A transparent approach to R_0 in structured populations

Nicholas F. Britton

University of Bath, United Kingdom, n.f.britton@bath.ac.uk

Epidemics in initially completely susceptible populations are most simply modelled by assuming that every individual with whom an infective comes into contact is susceptible, on the grounds that the fraction who are not susceptible is very small. This assumption is true for infinite homogeneously mixing populations but false for real populations, as is well known. The assumption of homogeneous mixing breaks down in any population where spread is local, maybe simply because the population is distributed in space or maybe because transmission is concentrated in particular locations such as households or workplaces. We shall consider the latter situation, known as a population with two levels of mixing [1], where transmission is strong within households and weaker between households. We make the simplest assumption of homogeneous mixing both within and between households. We retain the assumption of an infinite population of households, but take into account, as we must for realism, that within-household populations are finite and of different sizes. Transmission between households is therefore an essentially deterministic process but stochastic effects are important within households.

Crucial to the analysis of the dynamics and control of any epidemic are various threshold parameters such as R_0, the basic reproduction number, which may be defined as the leading eigenvalue of an operator or as the expected number of infectious contacts made by a typical infected individual introduced into an otherwise completely susceptible population during his or her infectious lifetime. A typical infected individual may be thought of as some kind of weighted average of infected individuals introduced into households of different sizes and with different within-household outcomes. The required weighting is known [2], but is not transparent. We look at the problem from a new perspective that allows us to obtain a much more intuitive expression for R_0, and we discuss the insights that may be gained from this. We consider generalisations of the method to other more complex scenarios.

Bibliography

[1] F. Ball, D. Mollison and G. Scalia-Tomba, *Ann. Appl. Prob.* Epidemics with two levels of mixing, 7, 46–89, 1997.

[2] L. Pellis, F. Ball and P. Trapman, *Math Biosciences.* Reproduction numbers for epidemic models with households and other social structures. I. Definition and calculation of R_0, 235, 85–97, 2012.