

Exercises and solutions to CIMPA-course

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1 The exercises

Consider the standard stochastic epidemic model where λ denotes the close contact rate, $I \sim F$ the duration of the infectious period which is initiated by 1 infectious individual and n susceptibles, and assume n is large. Consider the case where the mean infectious period equals $\iota = 1$ (for example on average one weeks infectious period and the time unit being one week and $\lambda = 1.5$ per week). Consider two different infectious distributions of the infectious period, for example $I \sim Exp(1)$, the Markovia SIR model, and $I \equiv 1$, the continuous time Reed-Frost model (the mean was already defined to equal 1). Compute the following quantities for each of the two situations (labelled 1 and 2):

- a) The basic reproduction number R_0 . (3p)
- b) The critical vaccination coverage v_c (assuming a perfect vaccine). (3p)
- c) The probability of a major outbreak. (4p)

And, assuming that a major outbreak occurs:

- d) The mean and standard deviation of final number infected Z_n . (4p)
- e) The exponential growth rate r during initial phase. (4p)
- f) The two leading terms of the duration of and epidemic (corresponding to the initial phase $T_{Beg}^{(n)}$, and the end of the epidemic $T_{End}^{(n)}$). (4p)

2 The solutions

- a) The basic reproduction number, the expected number a typical infective infects during the early stage of an outbreak, equals $\lambda E(I) = \lambda \iota = \lambda = 1.5$. This is true for both 1 and 2. The fact that $\lambda = R_0$ will be used below in several places, so keep this in mind.
- b) The critical vaccination coverage v_c is given by $v_c = 1 - 1/R_0 = 1 - 1/1.5 = 0.33$. This holds true for both 1 and 2.
- c) The probability of a minor outbreak corresponds to the probability of extinction in the approximating branching process. This probability q was derived in Etienne Pardoux's lectures, by conditioning on the number k infected in the first generation, the offspring

distribution: if k get infected these all start new independent branching processes so the probability that all go extinct equals q^k . The general equation is hence

$$q = \sum_{k=0}^{\infty} q^k P(X = k).$$

The offspring distribution X depends on the infectious period distribution I . Given that $I = s$, X has a Poisson distribution with mean λs , so $X \sim \text{MixPoi}(\lambda I)$. In situation 2 (cont-time R-F) $I \equiv 1$ so $X \sim \text{Poi}(\lambda = 1.5)$. This implies gives the following equation

$$q = \sum_{k=0}^{\infty} q^k \frac{\lambda^k e^{-\lambda}}{k!} = \dots = e^{-R_0(1-q)} = e^{-1.5(1-q)}.$$

If this equation is solved numerically it gives the result that $q = 1 - 0.583 = 0.417$. So the answer to c) in situation 2, the probability of a major outbreak, equals 0.583.

As for the first situation, where $I \sim \text{Exp}(1)$ we get $P(X = k) = \int_0^{\infty} P(X = k | I = s) f_I(s) ds = \int_0^{\infty} \frac{(\lambda s)^k e^{-\lambda s}}{k!} e^{-s} ds = \dots = \frac{1}{1+\lambda} \left(\frac{\lambda}{1+\lambda} \right)^k$, i.e. the geometric distribution, which should not come as a surprise (each time, the event is either infection or recovery, and the latter has probability $1/(\lambda + 1)$). We then get

$$q = \sum_{k=0}^{\infty} q^k P(X = k) = q^k \left(\frac{\lambda}{\lambda + 1} \right)^k \frac{1}{\lambda + 1} = \frac{1}{1 + (1 - q)\lambda}.$$

As a consequence, the probability of a minor outbreak for the Markovian SIR hence equals $q = 1/\lambda = 1/R_0 = 1/1.5 = 0.67$. The probability of a major outbreak is hence only 0.33. The randomness of the infectious period hence reduces the risk for a major outbreak. It can actually be proven that having a constant infectious period maximizes the outbreak probability among all distributions of the infectious period.

d) The total number of infected in a major outbreak is approximately normally distributed. The mean equals nx where x is the strictly positive solution of the equation $1 - x = e^{-R_0 x}$. When $R_0 = 1.5$ the solution is $x = 0.583$, so the expected number who ultimately get infected equals $0.583n$, and this is true for both 1 and 2 (and any infectious period distribution). As for the standard deviation, it was shown in Etienna Pardoux's lecture that the variance equals

$$n \frac{x(1-x)}{(1-(1-x)R_0)^2} (1 + r^2(1-x)R_0),$$

where $r^2 = V(I)/(E(I))^2$ is the squared coefficient of variation of the infectious period. The Markovian SIR has $r = 1$ and the continuous time Reed-Frost has $r = 0$. When $x = 0.583$ and $R_0 = 1.5$ we hence get that the variance for the Markovian SIR equals $1.05n$, and for the continuous time Reed-Frost $0.649n$. The standard deviations are hence the square root of these expressions. Randomness in the infectious period hence affect the randomness in the infectious period somewhat.

e) The exponential growth rate (or decay rate if $R < 1$) r is the solution to the equation $\int_0^{\infty} e^{-rs} \beta(s) ds = 1$, where $\beta(s)$ is the rate of infectious contacts s units after infection. For the standard stochastic epidemic this rate equals λ while being infectious, so $\beta(s) =$

$\lambda P(I > s)$. For the Markovian SIR we hence have $\beta(s) = \lambda e^{-s/\iota} = 1.5e^{-s}$, and the solution equals $r = \lambda - 1/\iota = 0.5$. For the continuous time Reed-Frost model we have $\beta(s) = \lambda 1_{(s < \iota)}$. The equation then becomes $\int_0^\iota e^{-rs} \lambda ds = \frac{\lambda}{r} (1 - e^{-r\iota}) = 1$. The equation is hence $r/\lambda = 1 - e^{-(r/\lambda)R_0}$. This is the same equation as for the final size x (with x replaced by r/λ). When $R_0 = 1.5$ we thus get $r/\lambda = 0.583$, so $r = 0.874$ for the continuous time Reed-Frost. This epidemic hence grows much quicker. The main reason for this is that even if the two infectious periods have equal mean $\iota = 1$, the average time of the infectious contacts are not the same. For the Reed-Frost the mean time to infectious contact (the mean of the generation time distribution) is of course 0.5 (the generation time distribution is uniform on $[0, 1]$), whereas for the Markovian SIR it equals 1 (the generation time distribution is $Exp(1)$).

f) Finally, the two leading terms for the duration of the SIR (in a fixed community of size n) is the beginning and the end of the epidemic, and they are of the form $T_{Beg}^{(n)} = \log n/r$ and $T_{End}^{(n)} = -\log n/r_{End}$, where r_{End} is the (negative) exponential decay rate at the end of the outbreak which is the solution to the same equation as for the initial growth rate except that λ is replaced by $\lambda(1-x)$ (the infection rate at the end when a fraction $1-x$ are still susceptible. For the Markovian SIR the beginning and the end are hence equal to $\log n/0.5$ and $-\log n/(-0.375) = \log n/0.375$. For the continuous time Reed-Frost the beginning of the epidemic lasts $\log n/0.874$. As for the end this decay rate is the negative solution to the equation (similar to the beginning but λ replaced by $\lambda(1-x)$): $r_{End}/\lambda = 1 - e^{-(r_{End}/\lambda)R_0(1-x)}$. Since $R_0(1-x) < 1$ this will give a negative solution. I don't have available software to obtain this numerically when $R_0 = 1.5$, $\lambda = 1.5$ and $x = 0.583$, but the duration of the end of the continuous time Reed-Frost epidemic will be $\log n/r_{End}$ for this solution.