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Threshold Parameter for a Random Graph Epidemic Model

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Abstract:

Let us consider a stochastic SIR epidemic model in which individuals may make infectious contacts in two ways, both within households and along the edges of a random graph describing additional social contacts. Heuristically motivated branching process approximations are described. In case the number of initially infective individuals stays small, a branching process approximation for the number of infectives is in force. The network is modelled by a random intersection graph.

Keywords: Epidemics, branching process, coupling, Local and global contacts, threshold parameters.

1. Introduction:

The population grouped into households, with infectious contacts at a given per-pair rate, where individuals also make global contacts along the edges of a random graph over the whole population. The early stages of the epidemic can be approximated by a suitable branching process. A coupling argument is used to make this approximation precise in the limit as $n \to \infty$. If the relation between the number of individuals and the number of groups is chosen appropriately, this leads to a graph where the amount of clustering can be tuned by adjusting the parameters of the model. The threshold parameter R_* thus provides a natural generalization of R_o to two levels of mixing, but we must emphasize that R_* is a group-to-group or more precisely clump-to-clump reproductive ratio: it is the expected number of clumps contacted by all individuals in the clump of a random individual. Moreover, this approximation can be made precise by considering a sequence of epidemics in which the number of groups $m \to \infty$. This enables us to determine a threshold parameter R_* for our epidemic, such that, in the limit as $m \to \infty$, global epidemics occur with nonzero probability if and only if $R_* > 1$. Here, a global epidemic is one which affects infinitely many groups as $m \to \infty$. The probability that a global epidemic occurs and various properties of nonglobal

epidemics. Suppose that the population comprises of n individuals located in one-dimensional space. Label the individuals sequentially 1 through n and, to avoid boundary problems it is convenient to take the space to be the circumference of a circle, so that individuals 1 and n are neighbours. The epidemic is initiated by a number of individuals becoming infected at time t = 0, with the remaining individuals all assumed to be susceptible.

2. Branching process approximation:

Let us consider a sequence (E_n) of such epidemics, indexed by the population size n, in which the n^{th} epidemic has initially 1 infective and n-1 susceptibles, with the initial infective being chosen uniformly from the n individuals in the population.

The approximating branching process is based not on infectives but on clumps of infectives. Let δ^n_{ijk} and δ_{ijk} (i, j, k, n = 1, 2,.) be independent random variables, where for each n = 1, 2,, the $\{\delta^n_{ijk}\}$'s are independent and identically distributed with $Pr(\delta^n_{ijk} = l) = v^n_l$ (l = -[(n – 1) / 2], - [(n – 1) / 2] + 1,, [n/2]) and the $\{\delta_{ijk}\}$'s are independent and identically distributed with Pr ($\delta^n_{ijk} = l$) = v_l ($l \in z$). Consider a sequence of independent and identically distributed epidemics C_i (i = 1, 2,) constructed as follows. For fixed i, consider a population of infinitely many individuals in one-dimensional space, where each individual has two neighbours, one on each side. Assume that there is an initial infective at the origin while the rest of the population is initially susceptible.

3. Forward process:

The threshold parameter $R_* = E[\hat{C}]$. Label the individuals in a household 0, 1,, n -1, with individual 0 the initial infective, and define X_i to be the indicator of the event that individual i is infected in the local epidemic and C_i to be the number of global neighbours with which i makes infectious contact, if I were to become infected. Then

$$\hat{C} = C_o + \sum_{i=1}^{n-1} Xi\ Ci. \qquad (3.1)$$

Since C_1 and X_1 are independent and (C_1, X_1), (C_2, X_2),.. (C_{n-1}, X_{n-1}) are identically distributed, that

$$R_* = E[C_o] + E[T]\ E[C_1],.. \qquad (3.2)$$

Where T is the final size of the within-household epidemic.

3. 1. 1. Zero or infinite infectious period:

Suppose that $\mathbb{P}(I = \infty) = 1 - \mathbb{P}(I = 0) = p$ for some $p \in [0.\ 1]$. For the moment we ignore the differences between the initial and subsequent generations and denote the generic offspring random variable by unadorned C.

$$C = \begin{cases} 0, with\ probability\ 1-p, \\ C_0 + \sum_{i=1}^{n-1} C_i\ , with\ probability\ p, \end{cases}$$

Where Ci is the number of global neighbours infected by an infectious individual i. Thus C_0 equality distributed in K_0 and C_1, C_2,, C_{n-1} are independent and identically distributed with

$C_i = \begin{cases} 0, with\ probability\ 1-p, \\ K_i, with\ probability\ p. \end{cases}$

Also note that the number N say, of the n -1 C_i's which take the value K_i. i. e. the number of initially susceptible individuals in the household with I = ∞ is binomially distributed, with parameters n -1 and p. Therefore,

$f_C(s) = \mathbb{E}[s^C] = (1-p)\, s^0 + p\, \mathbb{E}[s^{C_0 + \sum_{i=1}^{n-1} K_i}]$

$= 1 - p + p\mathbb{E}[s^{C_0}]\ \mathbb{E}[s^{\sum_{i=1}^{N} K_i}]$

$= 1 - p + p\ f_{K_0}(s)\ f_N(f_D(s))$

$= 1 - p + p\ f_{K_0}(s)\ (1 - p + p f_D(s))^{n-1}$, (3. 3)

Where K_o is D or d in the initial generation and $\check{D}$ -1 in subsequent generations.

3. 1. 2. Fixed infectious period:

Suppose that ℙ (I = c) = 1 for some c > 0. Again temporarily ignore the differences between the initial and subsequent generations, label the individuals 0, 1,, n-1 and denote by C_i the number of global neighbours infected by an infections individual i. Then, letting T denote the finial size of the within-household epidemic. $C = C_0 + \sum_{i=1}^{T} C_i$ and, conditional on the final size, C_1, C_2,., C_T are mututally independent. Now $C_i \mid K_i \sim$ Bin (K_i, 1 - $e^{-c\lambda_G}$).

So $f_{c_i}(s) = f_{k_i}(1\text{-}p_G + sp_G)$, where p_G = 1 - $e^{-c\lambda_G}$. Thus, by the usual formula for the probability generating functions of a random sum.

$f_C(s) = f_{C_0}(s)\ f_T(f_{c_1}(s)) = f_{k_0}(1 - p_G + sp_G)\ f_T(f_D(1 - p_G + sp_G))$ (3. 4)

Where again K_o is D or d in the initial generation and $\check{D}$ -1 in subsequent generations.

4. Backward processes:

The infectious period distribution and then the relevant Poisson processes, make a list of other individuals it would infect were it to be infected itself. The vertices represent individuals in the population and we put a directed arc from i to j when, were i to become infected, it would make infectious contact with j, if j is in i's list. The susceptibility set of individual i consists of those individuals from which there exists a path to in the digraph. Approximate the size of the susceptibility set of an individual chosen uniformly at random from the population by the total progeny of an appropriate branching process. Each individual j that joins the susceptibility set by virtue of a global contact is in a household not previously associated with the susceptibility set with high probability, the number of households in each generation is approximated well by the branching process.

5. The final outcome of the epidemic:

Let us consider an edge percolation process on the underlying graph, where each edge in the graph is independently removed with probability $1-p$ and kept with probability p. The vertices that belong to the component of the initial infective in the graph so obtained correspond to the individuals that have experienced the infection at the end of the epidemic. This observation might be useful investigating the final size of the

epidemic. If there is a unique giant component in the thinned graph. The outcome of the percolation process contains a unique cluster of order n – then the relative size of this component gives the probability of an outbreak of order n in the epidemic. Such an outbreak coincides with the probability of explosion in the branching process describing the initial stages of the epidemic.

Consider an arbitrary graph with n vertices and k = O (n) edges and assume that the clustering equals 1. This implies that all subgraphs are complete. Hence, with n_{max} denoting the size of the largest subgraph, It follows that $n_{max} \leq O(\sqrt{k}) = O(\sqrt{n})$, that is, the relative size of the largest component tends to zero.

6. Early stages-Threshold parameter:

Let T b e the final size of a local epidemic amongst n -1 initial susceptible, we find that

$R_* = E\,C_o + E\,C_1$

$= (\mu_{\check{D}-1} + \mu_T \mu_D)(1 - \phi(\lambda_G))$

$= (\mu D(\mu T + 1) + \frac{\sigma 2D}{\mu D} - 1)(1 - \phi(\lambda_G)),..$ (6. 1)

Since $E\check{D} = ED + Var\,D / ED..$ (6. 2)

Unless n is very small any analytical formula for μ_T is very complicated, so we evaluate this quantity numerically.

7. Analysis of forward process:

7. 1. 1. Threshold theorem for the epidemic $E^{(m)}$.

Threshold theorem for the epidemic to establish a bound for the size of the bad set of half-edges after k generations of the epidemic $E^{(m)}$. The number of half-edges in this set is bounded by $2\check{T}_{k+1}^{(m)}$.

Theorem 7. 1:

For k=1, 2.

(i) for all $\omega_1 \epsilon A_1$, $\lim_{n\to\infty} \mathbb{P}_{\omega_{(\omega_1)}}(\check{Z}^{(m)} = k) = \mathbb{P}(\hat{Y} = k)$;

(ii) $\lim_{m\to\infty} \mathbb{P}(\check{Z}^{(m)} = k) = \mathbb{P}(\hat{Y} = k)$.

Proof:

Fix $\omega_1 \epsilon A_1$ and let $\gamma^{(m)}$ be the number of households infected by $E^{(m)}$ before a bad half-edge is chosen. Fix $k \epsilon \mathbb{N}$. Then,

$\mathbb{P}_{D(\omega_1)}(\check{Z}^{(m)} = k) = \mathbb{P}_{D(\omega_1)}(\check{Z}^{(m)} = k, \gamma^{(m)} \leq k) + \mathbb{P}_{D(\omega_1)}(\check{Z}^{(m)} = k, \gamma^{(m)} > k)$. (7. 1)

Let $\mathcal{J}_l^{(m)}$ (l= 1, 2,) be the set of half-edges we should to avoid when choosing the lth household to spread the epidemic to. Then

$J_k^{(m)} = \left|\mathcal{J}_k^{(m)}\right| \leq 2\check{T}_k^{(m)}$ .. (7. 2)

So, $\mathbb{P}_{D(\omega_1)}(J_k^{(m)} \leq 2\log m) \geq \mathbb{P}_{D(\omega_1)}\check{T}_k^{(m)} \leq \log m) \to 1.$ (7. 3)

as m $\to\infty$. And g$(m) = k$, h$(m) = 2\log m$, $\lim_{m\to\infty}\mathbb{P}_{D(\omega_1)}(\gamma^{(m)} > k) = 1.$ (7. 4)

Therefore, $\lim_{m\to\infty}\mathbb{P}_{D(\omega_1)}(\check{Z}^{(m)} = k, \gamma^{(m)} \leq k) = 0.$ (7. 5)

and using equation (7. 1),

$\lim_{m\to\infty}\mathbb{P}_{D(\omega_1)}(\check{Z}^{(m)} = k) = \lim_{m\to\infty}\mathbb{P}_{D(\omega_1)}(\check{Z}^{(m)} = k, \gamma^{(m)} > k)$ (7. 6)

$= \lim_{m\to\infty}\mathbb{P}_{D(\omega_1)}(\hat{Y}^{(m)} = k, \gamma^{(m)} > k)$

$= \lim_{m\to\infty}\mathbb{P}_{D(\omega_1)}(\hat{Y}^{(m)} = k)$

$= \mathbb{p}(\hat{Y} = k),$ (7. 7)

Further,

$\lim_{m\to\infty}\mathbb{P}(\check{Z}^{(m)} = k) = \lim_{n\to\infty}\mathbb{E}[\mathbb{P}_D(\check{Z}^{(m)} = k)] = \mathbb{P}(\hat{Y} = k).$ (7. 8)

8. Analysis of backward process:

8. 1. 1. Lower bounding branching processes:

The generation wise growth of the susceptibility set of a typical individual that is susceptible at time t_m in the forward process, in order to find the asymptotic probability that such as individual is ultimately infected, given that major outbreak occurs. A branching process $\varepsilon^{X^{(m)}}$ which asymptotically bounds $S^{(m)}$ from below until the susceptibility set covers a proportion ε of the households in the population. An almost sure bound, the proportion of households that are neighbours of the susceptibility set when the size of the susceptibility set is at most εm.

9. Local infectious clumps and susceptibility sets:

Let G be the random directed graph on N in which for any ordered pair (i, j) of distinct individuals there is a directed arc from i to j if and only if i, if infected, contacts j locally. For i, j $\in$N, wirte i$\rightsquigarrow$j if and only if there is a chain of directed arcs from i to j in G, with the convention that i$\rightsquigarrow$i. For i$\in$N, define i's local infectious clump and susceptibility set by $\mathcal{C}i = \{j \in \mathrm{N} : \mathrm{i} \rightsquigarrow \mathrm{j}\}$. The set of individuals who ultimately would be infected by the epidemic if there is no global infection, (i. e. λ_G = 0) and only individual i is initially infected. In household model, if λ_L and n are held fixed as m varies, then the distribution of C_i, S_i, and A_i are each invariant to N.

10. Threshold Behaviour:

Suppose that the C_i (i $\in$N) are each identically distributed. Let C, S and A be distributed according to C_1, S_1 and A_1, respectively. Suppose also that P (i$\rightsquigarrow$j) = P (j$\rightsquigarrow$i) (i, j $\in$ N). A sufficient condition for this is $\lambda^L_{ij} = \lambda^L_{ij}$ (i, j $\in$N).

Consider an epidemic initiated by a small number of infectives in a large population. Suppose that P(C < ∞) = 1. Each global infection initiates a new local infectious clump. During the early stages of the epidemic, the probability that these clumps intersect is very small, zero in the limit as N $\to\infty$. Thus, the process of

infected clumps can be approximated by a branching process, in which the offspring of a given clump are the global contacts. Let R be the total number of global contacts emanating from a typical clump. Since infectious individuals make global contacts independently at the points of Poisson processes with rate λ_G, R follows a Poisson distribution with random mean $\lambda_G A$. A global epidemic occurs if in the limit as $N \to \infty$ the epidemic infects infinitely many individuals. Thus, a global epidemic occurs if and only if the branching process does not go extinct.

11. Vaccination strategies in relation to local thresholds:

In a homogeneously mixing population, the minimum proportion v that to vaccinate to render the remaining susceptible population sub-threshold is given by $R'_G = (1 - v) R_G = 1$, that is we require $v \leq 1 - 1 / R_G$. The two levels of mixing, the basic reproductive ratio is $R_* = {}_{\mu}R_G$. For a population divided into large groups, R_* can take large values, since μ will be significant proportion of group size.

For the groups or households model, one strategy is to vaccinate whole groups. Let us assume for simplicity that if they are of different sizes, we choose groups at random, that is, according to the distribution $\{\pi_k\}$. Then μ will be unchanged, so that the overall reproductive ratio will simply become $R'_* = (1 - v) R_*$.

12. Final outcome of the epidemic process E_n:

Suppose that the epidemic process E_n is initiated by exposing the population to T^n_o units of global infectious pressure. The local epidemics created by individuals who succumb to T^n_o units of global infectious pressure will give rise to $A_n(T^n_o)$ further units of global infectious pressure. For k = 0, 1,., let $T^n_{k+1} = T^n_o + A_n (T^n_k)$. Thus T^n_1 is the total amount of infectious pressure that has been generated in the population after the local epidemics initiated by the initial T^n_o units of infectious pressure have occurred. These T^n_1 units of infectious pressure may infect further individuals globally leading to further local epidemics, after which there will have been a total of T^n_2 units of infecstious pressure generated in the population. The process continues until the additional infectious pressure generated by a set of local epidemics is insufficient to infect further individuals globally. Then $k_* = \min \{k: T^n_k+1 = T^n_k \}$ is well defined. Since the population is finite. Let $T^n_\infty = T^n_{k*..}$ Tn∞ represents the severity of the epidemic En and $R_n (T^n_\infty)$ its final size. Note that T^n_∞ satistifes $T^n_\infty = \min \{ t \geq 0: t = T^n_o + A_n (t) \}$.

13. Susceptibility sets and final size:

Susceptibility set size is again important in determining the mean final size of a major outbreak. We can construct the susceptibility set of an individual by generations in a manner similar to our analysis of the early stages of the epidemic. This leads to a branching process aproximation for the size of an individual's susceptibility set in the limit as $m \to \infty$. The offspring distribution for this branching process is the same as

the distribution of the number of individuals that make global contact with the members of a given individual's local susceptibility set.

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