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Stochastic SIR Epidemic on a Random Network and Household Structure

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Abstract

Let us consider a stochastic SIR model for the spread of an epidemic amongst a population of individuals, with a random network of social contacts, that is also partitioned into households. A threshold parameter which determines whether or not an epidemic with few initial infectives can become established and lead to a major outbreak is obtained, as are the probability that a major outbreak occurs and the expected proportion of the population that are ultimately infected by such an outbreak, together with methods for calculating these quantities. The asymptotic situation in which the local contact distribution remains fixed as the population becomes large is considered. The concepts of local infectious clump and local susceptibility set are used to develop a unified approach to the threshold behavior of this class of epidemic models.

Keywords: SIR epidemics, Threshold behaviour, local and global contacts, branching processes, random social network.

1. Introduction

The population partitioned into household within which local infectious contacts occur and by using a random graph to model contacts, social structures through which global infectious contacts might take place. The epidemic model featuring mixing on two level local contact with individuals in the same household and global contacts with an individuals neighbours in a random network with specified degree distribution. The branching process approximations are developed which lead to a threshold theorem determining whether a major outbreak is possible and the probability of such an outbreak, as well as results which allow one to determine the expected proportion of the population that will be infected by such a major outbreak. Moreover, this approximation can be made precise by considering a sequence of epidemics in which the number of graphs m→∞. This enables us to determine a threshold parameter R_* for our epidemic, such that in the limit as m→∞, global epidemics occur with nonzero probability if and only if $R_* > 1$. Here, a global epidemic is one which affects infinitely many groups as m→∞. The probability that a global epidemic occurs and the mean proportion of initial susceptible that are ultimately infected by a global epidemic.

2. Epidemic Model

SIR (Susceptible→infective→removed), infectious period I_1, I_2, I_n infected individual i makes local contacts along each of the D_i edges emanating from independently at rate λ_L for each edge, global contacts at rate λ_G, with individuals chosen independently and uniformly from **N**.

Let us see Approximate determinisitic model and Exact deterministic model.

2.1 Approximate determinisitic Model

For t≥0, Let x_i(t) and y_i(t) be the proportion of the population that have degree i and are susceptible an d infective, respectively, at time t and $y(t) = \sum_{i=1}^{\infty} y_i(t)$.

$$\frac{dx_i}{dt} = -\lambda_G\, y x_i - \frac{\lambda_L\, i x_i}{\mu_D} \sum_{j=1}^{\infty} (j-1)\, y_j \tag{2.1}$$

$$\frac{dy_i}{dt} = -\lambda_G\, y x_i + \frac{\lambda_L\, i x_i}{\mu_D} \sum_{j=1}^{\infty} (j-1)\, y_j - \frac{1}{\mu_I} y_i \; (i = 0,1,) \tag{2.2}$$

This model make three approximations

(i)Globally contacted individuals loss one neighbour on infection

(ii) Allows repeated local transmission down same edge

(iii)Effective degrees of individuals do not decrease as epidemic progresses.

2.2 Exact deterministic model

Let us consider x_i(t) and y_i(t) be the proportion of the population that have effective degree i and are susceptible and infective, respectively, at time t.

$$\frac{dy_i}{dt} = -\lambda_G\, y x_i + \lambda_L[(i+1) y_{i+1} - i y_i] - \gamma y_i + E(t)\{(i+1)[\lambda_L(x_{i+1} + y_{i+1}) + \gamma y_{i+1}] - i(\lambda_L + \gamma) y_i(t)\}, \tag{2.3}$$

$$\frac{dx_i}{dt} = -\lambda_G\, y x_i - \rho E(t)[(\lambda_L + \gamma) i x_i - \gamma(i+1)\, x_{i+1}], (i = 0,1,.), \tag{2.4}$$

$$\text{Where } \gamma = \frac{1}{\mu_I}, \rho E(t) = \left(\sum_{i=1}^{\infty} i y_i(t)\right) / \sum_{i=1}^{\infty} i\,(y_i(t) + x_i(t)) \quad .(2.5)$$

and $y(t) = \sum_{i=1}^{\infty} y_i(t)$. (2.6)

3. Branching Process Approximation

The early stages of an epidemic by comparing it with a branching process which approximates the proliferation of infected households. The local epidemic initiated by the initial infective, then let the individuals so infected make their global contacts.Then the households infected by an individual itself infected in the within-household epidemic in a household in generation n are in generation n+1.

The degree distribution of a type- j primary individual is different to that of a type-j secondary individual. The distribution of the number of susceptible neighbours of such a secondary individual is the same as that of $\mathbf{D}^{(j)}$, this is also true of the primary individual in generation zero, the initial case in the epidemic. However, the primary case in a subsequently infected household, supposing it is a type-j individual and was infected by a type-i individual, has the size-biased degree distribution $\tilde{\boldsymbol{D}}^{(ji)}$, where, for $\mathbf{d} \in \mathbb{Z}_{+}^{J}$, P $(\tilde{\boldsymbol{D}}^{(ji)}=\mathbf{d}) = d_i p_d^{(j)} / \mu_i^{(j)}$. The distribution of the number of susceptible neighbours of such a primary individual in the early stages of an epidemic is thus the same as that of $\boldsymbol{D}^{(ji)} = \tilde{\boldsymbol{D}}^{(ji)} - e_i$. The probability generating functions $f_{D^{(ji)}}(s) = f_{D^{(j)}}^{(ei)}(s) / \mu_i^{(j)}$.In addition, we define $\mu_k^{(ij)}$=E[$\boldsymbol{D}_k^{(ji)}$]. It follows easy that

$$\mu_k^{(ij)} = \frac{f_{D^{(j)}}^{(e_i+e_k)}(s)|s=1}{\mu_i^{(j)}} = \begin{cases} E\left[D_i^{(j)} D_k^{(j)}\right]/\mu_i^{(j)} \ if \ i \neq k, \\ E\left[D_i^{(j)}\left(D_i^{(j)} - 1\right)\right]/\mu_i^{(j)} \ if \ i = k. \end{cases} \tag{3.1}$$

The dependence of the primary individual's degree distribution on both its type and also that of the individual who infected it means that the households in the branching process approximation must be typed according to both of these features. Thus, in the multitype branching processes of infected households there are J^2 types, a type (i, i') households $(i, i' \in J)$ being one where the primary individual is of type i' and was infected by a type i individual. If, $\lambda_{ii'}^{(G)} \mu_{i'}^{(i)}$=0 then type(i, i') households cannot appear in the branching processes.

4. Threshold Parameter

To calculate R_* let us first condition on the size of the household that the globally infected individual is in, i.e,

$$\mathbb{E}[\tilde{C}] = \sum_{n=1}^{\infty} \tilde{\rho}_n \, \mathbb{E}[\tilde{C}^{(n)}], \quad .(4.1)$$

Where $\tilde{C}^{(n)}$ is the random variable $\tilde{C}$ conditional on the household being of size n and $\tilde{\rho}_n$ is the size-biased household size distribution, given by $\tilde{\rho}_n = n\rho_n / \sum_{j=1}^{\infty} j\,\rho_j$. This size biasing arises because an individual chosen uniformly at random from the population is in a household of size n with probability proportional to $n\rho_n$. Then,let us decompose $\tilde{C}^{(n)}$ into the number of global infections emanating from each member of the household.

$$\tilde{C}^{(n)} = C_0 + \sum_{i=1}^{n-1} \chi_i \ C_{i,} \tag{4.2}$$

Where we have labeled the individuals in the household 0,1,.,n-1, with individual 0 being the globally infected initial infective χ_i is the indicator of the event that individual i is infected by the local epidemic intiated by the primary infective and C_i is the number of global infections made by individual i. The random variables $(C_1, \chi_1), (C_2, \chi_2), . (C_{n-1}, \chi_{n-1})$ have the same distribution. Also, for each i= 1,2,,n-1, whether individual i is infected by the local epidemic is clearly independent of individual i's infectious period if it becomes infective, so χ_i and C_i are independent. Thus, taking expectations of equation (5.2),

$$\mathbb{E}[\tilde{C}^{(n)}] = \mathbb{E}[C_0] + \mathbb{E}[T^{(n)}]\ \mathbb{E}[C_1], \tag{4.3}$$

Where $T^{(n)} = \sum_{i=1}^{n-1} \chi_i$ is the final size of the local epidemic amongst the initial susceptible in the household.

4.1 Threshold parameter and probability of a major outbreak

The threshold parameter R_* for our epidemic model, the largest eigenvalue of the $J^2 \times J^2$ mean matrix M. The entries $\widehat{m}_{(ii')(jj')}$=E$[ii'^{\tilde{C}_{jj'}}]$ ((i, i'), $(j, j') \in \mathcal{J}^2$) of the mean matrix can be written as

$$\widehat{m}_{(ii')(jj')} = \sum_{n \epsilon \mathcal{N}} \tilde{\rho}_n^{(i')} \ (\delta_{i'j} \mu_{j'}^{(i'\ i)} + (\mathrm{E}[T_n^{e_{i'}}]) j^{\mu_{j'}^{(j)}})\ p_{jj'}^{(G)}, \qquad . (4.4)$$

Where $\tilde{\rho}_n^{(i)} = n_i \rho_n / \sum_{n' \epsilon \mathcal{N}} n_i' \ \rho n'$ is the probability that a type-i individual chosen uniformly at random from all type-i individuals is in a household of category $\boldsymbol{n}$, $\boldsymbol{T_n^a}$ is the final size of a standard $\boldsymbol{J}$- type SIR epidemic with $\boldsymbol{n}$ individuals, $\boldsymbol{a}$ of which are initially infective, $p_{ij}^{(G)}$=1 $- \phi^{(i)}$ $(\lambda_{ij}^{(G)})$ is the marginal probability that an infectious type i individual contacts a given type j global neighbour and δ_{ij} is the Kronecker delta.

5. Expected Relative Final Size of a Major Outbreak

The offspring of a household in which individual i is the primary individual either the individual whose susceptibility set we are considering or one that has joined the susceptibility set of interest by way of a global contact in this process are those households with a member who globally infects a member of i's local susceptibility set.

Theorem 5.1.1
For s ϵ [0,1], the PGFs of B and $\tilde{B}$ are given, respectively, by

$$f_B(s) = \sum_{n=1}^{\infty} \tilde{\rho}_n f_D\,(1 - p_G + sp_G)\, f_{M^{(n)}}\,(f_D\,(1 - p_G + sp_G)) \tag{5.1}$$

and

$$f_{\tilde{B}}(s) = \sum_{n=1}^{\infty} \tilde{\rho}_n f_{\tilde{D}-1}\,(1 - p_G + sp_G)\, f_{M^{(n)}}\,(f_D\,(1 - p_G + sp_G)), \quad .(5.2)$$

Where the random variable $M^{(n)}$ is the size of the local susceptibility set of a typical individual residing in a household of size n, not counting that individual.

Proof
Let us consider B be a random variable which could be either B or $\tilde{B}$ the differences in the calculation are only slight and are pointed out when they arise. The first step is to condition on the size of the household individual i is in, so

$$f_B(s) = \sum_{n=1}^{\infty} \tilde{\rho}_n \; f_{B^{(n)}}\,(s), \tag{5.3}$$

Where $B^{(n)}$ is the quantity B conditioned on the household size of individual i being n, then decompose $B^{(n)}$ into the number of global contacts made with each member of i's local susceptibility set, i.e.

$$B^{(n)} = B_0 + \sum_{j=1}^{M^{(n)}} B_j, \tag{5.4}$$

Where B_j is the number of contacts made with individual j and $M^{(n)}$ is the size of i's local susceptibility set, not counting i itself. If $M^{(n)}$=0 theni's local susceptibility set consists only of i itself and the sum in (6.4) is empty and equal to 0. Now $B_j \mid K_j \sim$ Bin(K_j, p_G), where K_j is the number of global neighbours of j not already in the susceptibility set and $p_G = 1 - \phi(\lambda_G)$ is the probability that a given global contact is made. Let us do not need to condition on the infection on the infectious period of individual j because the contacts we are considering come from other individuals, the independence of the infectious periods of these individuals implies that the events that each of these individuals contacts j are also independent.

Let us first note that, by independence, $f_{B^{(n)}}\,(s) = \mathbb{E}[s^{B^{(n)}}]$

$$=\mathbb{E}[s^{B_0}]\,\mathbb{E}[s\sum_{j=1}^{M^{(n)}} B_j].$$

Now,

$$\mathbb{E}[s^{B_0}]=\mathbb{E}[\mathbb{E}[s^{B_0}\,|K_0]]=\mathbb{E}[(1-(1 - p_G + sp_G)^{K_0}]$$
$$=f_{k_0}(1 - p_G + sp_G), \quad .(5.5)$$

Where f_{k_0} is either f_D or $f_{\tilde{D}-1}$, as above.
Similarly,

$$\mathbb{E}[s^{\sum_{j=1}^{M^{(n)}} B_j}] = \mathbb{E}\Big[\mathbb{E}\Big[s^{\sum_{j=1}^{M^{(n)}} B_j}\Big| M^{(n)}, K_1, K_2, ., K_n\Big]\Big] \qquad .(5.6)$$

$$= \mathbb{E}\Big[\prod_{i=1}^{M^{(n)}} (1 - p_G + sp_G)^{K_i}\Big] \qquad (5.7)$$

$$= \mathbb{E}[(f_D(1 - p_G + sp_G))^{M^{(n)}}] \qquad (5.8)$$

$$= f_{M^{(n)}}(f_D(1 - p_G + sp_G)). \qquad (5.9)$$

Thus,

$$\mathbb{E}[s^{B_n}] = f_{k_0}(1 - p_G + sp_G)\, f_{M^{(n)}}(f_D(1 - p_G + sp_G)) \qquad (5.10)$$

So, now denoting the offspring distribution random variable for the first generation by B and for subsequent generations by $\tilde{B}$ and substituting equation (5.10) into equation (5.3) we get the equation (5.1) and (5.2).

6. Standard Household Model and Networked Household model with the same Outcomes

The models are effectively the same if the corresponding approximating branching processes have the same distribution in both models, which is equivalent to their offspring distributions having the same distribution. To simplify the presentation we assume that the household size distributions are the same, so it is sufficient to consider the case where the household size n is fixed. The parameters of the NHM by I, D, λ_G and λ_L and those of the SHM by I', λ'_G and λ'_L . Note that although λ_L and λ'_L have the same interpretation,, λ'_G is a total contact rate whilst λ_G is a per-pair contact rate. We observe first that the decomposition (6.4) of the random variable for the offspring in the backward branching processes in the NHM is $B^{(n)} = B_0 + \sum_{j=1}^{M^{(n)}} B_j$, where $B_0, B_1, , B_{n-1}$ are independent, with $B_1, , B_{n-1}$ ~ Bin(D,p_G) and B_0~ Bin(D,p_G) or B_0~ Bin($\tilde{D} - 1, p_G$) according as we are looking at the first or subsequent generations.

It follows from the homogeneously mixing nature of the global contacts in the SHM that the corresponding decomposition,$B^{(n)'} = B'_0 + \sum_{j=1}^{M^{(n)'}} B'_j$, has $B'_0, B'_1, , B'_{n-1}$ as independent and identically distributed Poi($\lambda'_G \mu_{I'}$) random variables. By considering the PGFs of $B^{(1)}$ and $B^{(1)'}$, and in particular their factorial moments, the distributions of $B^{(1)}$ and $B^{(1)'}$ are different unless $\tilde{D} - 1$ ~ Poi(μ_D), which implies that D ~ Poi(μ_D), and $\mu_D p_G = \lambda'_G \mu_{I'}$. If D ~ Poi($\mu_D$) then B_i ~ Poi($\mu_D p_G$). The backward processes agree if and only if

$$\lambda'_G \mu_I = \mu_D(1 - \phi(\lambda_G)), \qquad (6.1)$$

where $\mu_I = \mathbb{E}[I]$. Note that if this is the case then the expected relative final size of a major outbreak z is the same for the two models, as is the threshold parameter R_*.

7. Vaccination

The two aspects of vaccination that need to be specified are the vaccine action model, i.e. the effect of vaccination on an individual's susceptibility and infectivity, and the vaccine allocation model that describes which members of the population are actually vaccinated. Initially we restrict our attention to a vaccine action known as non-random, where vaccinated individuals of the same type all have the same response to vaccination. We assume that, for each $i \epsilon \mathcal{J}$, a vaccinated type-i individual has relative susceptibility a_i and, if it becomes infected, relative infectivity b_i. The rate of each Poisson process associated with infection of such a vaccinated individual is multiplied by a_i and, if infected, the rates at which it makes infectious contacts are all multiplied by b_i. Typically a_i and b_i are both in the interval [0,1], but this is not necessary, and for convenience we write $\boldsymbol{a}=(a_j,\ j \epsilon \mathcal{J})$ and $\boldsymbol{b} = (b_j,\ j \epsilon \mathcal{J})$. If $\boldsymbol{a}=\mathbf{0}$ the vaccine is called perfect, whilst if $\boldsymbol{b} = \mathbf{1}$ so vaccination affects only susceptibility, it is called leaky.

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