation for dynamic networks, and find that it performs reasonably well for low to medium mixing rates. When mixing rate is very high, the approximation breaks down, but other simple models become possible (Volz & Meyers 2007; Volz 2008*b*).

These results have practical implications. Many populations exhibit not only extreme heterogeneity in contact rates but also dynamic extended duration partnerships. In Volz & Meyers (2007), the NE model was applied to a syphilis outbreak in an urban adolescent population, and in Volz (2008*b*), to a hypothetical smallpox outbreak in a simulated urban network. In both cases, the quantities derived above (the reproductive ratio and epidemic threshold) allow us to evaluate and improve vaccination and other public health strategies.

Future work might consider relaxing the assumption that NE occurs at a constant rate. In reality, partnerships may have characteristic survival times that differ from the exponentially distributed survival times implicit in our model. This could have unpredictable effects on epidemic dynamics, depending on the exact distribution and the transmission and mixing rates. Furthermore, our derivations rely on the assumption that partnerships are uncorrelated and that the network topology is locally tree-like. For many networks, these quantities will offer reasonable approximations (Volz & Meyers 2007), but ideally we will eventually develop similar methods that relax this assumption.

This work complements a related model with dynamic extended duration partnerships that change independently of a homogeneous set of nodes (Altmann 1995). Although the model in Altmann (1995) lacked the heterogeneous network structure of the NE model, it had the advantage that the concurrent number of partnerships for a given node was not fixed. This motivates future development of a more general model in which the numbers of concurrent contacts vary

within a population with heterogeneous contact rates. The case of serial monogamy has also been investigated in Eames & Keeling (2004), a framework based on pair approximation, which was subsequently extended to the case of random numbers of concurrent contacts. Similarly, we are optimistic that our model can be extended to a scenario where there is a random number of cumulative partnerships over the lifetime of an individual, many of which overlap in a stochastic manner, but such that the number of concurrent partnerships at any time is not fixed.

REFERENCES

Altmann, M. 1995 Susceptible–infected–removed epidemic models with dynamic partnerships. *J. Math. Biol.* **33**, 661–675. (doi:10.1007/BF00298647)

Altmann, M. 1998 The deterministic limit of infectious disease models with dynamic partners. *Math. Biosci.* **150**, 153–175. (doi:10.1016/S0025-5564(98)00012-1)

Anderson, R. M. & May, R. M. 1991 *Infectious diseases of humans: dynamics and control*. Oxford, UK: Oxford University Press.

Andersson, H. 1997 Epidemics in a population with social structure. *Math. Biosci.* **140**, 79–84. (doi:10.1016/S0025-5564(96)00129-0)

Andersson, H. 1998 Limit theorems for a random graph epidemic model. *Ann. Appl. Probab.* **8**, 1331–1349. (doi:10.1214/aoap/1028903384)

Andersson, H. 1999 Epidemic models and social networks. *Math. Sci.* **24**, 128–147.

Aparicio, J. P., Capurro, A. F. & Castillo-Chavez, C. 2000 Transmission and dynamics of tuberculosis on generalized households. *J. Theor. Biol.* **206**, 327–341. (doi:10.1006/jtbi.2000.2129)

Bansal, S., Grenfell, B. T. & Meyers, L. A. 2007 When individual behaviour matters: homogeneous and network models in epidemiology. *J. R. Soc. Interface* **4**, 879–891. (doi:10.1098/rsif.2007.1100)

Bauch, C. T. 2002 A versatile ODE approximation to a network model for the spread of sexually transmitted diseases. *J. Math. Biol.* **45**, 375–395. (doi:10.1007/s002850200153)

Callaway, D. S., Newman, M. E. J., Strogatz, S. H. & Watts, D. J. 2000 Network robustness and fragility: percolation on random graphs. *Phys. Rev. Lett.* **85**, 5468–5471. (doi:10.1103/PhysRevLett.85.5468)

Callaway, D. S., Hopcroft, J. E., Kleinberg, J. M., Newman, M. E. J. & Strogatz, S. H. 2001 Are randomly grown graphs really random? *Phys. Rev. E* **64**, 041 902. (doi:10.1103/PhysRevE.64.041902)

Catanzaro, M., Boguñá, M. & Pastor-Satorras, R. 2005 Generation of uncorrelated random scale-free networks. *Phys. Rev. E* **71**, 027 103. (doi:10.1103/PhysRevE.71.027103)

Chung, F. & Lu, L. 2002 The average distances in random graphs with given expected degrees. *Proc. Natl Acad. Sci. USA* **99**, 15 879–15 882. (doi:10.1073/pnas.252631999)

Diekmann, O. & Heesterbeek, J. A. P. 2000 *Mathematical epidemiology of infectious diseases. Model building, analysis and interpretation*. Chichester, UK: Wiley.

Durrett, R. 2006 *Random graph dynamics*. Cambridge, UK: Cambridge University Press.

Eames, T. D. & Keeling, M. J. 2002 Modeling dynamic and network heterogeneities in the spread of sexually transmitted diseases. *Proc. Natl Acad. Sci. USA* **99**, 13 330–13 335. (doi:10.1073/pnas.202244299)

Eames, K. T. D. & Keeling, M. J. 2004 Monogamous networks and the spread of sexually transmitted diseases. *Math. Biosci.* **189**, 115–130. (doi:10.1016/j.mbs.2004.02.003)

Evans, T. S. & Plato, A. D. K. 2007 Exact solution for the time evolution of network rewiring models. *Phys. Rev. E* **75**, 056 101. (doi:10.1103/PhysRevE.75.056101)

Ferguson, N. M. & Garnett, G. P. 2000 More realistic models of sexually transmitted disease transmission dynamics: sexual partnership networks, pair models, and moment closure. *Sex. Transm. Dis.* **27**, 600–609. (doi:10.1097/00007435-200011000-00008)

Gross, T., D'Lima, C. J. D. & Blasius, B. 2006 Epidemic dynamics on an adaptive network. *Phys. Rev. Lett.* **96**, 208 701. (doi:10.1103/PhysRevLett.96.208701)

Gupta, S., Anderson, R. M. & May, R. M. 1989 Networks of sexual contacts: implications for the pattern of spread of HIV. *AIDS* **3**, 807–817. (doi:10.1097/00002030-198912000-00005)

Holme, P. & Zhao, J. 2007 Exploring the assortativity-clustering space of a network's degree sequence. *Phys. Rev. E* **75**, 046 111. (doi:10.1103/PhysRevE.75.046111)

Jones, S. J. 2005 Analysis of a syphilis outbreak through the lens of percolation theory. Master's thesis, University of Texas-Austin.

Kenah, E. & Robins, J. 2007 Second look at the spread of epidemics on networks. *Phys. Rev. E* **76**, 036 113. (doi:10.1103/PhysRevE.76.036113)

Liljeros, F., Edling, C. R., Amaral, L. A. N., Stanley, H. E. & Aberg, Y. 2001 The web of human sexual contacts. *Nature* **411**, 907–908. (doi:10.1038/35082140)

Maslov, S. & Sneppen, K. 2002 Specificity and stability in topology of protein networks. *Science* **296**, 910–913. (doi:10.1126/science.1065103)

Meyers, L. A. & Newman, M. E. J. 2003 Applying network theory to epidemics: control measures for *Mycoplasma pneumoniae* outbreaks. *Emerg. Infect. Dis.* **9**, 204.

Meyers, L. A., Pourbohloul, B., Newman, M. E. J., Skowronski, D. M. & Brunham, R. C. 2005 Network theory and SARS: predicting outbreak diversity. *J. Theor. Biol.* **232**, 71–81. (doi:10.1016/j.jtbi.2004.07.026)

Meyers, L. A., Newman, M. E. J. & Pourbohloul, B. 2006 Predicting epidemics on directed contact networks. *J. Theor. Biol.* **240**, 400–418. (doi:10.1016/j.jtbi.2005.10.004)

Molloy, M. & Reed, B. 1995 A critical point for random graphs with a given degree sequence. *Random Struct. Algor.* **6**, 161.

Molloy, M. & Reed, B. 1998 The size of the giant component of a random graph with a given degree sequence. *Comb. Probab. Comput.* **7**, 295–305. (doi:10.1017/S0963548398003526)

Newman, M. E. J. 2002 The spread of epidemic disease on networks. *Phys. Rev. E* **66**, 016 128. (doi:10.1103/PhysRevE.66.016128)

Newman, M. E. J. 2003 The structure and function of complex networks. *SIAM Rev.* **45**, 167–256. (doi:10.1137/S0036144502342480)

Newman, M. E. J., Strogatz, S. H. & Watts, D. J. 2001 Random graphs with arbitrary degree distributions and their applications. *Phys. Rev. E* **64**, 026 118. (doi:10.1103/PhysRevE.64.026118)

Newman, M. E. J., Watts, D. J. & Strogatz, S. H. 2002 Random graph models of social networks. *Proc. Natl Acad. Sci. USA* **99**, 2566–2572. (doi:10.1073/pnas.012582999)

Serrano, M.Á. & Boguñá, M. 2006 Percolation and epidemic thresholds in clustered networks. *Phys. Rev. Lett.* **97**, 088 701. (doi:10.1103/PhysRevLett.97.088701)

Strogatz, S. H. 2001 Exploring complex networks. *Nature* **410**, 268–276. (doi:10.1038/35065725)

Trapman, P. 2007 On analytical approaches to epidemics on networks. *Theor. Popul. Biol.* **71**, 160–173. (doi:10.1016/j.tpb.2006.11.002)

Volz, E. 2008*a* SIR dynamics in random networks with heterogeneous connectivity. *J. Math. Biol.* **56**, 293–310. (doi:10.1007/s00285-007-0116-4)

Volz, E. 2008*b* Susceptible–infected–removed epidemics in populations with heterogeneous contact rates. *Eur. Phys. J. B.* **63**, 381–386. (doi:10.1140/epjb/e2008-00131-0)

Volz, E. & Meyers, L. A. 2007 Susceptible–infected–removed epidemics in dynamic contact networks. *Proc. R. Soc. B* **274**, 2925–2933. (doi:10.1098/rspb.2007.1159)

Watts, D. J. & Strogatz, S. H. 1998 Collective dynamics of small-world networks. *Nature* **393**, 409–410. (doi:10.1038/30918)

Wilf, H. S. 1994 *Generating functionology*, 2nd edn. Boston, MA: Academic Press.