

# THE RATE OF SPATIAL PROPAGATION OF SIMPLE EPIDEMICS

DENIS MOLLISON

KING'S COLLEGE RESEARCH CENTRE, CAMBRIDGE

## 1. Introduction

The work described here concentrates on one aspect of the development of epidemics, namely, spatial propagation, ignoring such features as variable density of population, the gradual introduction of fresh susceptibles, and, for the most part, the removal of infected cases. (For an introduction to more sophisticated models for epidemics see Bailey [1].)

The basic feature of the mathematical models considered here is that the rate of infection of susceptibles is assumed to be proportional to the product of the number of susceptibles with the number of infectious individuals. This follows immediately from the assumption that the infectious influence of an infectious individual on a susceptible is independent of the state of other members of the population. Thus, if there are  $X$  susceptibles and  $Y$  infectious individuals living at an isolated point—the significance of “at a point” is that they should live so close together as to affect each other equally—then  $\dot{X}$ , the rate of change of  $X$  with time, is proportional to (minus)  $XY$ .

If we wish to study the spatial propagation of infection for such an epidemic model, we must allow for the dependence of this infectious influence on the distance between the individuals concerned, so that the rate of infection of susceptibles at a point  $s$  at time  $t$ , namely,  $-\dot{X}(s, t)$ , is proportional to the product  $X\bar{Y}$  of the number of susceptibles at  $s$  with an average value  $\bar{Y}$  of the numbers of infectious individuals at all points, weighted according to their distances from  $s$ . This weighting function may be taken to be a probability distribution function  $V$ ; then  $\bar{Y}$  is the convolution of  $Y$  with  $dV$ , that is,  $\int_{\text{space}} Y(s-r) dV(r)$ .

The introduction of such a weighted average  $\bar{Y}$  to our equations causes considerable difficulties in their analysis which have not, to the best of my knowledge, been tackled hitherto (Neyman and Scott [12] make allowance for such a dependence on distance as is considered here, but their approach otherwise differs widely). I have, accordingly, concentrated on the most simple type of epidemic model which incorporates this feature, namely, a *simple epidemic* in which there are only two types of individual, *susceptible* and *infected*; infected and infectious individuals are taken to be the same. For the most part, too, I have restricted attention to a deterministic model.

The work described here was carried out during the tenure of an S.R.C. grant in the Department of Pure Mathematics and Mathematical Statistics at Cambridge University, and (more recently) of a Research Centre Fellowship at King's College.