Population and disease models

A. D. Barbour*
Universität Zürich

3 Branching process approximations.

3.1 Whittle's threshold theorem.

Back to the SIR-epidemic, in the case $R_0 > 1$, or $\beta < \alpha$, which should lead to large epidemics. However, this is not certain, because of chance elements. *Whittle's stochastic threshold theorem* says the following, for an epidemic with I_0 small and with N large:

If $R_0 < 1$, then the probability of having $N - S(\infty)$ as big as any non-zero fraction of N is very small: if $R_0 > 1$, then $N - S(\infty)$ will be some positive fraction of N with probability close to $(\beta/\alpha)^{I_0}$.

More precisely, Whittle noted that, given any $\varepsilon > 0$, the process $I(\cdot)$ can be bounded above and below by birth and death processes X^u and $X^{l,\varepsilon}$, until the first time that $S < (1-\varepsilon)N$:

1. *above* by the process X^u with per capita birth rate α and death rate β;
2. *below* by the process $X^{l,\varepsilon}$ with smaller birth rate $(1-\varepsilon)\alpha$, but the same death rate β.

*Angewandte Mathematik, Winterthurerstrasse 190, CH–8057 ZÜRICH, Switzerland: a.d.barbour@math.unizh.ch

He then showed that, for either of the birth and death processes, provided that $\alpha(1-\varepsilon) > \beta$, the events of extinction and of becoming extinct with only εN individuals ever born differ on a set of probability geometrically small with N. Hence, comparing the extinction probabilities of the two birth and death processes, he concluded that

$$\left(\frac{\beta}{\alpha}\right)^{I_0} + \eta_N^1 \;\leq\; \mathbb{P}[\text{the epidemic ends with } S(\infty) \geq (1-\varepsilon)N] \;\leq\; \left(\frac{\beta}{\alpha(1-\varepsilon)}\right)^{I_0} + \eta_N^2,$$

where both η_N^1 and η_N^2 are geometrically small. This argument can be adapted for $\varepsilon = \varepsilon_N$; taking for instance $\varepsilon_N = N^{-1/2}$ gives

$$\mathbb{P}[\text{the epidemic is small}] \;\sim\; (\beta/\alpha)^{I_0},$$

when $R_0 > 1$. Of course, for $R_0 < 1$, both birth and death processes die out fast with probability geometrically close to 1.

The time τ to reach $S = (1-\varepsilon)N$, if this happens, is in distribution larger than

$$(\log(\varepsilon N) - \log W^u)/(\alpha - \beta)$$

and smaller than

$$(\log(\varepsilon N) - \log(W^{l,\varepsilon}))/(\alpha(1-\varepsilon) - \beta),$$

by the same comparison, where, by the usual martingale convergence argument,

$$\begin{aligned} e^{(\beta-\alpha)t} X^u(t) &\;\to\; W^u \quad \text{a.s.} \\ e^{(\beta-\alpha\{1-\varepsilon\})t} X^{l,\varepsilon}(t) &\;\to\; W^{l,\varepsilon} \quad \text{a.s.} \end{aligned}$$

Thus the time to reach, say, $S = N - N^{1/2}$ is of order $c \log N$ for some c; in any fixed time interval $[0, T]$, the change in $S(t)$ is only of order $O(1)$. This explains why the Kurtz theorem is consistent and correct for starting with $I_0 = O(1)$, but not helpful.

3.2 The Ball and Donnelly coupling.

In this approach, the epidemic is not just bounded by birth and death processes, but attached to one of them, path by path; this makes comparison arguments very direct. Start with X^u as before, with $X^u(0) = I_0$. Associate the epidemic process $(\widetilde{S}, \widetilde{I})$ with X^u by

1. choosing a label for each newborn individual and for each of the I_0 initial indviduals *uniformly and indpendently* from $\{1, 2, \ldots, N+1\}$ (*excluding the parent's label*).

2. marking individuals that are assigned a label that has previously been assigned to an *unmarked* individual, or that are offspring of a marked individual.

Set

$$\begin{aligned} \widetilde{I}(t) &:= \text{number of } \textit{unmarked} \text{ individuals alive at } t; \\ \widetilde{S}(t) &:= S_0 - \#\{\text{unmarked individuals born up to time } t\}. \end{aligned}$$

The process $(\widetilde{S}, \widetilde{I})$ is clearly Markovian; it is easy to check that it is indeed an SIR-epidemic process.

The coupling: if τ denotes the first occasion on which a label is chosen for the second time, then we have

$$X^u(t) \;=\; \widetilde{I}(t) \quad \text{for all } 0 \le t < \tau :$$

the infective process is identical to the birth and death process X^u up to the random time τ (and $\widetilde{S}(t)$ decreases by 1 on each occasion when $\widetilde{I}(t)$ increases, so that it is also determined precisely by X^u up to the time τ).

For some choice of t_N, define

$$\Delta_N \;:=\; d_{TV}(\mathcal{L}(X^u(t), 0 \le t \le t_N), \mathcal{L}(\widetilde{I}(t), 0 \le t \le t_N)),$$

and note that, from the coupling above,

$$\Delta_N \;\le\; \mathbb{P}[\tau < t_N].$$

When is this probability small?

If M labels are sampled as above, then the probability of having a coincident pair is the solution to a *birthday problem*, with great Poisson approximation using the Stein–Chen method. In particular,

$$\mathbb{P}[\text{no coincident pair}] \;\sim\; e^{-\frac{1}{N}\binom{M}{2}}.$$

So Δ_N is small if $M \ll \sqrt{N}$, i.e. as long as

$$N - \widetilde{S} \;\ll\; \sqrt{N},$$

then the infectives process in the epidemic is indistinguishable from the birth and death process X^u, with high probability.

3.3 The Radon–Nikodym coupling.

For the epidemic process, the probability density of a path having its first m jumps at times

$$0 < t_1 < t_2 < \cdots < t_m,$$

with sequence of states $(S_1, I_1), \ldots, (S_m, I_m)$ is

$$\prod_{i=0}^{m-1} \left\{ e^{-I_i[\alpha s_i + \beta](t_{i+1} - t_i)} \frac{(\alpha s_i)^{u_i} \beta^{1-u_i}}{\alpha s_i + \beta} \right\},$$

where $t_0 = 0$, $s_i = S_i/N$ and

$$u_i \;=\; \mathbf{1}\{I_{i+1} = I_i + 1\}.$$

For the linear birth and death process X^u and the state sequence $\{I_i,\, 1 \le i \le m\}$, the formula is the same, but with s_i replaced by 1. Hence the likelihood ratio of the two processes at such a path is

$$r_m \;:=\; \prod_{i=0}^{m-1} (1 + z_i),$$

where

$$1 + z_i \;=\; \frac{e^{I_i(1-s_i)(t_{i+1}-t_i)} s_i^{u_i}}{1 - \frac{\alpha(1-s_i)}{\alpha+\beta}}. \tag{3.1}$$

Note that

$$(I_0 - 1)/N \;\le\; 1 - s_i \;\le\; (I_0 - 1 + i)/N \quad \text{for all } i,$$

and that, under the birth and death probability measure,

$$I_i(\alpha + \beta)(t_{i+1} - t_i)$$

is a realization of a random variable $E_i \sim \exp(1)$, and that the E_i are all independent: thus, 'typically',

$$z_i = O((I_0 + i)/N)$$

is small.

So consider sampling paths from the process X^u of length m; the quantity r_m is then a realization of a likelihood ratio martingale R_m, the corresponding random variables Z_i have zero mean, and have variance

$$\operatorname{Var} Z_i \;\le\; c(\alpha,\beta)(1-s_i)^2 \;\le\; c'(\alpha,\beta)(i+I_0)^2/N^2.$$

Hence

$$\mathbb{P}[\sup_{0\le m\le M}|R_m-1|\ge\varepsilon] \;\le\; \frac{(1+\varepsilon)^2c'(\alpha,\beta)}{N^2\varepsilon^2}\sum_{i=0}^{M}(i+I_0)^2 \;=\; O\left(\frac{(M+I_0)^3}{\varepsilon^2N^2}\right).$$

Thus, for $M+I_0 \ll N^{2/3}$, we can choose $\varepsilon \ll 1$ to make this probability small, and hence Δ_N also: the epidemic and birth and death processes can be coupled so as to be indistinguishable for $N-\widetilde{S} \ll N^{2/3}$, with high probability.