Advances in Applied Mathematical Biosciences.
ISSN 2248-9983 Volume 5, Number 1 (2014), pp. 27-33

http://www.irphouse.com

Stochastic Model for the Spread of an Epidemic around a Circle

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Abstract

Let us consider a Stochastic model for the spread of an epidemic among a population of n individuals that are equally spaced around a circle. Throughout its infectious period, a typical infective, i say, makes global contacts, with individuals chosen independently and uniformly from the whole population, and local contacts with individuals chosen independently and uniformly according to a contact distribution centered on i. The great circle model, in which individuals are equally spaced on a circle and local contacts are nearest-neighbour.

Keywords Epidemic process, local and global mixing, random graph, Poisson convergence, Branching process.

1. Introduction

The great circle model is considered and an informal argument given for its threshold behaviour. A formal threshold theorem and the mean final size of an epidemic that takes off in the limit as the population size $n\to\infty$. 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, that individuals 1 and n are neighbours. Assign to each individual independent and identically distributed life histories. $\mathcal{H} = (Q, \eta^G, \eta^L)$, where Q is the infectious period and η^G and η^L are point processes of times, relative to an individual's infection, at which global and local infectious are made. Each global contact is with an individual chosen independently and uniformly from the initial n individuals in the population.

2. Branching Process

Let us consider a sequence (En) 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 epidemics and associated global contact processes, (C_i, ξ_i) (i=1, 2), can be used to construct a realization of a general branching process. Let $0 < s_2 \leq s_3 \leq$. denote the times of births in the branching process. Let (D_2, J_2, ξ_2), (D_3, J_3, ξ_3),. denote the successive histories of individuals born into the branching process.

Thus individuals in the branching process are labeled in the order in which they are born, with the label 1 being attached to the initial ancestor. The i^{th} individual in the branching process has lifetime D_i and reproduces fat the points of ξ_i. The J_i's play no role in the branching process, but are instrumental in coupling the epidemic process to the branching process.

3. Great Circle Model

The great circle consists of alternating runs of susceptible and infected individuals, which from an alternating renewal process.

In the great circle model, the population is assumed to the equally spaced around a circle. During infectious period, a typical infective contacts any given susceptible that is located next to it on the circle at rate λ_L. It contacts any given susceptible in the whole population at rate λ_G/N. Thus the individual to individual infection rate for neighbouring and non-neighbouring individuals are λ_L+λ_G/N and λ_G/N respectively.

Households model, the population partitioned into m households, each of size n, so N=mn. The overlapping groups model the population into m_α households, each of size n_α, and also into m_β workplaces, each of size n_β, So N = $m_\alpha n_\alpha$ = $m_\beta n_\beta$, for each n≥1, the epidemic E_n is among n individuals located in one-dimensional space. Let us Consider the case where each individual has one neighbor one each side, so avoid boundary problems, it is convenient to take the space to the circumference of a circle.

The individuals are numbered sequentially around a circle 1 through n. So that individuals 1 and n are neighbours. Each local contact is with an individual chosen independently form a distribution

$$\{\omega_i^n;\ i = -\left[\frac{n-1}{2}\right], -\left[\frac{n-1}{2}\right]+1 .. \left[\frac{n}{2}\right]\} .. \qquad (3.\ 1.\ 1)$$

Where ω_i^n is the probability individual k on making a local infectious contact, so with individual $(k+i)_{\text{mod n}}$. So v_k, $(k+i)_{\text{mod n}} = \omega_i^n$.

Suppose that $\lim_{n\to\infty} \omega_i^n = \omega_i$ ($i\epsilon\mathbb{Z}$), where $\{\omega_i;\ i\epsilon\mathbb{Z}\}$ is a proper distribution with ω_0=0 for n=1, 2,., $\omega_i^n \geq \omega_i$(i=-$\left[\frac{n-1}{2}\right]$, -$\left[\frac{n-1}{2}\right]+1 .. \left[\frac{n}{2}\right]$) with $\omega_0^n = 0$. Therefore, for all $1 \leq i \leq n$,

$$P(|s_i^n| = 1) = .\ \Pi_j^{[n/2]} = -[(n-1)/2]^{\phi(}\omega_j^n\ \lambda_L^{n)} ... \qquad (3.\ 1.\ 2)$$

Theorem 3. 1.
Suppose that there exist $\alpha>0$, $0<\delta<\frac{1}{2}$ and $b>0$ such that $\lambda_L^n n^{-\alpha}\to 0$, $n^{\delta} P(|s_i^n|=1)\to\infty$ and $\lambda_G^n E[Q] - \log(h_n P|s_i^n|=1) + \log b \to 0$ as $n\to\infty$. Suppose also that there exist $\gamma\geq 0$ and $\rho > \frac{\delta+\alpha}{1+\gamma} + 2\delta$ such that $\gamma > \delta+\alpha-1$, $\sum_{i\in\mathbb{Z}}|i|^{1+\gamma}\omega_i<\infty$ and $h_n n^{-\rho}\to\infty$ as $n\to\infty$. Then $S_n \xrightarrow{D} Po(b)$ as $n\to\infty$.

Proof.
If $P(|s_i^n|=1) =. \Pi_L{}^{[n/2]} = -[(n-1)/2]^{\phi}(\omega^n, \lambda_L^n)$ $(1\leq i\leq n)$. So, $g(n) = P(|s_i^n|=1)$. Fix ε and c such that $\frac{\delta+\alpha}{1+\gamma} < \frac{\varepsilon}{1+\gamma} < c < \rho-2\delta$ and, for $1\leq i\leq n$.. Let $L_i^n = \{j \in \mathbb{N}: j \leq n$ and $-\frac{1}{10}n^c < (j-1)_{modn} < \frac{1}{10}n^c\}$. Then, for $n\geq 1$, $|L_i^n| \leq \frac{1}{3}n^c$ $(1\leq i\leq n)$.

For $n\geq 1$, $\omega_l^n \leq \omega_l$ $(l = -\left[\frac{n-1}{2}\right], -\left[\frac{n-1}{2}\right]+1.. \left[\frac{n}{2}\right])$. Thus for $1\leq i\leq n$.

$$\sum_{j\notin L_i^n} v_{i,j}^n = \sum_{|l|\geq\frac{n^c}{10}} \omega_l^n = 1-\sum_{|l|<\frac{n^c}{10}} \omega_l^n .. \quad (3.1.3)$$

$$\leq 1-\sum_{|l|<\frac{n^c}{10}} \omega_l . \quad (3.1.4)$$

$$= \sum_{|l|\geq\frac{n^c}{10}} \omega_l . \quad (3.1.5)$$

Now $\sum_{|l|\geq\frac{n^c}{10}} \omega_l < n^{-\varepsilon}$ for all sufficiently large n, since otherwise

$$\sum_{i\in\mathbb{Z}}|i|^{1+\gamma}\omega_i \geq \sum_{|i|\frac{n^c}{10}}|i|^{1+\gamma}\omega_i .. \quad (3.1.6)$$

$$\geq \frac{1}{10^{1+\gamma}} n^{c(1+\gamma)} \sum_{|i|\geq\frac{n^c}{10}} \omega_i .. \quad (3.1.7)$$

$$\geq \frac{1}{10^{1+\gamma}} n^{c(1+\gamma)-\varepsilon..} ..... \quad (3.1.8)$$

For arbitrarily large n, which contradicts $\sum_{i\in\mathbb{Z}}|i|^{1+\gamma}\omega_i < \infty$. Since $c(1+\gamma)-\varepsilon > 0$.

Thus, $\sum_{j\notin L_n^i} v_{i,j}^n < n^{-\varepsilon}$ for all sufficiently large n.

Further, $\sum_{j\notin L_n^i} v_{j,i}^n = \sum_{j\notin L_n^i} v_{i,j}^n$ by the symmetry of the great circle model. So, $\sum_{j\notin L_n^i} v_{j,i}^n < n^{-\varepsilon}$ for all sufficiently large n. Since, $c + 2\delta < \rho$, $h_n n^{-(c+2\delta)}\to\infty$ as $n\to\infty$.

4. The model with a general infectious period

Let the population consist of N individuals subdivided into m groups each of size n. The infectious periods of different infectives are independently and identically distributed according to a random variable T_1. Throughout its infectious period a given infective makes contact with each other susceptible in the population at the points of a homogeneous Poisson process having rate λ_G/N and, additionally with each susceptible in its own group at the points of a homogeneous Poisson process having rate λ_L. All the Poisson process describing infectious contacts, the random variables describing infectious periods, are assumed to be mutually independent. The great circle model where the population is not partitioned into groups.

5. Markov chain representation of the epidemic

A change of time scale and let us define a new artificial time t, t =1, 2, as the cumulative members of removals in the course of real time. Put $X_n(0)$ =n and for t≥1. Let $X_n(t)$ denote the number of individuals that escape infectious contacts with the first t infectives removed. For t≥1, let D_i be the length of the infectious period of the i^{th} infective removed, and denoted by $Z_{n,\,i}$ (t), 1 ≤i ≤ n.

$X_n(t) = \sum_{i=1}^{Xn(t-1)} Zn$, i (t), t≥1. (5. 1. 1)

Moreover, for t≥1 each vector $Z_n(t) = \{Z_{n,\,i}\ (t),\ 1 \le i \le n\}$ is a family of n exchangeable variables having mixed Bernoulli distributions with random parameter $Q_{n,\,t} = \exp(-\beta_n D_t)$.

$X_n(t) = d\mathcal{MB}(X_n\ (t\text{-}1), Q_{n,\,t})$, t≥1. (5. 1. 2)

Where $\mathcal{MB}$ denotes the mixed binomial. All the vectors $Z_n(t)$ are independent and all the $Q_{n,\,t}$'s are infected individuals and distributed as the variable $Q_n = \exp(\beta_n D)$. Let $I_n(t)$ denote the number of infected individuals. We have,

$T + X_n(t) + I_n(t) = n + m_n$, t≥1. (5. 1. 3)

T_n as the first time when there are no more infectives.

$T_n = \inf \{t: t + X_n(t) = n + m_n\}$. (5. 1. 4)

6. Final outcome of the epidemic process E_n

Suppose that the epidemic process E_n is initiated by exposing the population to T_0^n units of global infectious pressure. The local epidemics created by individuals who succumb to T_0^n units of global infectious pressure will be rise to $A_n(T_0^n)$ further units of global infectious pressure. For k = 0, 1,, let $T_{k+1}^n = T_0^n + A_n(T_k^n)$. Thus T_1^n is the total amount of infectious pressure that has been generated in the population after the local epidemics initiated by the initial T_0^n units of infectious pressure have occured. These T_1^n units of infectious pressure may infect further individuals globally leading to further local epidemics, after which there will have been a total of T_2^n units of infectious 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 $\{ k: T_{k+1}^n = T_k^n\}$ is well defined since the population is finite. Let $T_\infty^n = T_{k^*}^n$. Then T_∞^n represents the severity of the epidemic E_n and $R_n(T_\infty^n)$ its final size. Note that T_∞^n satisfies

$T_\infty^n = \min\{t \ge 0; t = T_0^n + A_n(t)\}$.. (6. 1. 1)

Lemma 6. 1.

Suppose that there exist γ>2 and δ>6/(γ-2) such that $\sum_{i\in\mathbb{Z}}|i|^{2+\gamma} v_i < \infty$ and $E[Q^{4+2\delta}] < \infty$. Then the epidemic process E_∞ is α-mixing. Furthermore, $\alpha_k(k \ge 1)$ can be chosen so that $D_\delta < \infty$.

Proof.

Let us consider fixed m, k ≥ 1, t ϵ $\mathbb{R}^m$ and α, β ϵ $\mathbb{R}$. For a $\epsilon\mathbb{Z}$, let$R_{a,k}$ ($L_{a,k}$) denote the furthest individual to the right(left) that is infected by the local epidemic having as initial infectives all individuals ≤ a + [(k+1)/2] (≥ a + [k/2] + 1).

Let $B_{a,k}$ = {$R_{a,k}$ ≥ a + k} ∪ {$L_{a,k}$ ≤ a}. Let $A_1 \in \mathcal{M}_{-\infty}^{a}$(t). Given $B_{a,k}^{c}$, A_2 is conditionally independent of A_1, i. e. $P_r(A_2 \mid B_{a,k}^{c})$.

Thus,

|Pr (A_1, A_2) – Pr (A_1) Pr (A_2)| (6. 1. 2)

= | Pr (A_1, A_2, $B_{a,k}^{c}$)(Pr ($B_{a,k}^{c}$)) + Pr (A_1, A_2, $B_{a,k}$)

-(Pr (A_1, $B_{a,k}^{c}$) + Pr (A_1, $B_{a,k}$)) (Pr(A_2, $B_{a,k}^{c}$)+ Pr(A_2, $B_{a,k}$))|. (6. 1. 3)

≤ | Pr (A_1, A_2, $B_{a,k}^{c}$) Pr ($B_{a,k}^{c}$)-Pr (A_1, $B_{a,k}^{c}$) Pr(A_2, $B_{a,k}^{c}$) | + 5 Pr($B_{a,k}$) (6. 1. 4)

= 5 Pr($B_{a,k}$).. (6. 1. 5)

Let R_0 (-L_0) be the furthest individual to the right(left) that is infected by the local epidemic in which the initial infectives are {i∈ $\mathbb{Z}$: i ≤ 0}). It shows that E[$R_0^{1+\gamma}$] < ∞, since $\sum_{i\in\mathbb{Z}}|i|^{2+\gamma} v_i < \infty$. Thus using Markov's inequality,

Pr($R_{a,k}$ ≥ a + k) = Pr($R_0 \geq [\frac{k}{2}]$) ≤ $[\frac{k}{2}]^{-(1+\gamma)}$ E[$R_0^{1+\gamma}$]. (6. 1. 6)

A similar argument shows that Pr($L_{a,k}$ ≤ a) ≤ $[\frac{k}{2}]^{-(1+\gamma)}$ E[$L_0^{1+\gamma}$], where E[$L_0^{1+\gamma}$] < ∞.

Now, Pr($B_{a,k}$) ≤ Pr($R_{a,k}$ ≥ a + k) + Pr($L_{a,k}$ ≤ a). So, |Pr (A_1, A_2) – Pr (A_1) Pr (A_2)| ≤ α_k, where α_k= $5[{}^{k}/_{2}]^{-(1+\gamma)}$(E[$R_0^{1+\gamma}$]. + E[$L_0^{1+\gamma}$]). (6. 1. 7)

Clearly, the epidemic is α-mixing, since $\alpha_k \to 0$ as k →∞. Moreover, since γ>2 and δ >6/(γ-2). Then, $D_\delta < \infty$.

7. Poisson Convergence

Poisson Limit theorem for $S_n(\infty)$ may be directly translated in terms of $X_n(T_n)$. This is equivalent to a Poisson limit theorem for $X_n(n+m_n)$ with the condition that {$S_n(\infty)$} is bounded in probability. Observe that $X_n(T_n) \geq X_n(n+m_n)$.

Lemma 7. 1.

For any α$\epsilon\mathbb{N}$ P [S_n (∞) ≠ X_n (n + m_n)] ≤ P [S_n (∞) > $\boldsymbol{a}$] + $\boldsymbol{a^2}$ [1 – E (Q_n)].

PROOF.

For $\boldsymbol{a}$ ∈$\mathbb{N}$,

P [S_n (∞) ≠ X_n (n + m_n)]

≤ P [S_n (∞) > $\boldsymbol{a}$] + P [S_n (∞) ≤ $\boldsymbol{a}$; Sn (∞) ≠ X_n (n + m_n)]

= P [S_n (∞) > $\boldsymbol{a}$]

+ $\sum_{k=1}^{a}$ $P[Xn\ (Tn)$ = k] P[X_n (n + mn) ≠ k | X_n (T_n) = k]. (7. 1. 1)

Let $T_n = n + m_n - k$, The process $\{ X_n (t), t \geq 0 \}$ is a decreasing Markov chain with,

$X_n (t) = {}_d \mathcal{MB} (n, \prod_{S=1}^{t} Q_n, S), t \geq 1..$ (7. 1. 2)

AT time T_n, the state $X_n (T_n)$ has the same law as the variable $S_n (\infty)$ for $t > \zeta \geq 0$,

$P[X_n (t) \neq k \mid X_n (t - \zeta) = k] = 1 - P[X_n (t) = k \mid X_n (t - \zeta) = k]$ (7. 1. 3)

$= 1 - P[\mathcal{MB} (k, \prod_{S=t-\zeta+1}^{t} Q_n, S) = k]$ (7. 1. 4)

$= 1 - [E(Q^k_n)]^{\zeta.}$ (7. 1. 5)

$\leq k \zeta[1 - E(Q_n)]..$ (7. 1. 6)

Using equation (7. 1. 7)

$P[S_n (\infty) \neq X_n (n + m_n)] \leq P [S_n (\infty) > \boldsymbol{a}] + [1 - E (Q_n)] \sum_{k=1}^{a} k2 \; P [X_n (T_n) = k]$

7. 2. 1Threshold behaviour

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

Let us consider an epidemic initiated by a small number of infectives in a large population. Suppose that $P (C < \infty) = 1$. 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. Thus the process of infected clumps can be approximated by a branching process. Let R be the total number of global contactsindependently 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 $N \rightarrow \infty$, the epidemic infects infinitely many individuals. Thus a global epidemic occurs if and only if the branching process does not go extinct.

Let $R_* = E[R]$ and $f_R (S) = E[S^R]$ be respectively the mean and probability generating function of the offspring distribution of the branching process.

Then,

$R_* = E[E [R|A]] = \lambda_G E[A] = \lambda_G E[A] = \lambda_G E[C] E[T_1].$ (7. 2. 2)

and

$f_R(S) = E[S^R] = E [E[S^R \mid A]] = E[\exp (-\lambda_G A (1 - S))].$ (7. 2. 3)

Since conditional upon A, R has a Poisson distribution with mean $\lambda_G A$. Thus,

$f_R(S) = \psi (\lambda_G (1 - S) (S \in [0, 1])...$ (7. 2. 4)

where $\psi(\theta) = E [\exp(-\theta A)]$ $(\theta \geq 0)$ is the moment generating function of A. A global epidemic occurs with non-zero probability if and only if $R_* > 1$, and if the epidemic is initiated by a single infective, the probability that a global epidemic occurs is $1 - p$, where p is the smallest root of $f_R(S) = S$ in $[0, 1]$.

7. 3. 1. Poisson Approximation for Survivors of the Epidemic

Let $\psi_i^n (t) = 1$ if individuals i's Susceptibility set avoids global infection from the first

t infectives in a population of size n and ψ_i^n (t) = 0.

Let Y_n (t) = $\sum_{i \in U_n} \psi_i^n$(t) = 0. Clearly for all t ≥ 0.

ψ_i^n (t) ≤ θ_i^n (t) (1 ≤ i ≤ n).

T_n infectives in the epidemic infects any of the remaining S_n Susceptibles either locally or globally. Then T_n infectives belongs to the Susceptibility set of a remaining Susceptible. Therefore, θ_i^n (T_n) = 1 implies that ψ_i^n (T_n) = 1.

So, ψ_i^n (T_n) = θ_i^n (T_n). Then, Y_n (T_n) = X_n (T_n). Also, note that both X_n and Y_n are increasing in t.

Let R_n be the set of individuals who remain susceptible during E_n and let W_n be the set of initial susceptibles who avoid global infection from the first n – [n^δ] infectives. Then, if $T_n \geq n - [n^\delta]$. That $R_n \subseteq W_n$.

Let A_n = { ∃i, j ∈ U_n : i, j ∈ R_n, i ≠ j, j ∈ S_i^n }, B^c_n = { the individuals in R_n fail to become infectious} and D_n = { ∃i, j ∈ U_n : i, j ∈ W_n, i ≠ j, j ∈ S_i^n }.

References

[1] Ball, F. G., Neal, P. J., (2002a). A general model for stochastic SIR epidemics with two levels of mixing. Math. Biosci. 180, 73 – 10

[2] Ball, F. G., Neal, P. J., (2002b). Poisson approximations for epidemics with two levels of mixing. Ann. Probab., accepted.

[3] Lefevre, C., Utev, S., (1995). Poisson approximation for the final state of a generalised epidemic process. Ann. Probab. 23, 1139 – 1162.

[4] Peligrad, M., Utev, S., (1997). Central limit theorem for linear processes. Ann. Prob. 25, 443–456.

[5] Ball, F. G. And Neal, P. J. (2003). The great circle epidemic model. Stochastic Process. Appl. 107, 233 – 268.

[6] Ball, F. G. And Barbour, A. D. (1990). Poisson approximation for some epidemic models. J. Appl. Probab. 27 479–490.

[7] Ball, F. G., Mollison, D. And Scalia – Tomba, G. (1997). Epidemics with two levels of mixing. Ann. Appl. Probab. 7 46–89.

[8] Sellke, T. (1983). On the asymptotic distribution of the size of a stochastic epidemic. J. Appl. Probab. 20 390–394.

[9] Von Bahr, B. And Martin–L*ö*f, A. (1980). Threshold limit theorems for some epidemic processes. Adv. in Appl. Probab. 12 319–349.

[10] Bailey, N. T. J. (1975). The Mathematical Theory of Infectious Diseases and Its Applications. Griffin, London.