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Stochastic Epidemic in Large Communities

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Abstract:

We discuss in detail about SIR epidemic model in large population. The main insight from such large population approximates is the threshold limit theorem. The theorem states that as $n \to \infty$ one of two possible scenarios can occur, only few individuals will become infected or else a more or less deterministic positive proportion of the susceptible of smaller order, will have been infected by the end of the epidemic. The latter scenario is referred to as a large or major outbreak. The important task is to find out for which parameter values the asymptotic Probability of a major outbreak is 0. The parameter R_o called the basic reproduction number plays a crucial role in this context. The parameter R_o a function of the model, is the average number of new infections caused by a typical infective during the early stages of the epidemic. We discuss in detail about the basic reproduction number R_o in this paper.

Keywords: Basic reproduction number, Branching process, poisson Process.

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Introduction:

The main advantage of deterministic models lies in their simpler analysis. For a stochastic epidemic model to be mathematically manageable it has to be quite simple.

Deterministic models can be more complex, yet still possible to analyze, at least when numerical solutions are adequate.

Stochastic models are to be preferred when this analysis is possible since the most natural way to describe the spread of disease is stochastic. For example in a large community many models will lead either to a miner out break infecting more or less deterministic proportion of the community. To calculate the probability of the two events is only possible in a stochastic setting. Further when considering extinction of endemic diseases this can only be analyzed with stochastic models, since extinction occurs when the epidemic process deviates from the expected level. Knowledge about uncertainty in estimates requires a stochastic model.

So we, prefer stochastic models when their analysis is possible otherwise deterministic models should be used.

The Reed – Frost model:

We shall consider simplest epidemic model for the spread of an infectious disease say the common cold in a small group of individuals. This model is called the Reed – Frost. The model is an SIR epidemic model which means that individuals are at first susceptible to the disease. If an individual becomes infected he/she will first be infectious and called an infective for some time and then recover and become immune a state called removed.

The model is usually specified using discrete time scenario it is natural to think of the infections period as being short and preceded by a longer latent period. Then new infections will occur in generations, these generations being separated by the latent period as the discrete time unit. The event probabilities in a given generation depend only on the state of the epidemic in the previous generation and these events are specified by certain binomial probabilities. If we let X_j and Y_j denote the number of susceptible and infective respectively at time j, the chain – binomial Reed – Frost model has conditional probabilities.

$$P\ Y_{j+1} = y_{j+1} \mid X_0 = x_0, Y_0 = y_0, \ldots X_j = x_j, \mathrm{Y}_j = y_j$$

$$= P\ Y_{j+1} = y_{j+1} \mid X_j = x_j, Y_j = y_j$$

$$= \begin{pmatrix} x_j \\ y_{j+1} \end{pmatrix} \ 1 - q^{y_j \quad y_{j+1}} \quad q^{y_j \quad x_j - y_{j+1}}$$

and $X_{j+1} = X_j - Y_{j+1}$. This means that a given susceptible of generation j remains susceptible in the next generation if she escapes infective from all infective of generations j; these events are independent each occurring with probability q. Further different susceptible in a given generation become infected independently of one another and infectious individuals are removed in the next generation. Given the initial state $X_0 = n$ and $Y_0 = m$ the probability of the complete chain $y_1, \ldots . y_k, y_{k+1} = 0$ is obtained by conditioning sequentially and using the Markov property of the chain. If we let $x_{j+1} = x_j - y_{j+1}$ we have

$$P\ Y_1 = y_1,....Y_k = y_k, Y_{k+1} = 0 \mid X_0 = n, Y_0 = m$$
$$= P\ Y_1 = y_1 \mid X_0 = n, Y_0 = m\ \times .....\times P\ Y_{k+1} = 0 \mid X_k = x_k, Y_k = y_k$$
$$= \binom{n}{y_1} 1-q^{m\ \ y_1}\ \ q^{m\ \ n-y_1} \times ....\times \binom{x_k}{0} 1-q^{y_k\ \ 0}\ \ q^{y_k\ \ x_k}$$

From the mathematical point of view , the Spread of the disease does not have to occur in generations.

The necessary assumption is that each individuals who becomes infected has infectious contact with any other given individual with probability $p = 1-q$, and all such contacts occur independently. We shall use the formula $Z = \sum_{j\geq 1} Y_j$ to compute the total number of infected individuals. The quantity Z is also known as the final size of the epidemic.

To compute $P\ Z = z \mid X_0 = n, Y_0 = m$ we sum the probabilities of all chains for which $|\,y\,| = \sum_{j\geq 1} y_j = z$. From the defining equations it is seen that $Y_j = 0$ implies that $Y_{j+1} = 0$. Hence we know that the new infections may only occur whenever some individuals are infectious. So we include that the length of a chain cannot be longer than the total number infected, making the number of possible chains finite. The probability function for the final number of infected is given by

$$P\ Z = z \mid X_0 = n, Y_0 = m\ = \sum_{y=|y|=z} P\ Y_1 = y_1,...,Y_k = y_k, Y_{k+1} = 0 \mid X_0 = n, Y_0 = m$$

We calculate the probability function explicitly for Z in the following way. The final number infected among those initially susceptible when $Y_0 = m = 1$ and $X_0 = n = 1,2$ and 3.

We start with n = 1

$$P\ Z = 0 \mid X_0 = 1\ = P\ Y_1 = 0 \mid \mathrm{X}_0 = 1\ = q,$$
$$P\ Z = 1 \mid X_0 = 1\ = P\ Y_1 = 1, Y_2 = 0 \mid X_0 = 1\ = p$$

For n = 2, we have

$$P\ Z = 0 \mid X_0 = 2\ = P\ Y_1 = 0 \mid X_0 = 2\ = q^2$$
$$P\ Z = 1 \mid X_0 = 2\ = P\ Y_1 = 1, Y_2 = 0 \mid X_0 = 2\ = \binom{2}{1} pq \times q$$
$$P\ Z = 2 \mid X_0 = 2\ = P\ Y_1 = 2, Y_2 = 0 \mid X_0 = 2\ + P\ Y_1 = 1, Y_2 = 1, \mathrm{Y}_3 = 0 \mid X_0 = 2$$
$$= p^2 + \binom{2}{1} pq \times p$$

For n =3, we compute only the first three probabilities the final probability may be derived from the complement

$$P\ Z = 1 \mid X_0 = 3\ = P\ Y_1 = 1, Y_2 = 0 \mid X_0 = 3\ = \binom{3}{1} pq^2 \times q^2$$

$$P\ Z=2\mid X_0=3\ =P\ Y_1=2,Y_2=0\mid X_0=3\ +P\ Y_1=1,Y_2=1,Y_3=0\mid X_0=3$$
$$=\binom{3}{2}P^2q\times q^2+\binom{3}{1}pq^2\times\binom{2}{1}pq\times q$$

Stochastic Epidemic in Large Communities:

Theorem:

Consider a sequence of epidemic processes $E_{n,m_n}\ \lambda,I$. Assume that $m_n=m\ for\ all\ n$ and define τ as the nontrivial solutions to $1-e^{-\lambda_i\tau}=\tau$. Also denote the final epidemic size by Z_n and write $Z_n^{'}=Z_n+m$.

If $\lambda\imath\le 1 then\ Z_n\to Z$ almost surely, where $P\ Z<\infty\ =1 and\ Z$ is the total progeny in a continuous time branching process $E_m\ \lambda,I$ initialed by m ancestors in which individuals give birth at the rate λ during a lifetime distributed according to I.

If $\lambda\imath>1$ then Z_n still averages to Z , but now $P\ Z<\infty\ =q^m\ where\ q^m$ is the extinction probability of the branching process. With probability $1-q^m$, the sequence $\sqrt{n}\ \ Z_n^{'}/\ n-\tau$ averages to a normally distributed random variable with mean 0 and variance.

$$(\rho\ 1-\rho\ +\lambda^2\sigma^2\tau\rho^2)/\ 1-\lambda\imath\rho\ ^2\quad where\ \rho=1-\tau$$

From the theorem it follows in particular that in the case where $R_0>1$, ($R_0\ is\ given\ by\ \lambda\imath$) the final size proportion Z_n/n converges in distribution to a random variable with mass q^m at the point 0 and mass $1-q^m$ at the point τ . The theorem states that the distribution of the major outbreak sizes should be approximately Gaussian with mean $n\tau$ = 583 and standard deviation $\sqrt{3.139n}$ $\approx$ 56. Suppose n = 1000 m = 1 we have the above result.

The above theorem states that a major outbreak is large population is possible if and only if $R_o > 1$. Where R_o is called the basic reproduction number.

Standard SIR epidemic Model:

We consider a simple model for the spread of an infectious disease. In particular, the population is assumed to be closed, homogeneous and homogeneously mixing. Also the effects of latent periods, change in behavior, time varying infectivity and temporary or partial immunity are not taken in to account.

We assume that initially there are m infectious individuals and n susceptible individuals. The infections periods of different infective are independent and identically distributed according to some random variable I having an arbitrary but specified distributions. During her infections period an infective makes contact with a given individual at the time points of a time homogeneous Poisson process with

intensity λ/n. If a contacted individual is still susceptible, then she becomes infectious and is immediately able to infect other individuals. An individual is considered removed once her infectious period has terminated and is then immune to new infections, playing no further part in the epidemic spread. The epidemic ceases as soon as there are no more infectious individual present in the population. All Poisson processes are assumed to be independent of each other; they are also independent of the infectious periods.

We call this model the standard SIR epidemic model, the letters S, I, R standing for the terms susceptible, infections and removed respectively. We denote the process by $E_{n,m}(\lambda, I)$. Also denote the mean and the variance of the infections period I by ι and σ^2 respectively the rate of containing a given individual is set to λ/n in order to keep the rate at which a given infective makes contact with other individuals constant (=λ) independent of the population size. The final size of the epidemic Z is simply defined as the number of initially susceptible individuals that ultimately became infected. Thus Z is a finite random variable taking values between o and n. We shall derive a triangular linear system of equations for $P^n = P_0^n, P_1^n, ..., P_n^n$ *where* P_k^n is the probability that k of the initial susceptible are ultimately infected.

Let Z be the final size of the epidemic, and let $A = A(\infty) = (\lambda / n)\int_0^\infty Y(u)du$

be the total pressure of the epidemic. Both the final size and the total pressure can be expressed in terms of the infections periods and the individual thresholds.

First

$$Z = \min\left\{ i : Q_{i+1} > \lambda / n \sum_{j=-m-1}^{i} I_j \right\}$$

where $Q_{(1)}$, $Q_{(2)}$, …. $Q_{(n)}$ are the order statistics of Q_1, Q_2,….. Q_n since the epidemic stops as soon as the infection pressure generated by the previously infected individuals is insufficient to infect any more susceptible. Also

$$A = \lambda / n \sum_{j=-m-1}^{z} I_j$$

, which is just another way of writing A (∞)

Hence it is clear that the final size and the total pressure are intimately related.

Lemma

Consider the standard SIR epidemic $E_{n,m}$ λ, I and let A be as above

Then $E\left[e^{-\theta A} / \phi \ \lambda\theta / n \ ^{z+m} \right] = 1$

, $\theta \geq 0$ where ∅ (o) = E [exp (-θI)] is the Laplace transform of I.

Proof:

To prove the identity, we note that

$$\phi\ \lambda\theta/n\ ^{n+m} = E\left[\exp\left((-\lambda\theta/n)\sum_{j=-\ m-1}^{n} I_j\right)\right]$$

$$= E\left[\exp\left(-\theta\left(A+\ \lambda/n\ \sum_{j=z+1}^{n} I_j\right)\right)\right]$$

$$= E\left[e^{-\theta A}\ \phi\ \lambda\theta/n\ ^{n-z}\right]$$

Where the last identity follows since the variable $I_{i,j} \geq Z+1$ are both independent of both Z and A.

We are now in a position to derive the system of equations for $P^n = P_0^n, ...P_n^n$ For each k ≥ 1, define k to be the set { 1, 2,… k}; also let o be the empty set. The initial susceptible are labeled 1, 2,…n. P_k^n is the probability that k initial susceptible are infected in the $E_{n,m}\ \lambda, I$ epidemic and P_k^n is the probability at precisely the set k is infected.

By symmetry $P_k^n = \binom{n}{k} P_k^n$ Now fix k and choose l such that 0≤ k ≤ l ≤ n,

Implying $K \subseteq L \subseteq N$. We use the notation of infection pressure to compare an epidemic within N with a sub-epidemic within L. The event that an epidemic within N infects presently the set K is the same as the event that a sub-epidemic within L infects precisely K and that these k new infective, together with the m initial infective, fail to infect any of the individual s in the set N \L. We know from the sellke construction that the probability of avoiding the infection is given by exp (-a), given that the sub-epidemic has generated the infection pressure $A^l = a$. It follows that

$$P_K^n = P_K^l E\left[\exp\ -A^l\ \ n-l\ \ |Z^l = k\right] \textit{ where } Z^l \textit{ is the final size of the sub-epidemic.}$$

This equation is equivalent to

$$\binom{l}{k} P_k^n / \binom{n}{k} = P_k^l E\left[\exp\ -A^l\ \ n-l\ \ |z^l = k\ \right]\ \rightarrow\ 1$$

Now let us use the wald's identity applied to the sub-epidemic and with $\theta = n-l$ to get

$$E\left[e^{-A^l\ n-l}\ /\left[\phi\ \lambda\ \ n-l\ \ /n\ \right]^{z^l+m}\right] = 1$$

or conditioning on the final size z^l

$$\sum_{k=0}^{l} P_k^l E\left[\exp\ -A^l\ \ n-l\ \ |z^l = k\right]\ /\left[\phi\ \lambda\ \ n-l\ \ /n\ \right]^{k+m} = 1 \rightarrow\ 2$$

Equations (1) and (2) immediately give us

$$\sum_{k=0}^{l}\left(\binom{l}{k}P_k^n \Big/ \binom{n}{k}\left[\phi\ \lambda\ n-l\ /n\ \right]^{k+m}\right)=1$$

Finally noting that $\binom{l}{k}/\binom{n}{k}=\binom{n-k}{l-k}/\binom{n}{l}$

We arrive at the following result

Consider the standard SIR epidemic $E_{n,m}\ \lambda, I$ .Denote by P_k^n the probability that the final size of the epidemic is equal to k, $0 \le k \le n$. Then we have

$$\sum_{k=0}^{l}\binom{n-k}{l-k}P_k^n \Big/ \left[\phi\ \lambda\ n-l\ /n\ \right]^{k+m}=\binom{n}{l}\ ,0\le l\le n.$$

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