

SOME PROBLEMS IN  
STOCHASTIC MODELS FOR EPIDEMICS

by

R. Dunstan

A thesis submitted to the  
Australian National University  
for the degree of  
Doctor of Philosophy  
in the  
Department of Statistics  
Research School of Social Sciences  
Canberra  
February 1981



STATEMENT

The material in this thesis is my own original work except where specific reference is made.

A handwritten signature in blue ink that reads "Ross Dunstan". The signature is written in a cursive style with a large initial 'R' and a long, sweeping underline.

Ross Dunstan

## ACKNOWLEDGEMENTS

The work in this thesis was carried out in the Department of Statistics (IAS) at the Australian National University. My financial support was provided by the Federal Government of Australia in the form of a Commonwealth Postgraduate Scholarship and by a supplement to this scholarship provided by the Australian National University. To these bodies I extend my thanks.

I especially wish to thank my supervisor Dr D.J. Daley for his help at all stages in the preparation of this thesis, in particular for always being ready to set aside his work when I wished to see him, for many interesting and invaluable discussions, and for his friendly and cheerful nature. I also wish to thank Professor P.A.P. Moran for his kindly willingness to be of any assistance. My thanks go to all the members of the Department for providing a relaxed and pleasant atmosphere in which to work.

I am indebted also to Dr A.J. Dobson for her help during my earliest attempts at research at the University of Newcastle, and to the Division of Mathematics and Statistics of the CSIRO in Canberra where I had a short but rewarding visit before beginning my studies at ANU.

Finally, I am very grateful to Mrs B. Geary for her skill and patience in typing this thesis.

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## PREFACE

With the exception of the final chapter, this thesis is concerned with the general epidemic model and some simple extensions of it. The main concern is with the stochastic case and the deterministic model is only of interest when it is useful in constructing approximations to the stochastic model or in providing insights into its behaviour.

The model itself is quite old, appearing first in a paper by Kermack and McKendrick (1927). It is the simplest of stochastic models incorporating the two features:

- (i) the rate of spread of infection is a function of the number of infectives and susceptibles present; and
- (ii) infectives may be removed from the process (corresponding to death, isolation or recovery with immunity).

These two features must be regarded as essential for any model which would hope to describe realistically the spread of infectious disease.

Despite its conceptual simplicity, the model presents enormous mathematical difficulties which we believe have not yet been successfully overcome and this has severely limited an analysis of its strengths and weaknesses in potential applications to real data. This is a very unhappy situation as such a model is merely the beginning of a satisfactory mathematical theory. We have attempted to solve some of these difficulties both by obtaining what theoretical results we could and by utilizing methods leading to approximations where theoretical results were either unobtainable or whose complexity rendered them useless.

Inevitably, because of the age of the model, some of these results come from applications and extensions of techniques and results obtained by

previous researchers. For instance the approximating model presented in chapter 3 arises by combining in a new way ideas of Kendall (1956) and Faddy (1978), resulting in a technique which gives good approximations for all the mathematical quantities of interest and which may be applied to the various extensions of the model which are discussed in later chapters. However, with the exception of chapter 1 which presents a brief survey of results needed for later work, and with a few exceptions where indicated, the material in this thesis is to the best of my knowledge original.

The remaining paragraphs of this preface are a brief summary of the contents of the thesis.

Chapter 2 presents some results of a theoretical nature on the general stochastic epidemic model. Solutions for the joint probability generating function (p.g.f.) of the stochastic variables of the general epidemic model were first found simultaneously by Gani and Siskind (1965). Each used a transform technique and the solution obtained was in a recursive form and extremely complicated. More recently, Billard (1973) obtained a solution in simpler form using matrix methods. Since the process is a finite Markov chain in continuous time and such processes may be described by a linear differential equation

$$\dot{p}(t) = Ap(t) ,$$

where  $p(t)$  is the state probability vector at time  $t$  and  $A$  is the transition matrix, and since the general theory of such processes is well known, it was felt that this theory could be used to find a solution. With the help of a (well-known) partial differential equation satisfied by the joint p.g.f. this was found to be the case. The solution obtained is in a simpler form than those already in existence (mentioned above) and we believe it is the simplest that could be hoped for.

Because of the Markovian structure of the process renewal-type arguments may be applied in many situations. For instance, simple recursive expressions may be obtained for the expected final size of the epidemic and for its expected duration time. These two examples are known results, however we have used this technique to deal with the second moments of the final size (in this chapter) and with various quantities arising in extensions of the model (in chapters 4 and 5). By purely algebraic methods we are able to use these recursive expressions for the moments of the final size to find their asymptotic series expansions as the population size becomes large. The expansions throw light on the behaviour of the process, particularly when its bimodal nature is taken into account. These asymptotic results will be published in a paper to appear in the *Journal of Applied Probability* in 1980. We have also been able to apply this algebraic technique to the probability of complete infection of the population and to the probability of early extinction of the epidemic. While in this first case the proof is incomplete, computer calculations indicate the correctness of the conjecture. Heuristic reasoning based on these asymptotic results leads to a simple technique giving the asymptotic form of the mean duration time of the process.

Because we wish to use this same heuristic technique, as an aside in this chapter we discuss briefly an extension of the model to include a non-zero latent period between an individual's becoming infected and becoming infectious.

We conclude the chapter by proving the convergence (as the population size becomes large) of the general epidemic model to limit processes under two different sets of initial conditions. The first of these arose from an attempt to put on a rigorous basis the idea of Kendall (1956) of using a birth and death process to approximate the early behaviour of the process.



The second comes simply from the application of a result of Barbour (1974). The result is of interest mainly because of its usefulness in an application in chapter 3.

The form of the solution obtained in chapter 2 is still too complicated to allow its use except for very small population sizes. The material in chapter 3 is largely concerned with developing and evaluating an approximating process. Faddy (1977) found that by replacing a stochastic variable in one of the two transition probability rates by its deterministic equivalent, the resulting process became a member of a general class of compartment models for which a simple solution was available. However, numerical results given by Faddy showed that the error introduced by the resulting loss of randomness was most apparent as a change in the initial behaviour of the process. We were able to rectify this by combining this idea with Kendall's (1956) explanation of the bimodal nature of the general epidemic process.

We evaluate the performance of the resulting approximating process with a series of graphs comparing real values (based on computer simulations) with their approximating values for various parameter values. As well as this we find the joint p.g.f. for the process of Faddy by standard arguments since the method is more direct and the result in this form is more easily manipulated to give the quantities that we require, e.g. the distribution of the duration time of the epidemic. The methods of Kendall (1956) are not applicable when the population is near critical (i.e. susceptible population size  $\approx$  relative removal rate). A suggestion is made for this situation which is supported by heuristic arguments and numerical results.

Chapter 4 deals with the application of the general epidemic model to rumours. The model is identical to that of the general epidemic model except that attention is directed to the sizes of the individual generations

of infection. Renewal arguments of the type used in chapter 2 are applied to find recursive expressions for the mean final generation sizes. For the deterministic model, a simple formula is found for each generation size at any time, the formula resulting from a simplification of an expression by Daley (1967). The asymptotic form of the final generation size is found, thus generalising a result of Daley (1967) whose result is for the case when the relative removal rate is zero (the simple epidemic model). The rest of the chapter deals with the application of the approximating method of chapter 3 and with the limiting result corresponding to that at the end of chapter 2.

In the general epidemic model it is implicitly assumed that the population mixes homogeneously. It is this assumption which is most likely to be unsatisfactory in any particular application. It is natural therefore to consider a modification of the model which allows for the existence of subgroups within which mixing is homogeneous but between which it is more restricted. Such a model is the subject of chapter 5. Mathematical difficulties are multiplied by the non-homogeneity, though some interesting results can still be obtained. The effect on the important threshold theorem is examined both in the stochastic and deterministic cases. The probability of containing infection in the group in which it originates is found approximately. The usual renewal arguments are applied yielding recursive expressions for mean final sizes of the epidemic in each subgroup and for the duration of the epidemic in the whole population. An analogous approximating technique to that of chapter 3 is applied and the limiting diffusion process is given.

In chapter 6 we look at three models for epidemics in which the assumption of homogeneous mixing of the population is completely abandoned.

The first of these is a model applicable to a population with little or no mobility. The model assumes that the disease is spread only by those infectives on or adjacent to the boundary of the infected area. The resulting process is a linear one and we are able to obtain expressions for the mean numbers of active infectives and also for the probability of extinction of the process.

The second of the models of chapter 6 is a two-type branching process model applicable to a population with family structure. Branching processes are useful in describing the early behaviour of an epidemic process. This is particularly interesting because it is the behaviour of the epidemic during its early stages which will determine if the outbreak will be minor or major. In the model we distinguish between infectives who were infected by members of their family and those infected by individuals not of their family. A special case of this model is the model of Bartoszyński (1972). Our approach here is different, using branching process theory to obtain results about the moments of the two types of infective and the probability that the process will become extinct.

The third is a model for an epidemic in a stratified population. The model of chapter 5 is very complicated mathematically and by making some realistic assumptions we are led to qualitative results about the final size of an epidemic in a stratified population.

## CHAPTER 1

### INTRODUCTION

#### 1.0 Introduction

The general epidemic model is a mathematical model to describe the spread within a population of some characteristic able to be transmitted from one individual to another. We usually imagine the characteristic to be a disease although for some applications it may be a rumour or a particular item of information. The model assumes that the population consists of three types of individuals: susceptibles who may become infected by contact with infectives; infectives who have the disease and may cause further infections by contact with susceptibles; and removed individuals who have, or have had, the disease and play no further part in the process because of immunity or isolation or death. Infectives become removed at a rate proportional to the size of the infective population. Members of the population, except for removed individuals, are assumed to mix uniformly, and hence susceptibles become infected at a rate which is proportional to the sizes of the susceptible and infective populations.

The model was first introduced in a paper by Kermack and McKendrick (1927). No further work appears to have been done on the model until Bailey (1953) published a paper on the final size of the general epidemic. Shortly after, Whittle (1955) generalised the threshold theorem of Kermack and McKendrick to the stochastic case and Kendall (1956) introduced an approximating process based on the consequences of the threshold theorem. Gani (1965) and Siskind (1965) simultaneously derived expressions for the joint p.g.f. associated with the process and more recently Billard (1972) found an expression for it in simpler form. The distribution of the number

remaining uninfected by the process of the general epidemic model (hereafter simply called "the general epidemic") was investigated by Daniels (1965). Ridler-Rowe (1967) found the asymptotic form of the mean duration time of the process. Asymptotic limiting processes were the subject of work by Nagaev and Startsev (1970) and Barbour (1975). Abakuks (1973) investigated the cost of the general epidemic and Watson (1972) studied a generalisation of the model in which the population is assumed to be stratified.

The rest of this chapter is a brief survey of known results about the general epidemic model which must be referred to in subsequent chapters.

## 1.1 The model

### THE STOCHASTIC FORM

Let the number of susceptibles and infectives at time  $t$  be  $X(t)$  and  $Y(t)$  respectively (for convenience  $t$  will usually be suppressed). The transitions from the state  $(X, Y)$  in the time interval  $(t, t+\delta t)$  are given by

$$1.1 \quad (X, Y) \rightarrow \begin{cases} (X-1, Y+1) & \text{with probability } \mu XY\delta t + o(\delta t) , \\ (X, Y-1) & \text{with probability } \gamma Y\delta t + o(\delta t) , \end{cases}$$

as  $\delta t \rightarrow 0$ .

The initial conditions are  $(X(0), Y(0)) = (n, a)$ . (The parameters  $\mu$  and  $\gamma$  are known as the contact rate and the removal rate respectively. It is more convenient and more common to use the relative removal rate  $\rho = \gamma/\mu$  instead of the two parameters  $\mu$  and  $\gamma$ . Thus it merely requires a change in time scale to write the above infinitesimal transition rates as  $XY$  and  $\rho Y$ .)

Let

$$p_{rs}(t) = \Pr\{(X(t), Y(t)) = (r, s)\},$$

$$r = 0, 1, \dots, n, \quad s = 0, 1, \dots, n+a-r.$$

Considering the possible transitions in the time interval  $(t, t+\delta t)$  and letting  $\delta t \rightarrow 0$  leads to

$$1.2 \quad \dot{p}_{rs}(t) = -s(r+\rho)p_{rs}(t) + (r+1)(s-1)p_{r+1,s-1}(t) + \rho(s+1)p_{r,s+1}(t),$$

$$r = 0, 1, \dots, n, \quad s = 0, 1, \dots, n+a-r,$$

where  $p_{rs}(t)$  is defined to be zero if  $s$  is negative.

Let  $P(w, z; t) = E(w^X z^Y)$  be the joint p.g.f. of  $(X, Y)$ . Multiplying 1.2 by  $rs$  and summing over the possible values of  $r$  and  $s$  shows that  $P$  satisfies the partial differential equation

$$1.3 \quad \frac{\partial P}{\partial t} = z(z-w) \frac{\partial^2 P}{\partial w \partial z} + \rho(1-z) \frac{\partial P}{\partial z},$$

where  $P(w, z; 0) = w^n z^a$ .

Equations 1.2 and 1.3 are well known (see e.g. Bailey (1954)). Their solution has proved to be extremely difficult. Gani (1965) and Siskind (1965) obtained solutions using transform techniques. More recently Billard (1972) used matrix methods to find a solution in simpler form.

#### THE DETERMINISTIC FORM

From 1.3 it follows easily that

$$\frac{dEX}{dt} = -EXY,$$

$$\frac{dEY}{dt} = EXY - \rho EY, \text{ and}$$

$$\frac{dEZ}{dt} = \rho EY,$$

where  $Z$  is the number of removed at time  $t$ .

Assuming that we may write  $EXY = EXEY$  (which holds to a good approximation in large populations), and writing  $x, y$  and  $z$  for  $EX, EY$  and  $EZ$  respectively, we obtain the following equations which define the deterministic model corresponding to the stochastic model defined by 1.1:

$$1.4a) \quad \dot{x} = -xy,$$

$$1.4b) \quad \dot{y} = xy - \rho y,$$

$$1.4c) \quad \dot{z} = \rho y,$$

where  $(x(0), y(0), z(0)) = (n, a, 0)$ .

It is easily seen that if  $n \leq \rho$ ,  $y$  is always decreasing. This lies behind the important threshold theorem of Kermack and McKendrick which says that a major outbreak is only possible if  $n > \rho$ .

Combining 1.4a) and 1.4b) we have

$$1.5 \quad -\rho \ln \frac{x}{n} = z = n + a - x - y.$$

Substituting for  $y$  from 1.5 into 1.4a) and integrating gives

$$1.6 \quad \int_x^n \frac{ds}{s(n+a-s+\rho \ln(s/n))} = \mu t,$$

a result due to D.G. Kendall which defines  $x(t)$  implicitly. Explicit solutions for  $x, y$  and  $z$  are not available.

From equations 1.4 it follows easily that  $y(\infty) = 0$ . Hence from 1.5 we see that  $\theta (= x(\infty))$ , the number of susceptibles left after the epidemic has become extinct, is the unique solution between 0 and  $n$  of the equation

$$1.7 \quad -\rho \ln \frac{\theta}{n} = n + a - \theta ,$$

and we note that it is readily shown that

$$1.8 \quad \theta \sim n \exp\left[-\frac{n+a}{\rho}\right] , \text{ as } n \rightarrow \infty .$$

## 1.2 The distribution of the final size

The final size of the epidemic,  $W$ , is defined to be the number of further infections (not counting the initial infections) that have occurred at the time of extinction of the process. Let

$$p_r(n, a) = \Pr\{W = r \mid (X(0), Y(0)) = (n, a)\} .$$

It is easily shown by a backwards equation argument that for  $r = 0, 1, \dots, n$ ,

$$1.9 \quad p_r(n, a) = \frac{n}{n+\rho} p_{r-1}(n-1, a+1) + \frac{\rho}{n+\rho} p_r(n, a-1) , \quad n, a = 1, 2, \dots ,$$

and

$$p_r(n, 0) = p_r(0, a) = \delta(r) ,$$

where

$$\delta(\alpha) = \begin{cases} 1 & \text{if } \alpha = 0 , \\ 0 & \text{if } \alpha \neq 0 , \end{cases}$$



and where we define  $p_{-1}(n, a) \equiv 0$ , and  $p_r(n, a) \equiv 0$  if  $r > n$ . Equation 1.9 may be found in Daniels (1965) where it was further established that

$$1.10 \quad p_{n-r}(n, a) = \sum_{k=0}^{n-r} A_k \binom{n}{r+k} \left( \frac{\rho}{\rho+r+k} \right)^{n+a-r},$$

$$n, a = 1, 2, \dots, \quad r = 0, 1, \dots, n,$$

where the  $A_k$  are defined recursively by

$$1.11 \quad \delta(n-r) = \sum_{k=0}^{n-r} A_k \binom{n}{r+k} \left( \frac{\rho}{\rho+r+k} \right)^{n-r}, \quad n = 1, 2, \dots, \quad r = 0, 1, \dots, n.$$

Daniels shows that the  $A_k$  are functions of  $k$ ,  $r$  and  $\rho$  only.

It was shown in Bailey (1954) that

$$1.12 \quad \sum_{r=0}^m \binom{n-r}{n-m} \left( \frac{n-m+\rho}{\rho} \right)^{r+\alpha} p_r(n, a) = \binom{n}{m}, \quad n = 1, 2, \dots, \quad m = 0, \dots, n.$$

Using a heuristic argument Daniels conjectured that as  $n \rightarrow \infty$ ,

$$1.13 \quad p_{n-r}(n, a) \sim \left[ 1 - \left( \frac{\rho}{n} \right)^\alpha \right] \frac{(ne^{-n/\rho})^r}{r!} \exp(-ne^{-n/\rho}).$$

It is well-known that in the supercritical case ( $n > \rho$ )  $W$  has a bimodal distribution. Epidemics of intermediate size occur with very low probability and the epidemic will with high probability affect either a very small proportion of the susceptibles in the population or a very large proportion.

#### THE MEAN OF THE FINAL SIZE

Let

$$C_\rho(n, a) = E(W \mid (X(0), Y(0)) = (n, a)) = \sum_{r=0}^n r p_r(n, a) .$$

(We shall usually suppress  $\rho$ .) Multiplying 1.9 by  $r$  and summing over  $r = 0, 1, \dots, n$  yields

$$1.14 \quad C(n, a) = \frac{n}{n+\rho} [1+C(n-1, a+1)] + \frac{\rho}{n+\rho} C(n, a-1) , \quad n, a = 1, 2, \dots ,$$

and

$$C(n, 0) = C(0, a) = 0 .$$

Substituting successively for the final term gives

$$1.15 \quad C(n, a) = \frac{n}{n+\rho} \sum_{k=0}^{a-1} \left( \frac{\rho}{n+\rho} \right)^k [1+C(n-1, a+1-k)] ,$$

from which it is readily shown by induction that

$$1.16 \quad C(n, a) = n - \sum_{k=1}^n \binom{n}{k} k a_k \left( \frac{\rho}{k+\rho} \right)^{n+a-k} ,$$

where the  $a_k$  are defined recursively by

$$1.17 \quad \sum_{k=1}^n \binom{n}{k} k a_k \left( \frac{\rho}{k+\rho} \right)^{n-k} = n , \quad n = 1, 2, \dots .$$

The results of this section may be found in Abakuks (1973) where 1.16 first appeared. It was later found as a special case in Lefèvre (1978).

### 1.3 The distribution of the time to extinction

The epidemic is defined to be extinct when there are no more infectives left in the population. It is readily shown that the general epidemic will

become extinct with probability one. Let  $T$  be the time to extinction and  $F_T(t)$  its distribution function. Since

$$1.18 \quad F_T(t) = \sum_{r=0}^n p_{r0}(t) = P(1, 0; t),$$

and  $P(x, y; t)$  is known, in theory  $F_T(t)$  is known. In practice however, the existing solutions for  $P(x, y; t)$  mentioned in section 1.1 (and see section 2.1) are so complicated that this expression is completely useless except for very small values of  $n$  and  $a$ . Barbour (1975) has shown that in the case where the initial conditions are  $(X(0), Y(0)) = (n, nh)$ , where  $h$  is constant, and the contact rate is  $1/n$ , then as  $n \rightarrow \infty$ ,

$$(\rho - \phi)T - \ln n - k$$

converges in distribution to the random variable with distribution function  $\exp(-e^{-t})$ , where  $\phi$  satisfies

$$1 + h - \phi + \rho \ln \phi = 0,$$

and

$$k = \lim_{m \rightarrow \infty} \left[ -\ln m + (\rho - \phi) J \left[ \phi \left( 1 + \frac{1}{m(\rho - \phi)} \right), 1 \right] \right] + \ln \left( 1 - \frac{\phi}{\rho} \right),$$

where

$$J(\alpha, \beta) = \int_{\alpha}^{\beta} \frac{ds}{s(1+h-s+\rho \ln s)}.$$

The case when the initial number of infectives is constant is also treated but the result is not presented here because of its length.

## THE MEAN OF THE TIME TO EXTINCTION

Let

$$M(n, a) = E\{T \mid (X(0), Y(0)) = (n, a)\} .$$

The process may be looked upon as a random walk on the lattice  $(r, s)$  where  $r = 0, 1, \dots, n$  and  $s = 0, 1, \dots, n+a-r$ . From the state  $(r, s)$  the walk may go to  $(r-1, s+1)$  with probability  $r/(r+\rho)$  and to  $(r, s-1)$  with probability  $\rho/(r+\rho)$ . The time spent in  $(r, s)$  is an exponential variate with parameter  $s(r+\rho)$ . Hence it follows that

$$1.19 \quad M(n, a) = \frac{1}{a(n+\rho)} + \frac{n}{n+\rho} M(n-1, a+1) + \frac{\rho}{n+\rho} M(n, a-1) ,$$

$$n = 0, 1, \dots, \quad a = 1, 2, \dots ,$$

and

$$M(n, 0) = 0 .$$

This is a well known technique and equation 1.19 may be found in Billard (1977).

By considering the process as a competition process and using theorems of Reuter (1957), (1961), Ridler-Rowe (1967) has shown that

$$1.20 \quad M(n, a) \sim \frac{1}{\gamma} \ln(n+a) , \quad \text{as } n \rightarrow \infty ,$$

where  $a$  is not necessarily a constant.

## 1.4 The stochastic threshold theorem

Let

$$q_{ni} = \Pr\{W \leq ni\} ,$$

where  $0 \leq i < 1$ .

By considering birth and death processes that formed stochastic upper and lower bounds for the general epidemic process Whittle (1955) was able to show that for  $n$  large enough,

$$1.21 \quad \left[ \min\left(\frac{\rho}{n}, 1\right) \right]^a \leq q_{ni} \leq \left[ \min\left(\frac{\rho}{n(1-i)}, 1\right) \right]^a.$$

Hence if  $\rho \geq n$ , with probability 1 the process will become extinct before its size exceeds any given proportion of the initial susceptible population. This is the stochastic threshold theorem corresponding to the deterministic one of section 1.1.

Kendall (1956) introduced an approximating process by reasoning along similar lines as follows. In order to describe the early development of the process it is assumed that the effect of the depletion of the susceptible population during these early stages may be neglected. When  $X$  is held constant at its initial value  $n$  the process becomes a birth and death process  $Y'$  with birth rate  $n$  and death rate  $\rho$  (in fact  $Y'$  is a stochastic upper bound for  $Y$ ). If  $\rho \geq n$  extinction of  $Y'$  is certain so few further infections are expected and hence  $Y'$  is used as the approximation to  $Y$ . If  $\rho < n$  extinction of  $Y'$  occurs with probability  $(\rho/n)^a$  in which event it is known that  $Y'$  behaves like a birth and death process with birth rate  $\rho$  and death rate  $n$  (see O'N. Waugh (1958)) so this process is used as the approximation for  $Y$ . Also in the case  $\rho < n$ ,  $Y'$  will not become extinct with probability  $1 - (\rho/n)^a$  in which event we use the deterministic variable  $y$  (see equations 1.4) as the approximation for  $Y$ .

In the supercritical case ( $\rho < n$ ) the mean final size for this

approximating system,  $C'(n, a)$ , is given by

$$1.22 \quad C'(n, a) = \left[ 1 - \left( \frac{\rho}{n} \right)^a \right] (n - \theta) + \left( \frac{\rho}{n} \right)^a \frac{\rho a}{n - \rho}.$$

### 1.5 A quasi-deterministic approximation

Faddy (1978) considers an approximation to the general epidemic model as a special case in a more general discussion of a class of stochastic compartment models. In the infection probability rate the stochastic variable  $Y$  is replaced by its deterministic analogue  $y$ . The resulting process  $(X', Y')$  is mathematically tractable and it is shown that

$$1.23 \quad \Pr\{(X', Y_1) = (r, s_1)\} \\ = \frac{n!}{r!s_1!(n-r-s_1)!} [p_{11}(t)]^r [p_{12}(t)]^{s_1} [1-p_{11}(t)-p_{12}(t)]^{n-r-s_1},$$

and

$$1.24 \quad \Pr\{Y_2 = s_2\} = \frac{a!}{s_2!(a-s_2)!} [p_{22}(t)]^{s_2} [1-p_{22}(t)]^{a-s_2},$$

where

$$p_{11}(t) = \frac{x(t)}{n}, \\ p_{12}(t) = \frac{1}{n} (y(t) - ae^{-\rho t}),$$

and

$$p_{22}(t) = e^{-\rho t},$$

and where

$$Y' = Y_1 + Y_2 .$$

The distribution of the number of susceptibles remaining uninfected after the extinction of the process is a binomial random variable with mean  $\theta$  .

## 1.6 The application of the general epidemic model to rumours

In the application of the general epidemic model to the spread of news or rumours the characteristic transmitted from one individual to another is thought of as being a particular rumour or item of knowledge. Thus an infective is an individual who knows the rumour and a removed individual is one who has heard the rumour and forgotten it. It is important in this application to consider not only if an individual is infected but to which generation of infection he belongs. (The  $\alpha$  initial infections are regarded as belonging to the "0th" generation of infectives, those infected by them to the 1st generation etc.) This is relevant because it would be expected that the distortion of the rumour increases as the generation "distance" from the source increases.

The model is essentially no different from the general epidemic model. The only change is that attention is now directed to the individual generation sizes.

The following stochastic and deterministic models were first formulated by Daley (1967).

### THE STOCHASTIC MODEL

Let  $X$  and  $Y_g$  ,  $g = 0, 1, \dots$  , be the number of susceptibles and  $g$ th generation "knowers" respectively present in the population at time  $t$  .

Define

$$(X, Y) \equiv (X, Y_0, Y_1, \dots) .$$

The infinitesimal transition probability rates are given by

$$(X, Y) \rightarrow \begin{cases} (X-1, Y+\epsilon_{g+1}) & \text{at rate } \mu XY_g , \\ (X, Y-\epsilon_g) & \text{at rate } \gamma Y_g , \end{cases} \quad g = 0, 1, \dots ,$$

where  $\epsilon_g$ ,  $g = 0, 1, \dots$ , is the vector with 1 in the  $(g+1)$ th place and zero elsewhere. The initial condition is

$$(X(0), Y(0)) = (n, a, 0, 0, \dots) .$$

Define the final size of the  $g$ th generation,  $W_g$ ,  $g = 0, 1, \dots$ , to be the number of  $g$ th generation removed at the time of extinction of the process.

Let  $\mathbf{a} = (a_0, a_1, \dots, a_{m+1})$  and define

$$(n, \mathbf{a}) \equiv (n, a_0, a_1, \dots, a_{m+1}) .$$

Further, let  $\mathbf{r} = (r_0, \dots, r_{m+1})$ ,  $\mathbf{e}_k$  be the  $(k+1)$ th row of the  $(m+2) \times (m+2)$  identity matrix and

$$p_r(n, \mathbf{a}) = \Pr\left\{W_g = r_g, g = 0, 1, \dots, m,\right.$$

$$\left. \sum_{k=m+1}^{\infty} W_k = r_{m+1} \mid \left[ X(0), Y_0(0), \dots, \sum_{k=m+1}^{\infty} Y_k(0) \right] = (n, \mathbf{a}) \right\} .$$

By the usual argument it is shown that for  $m = 0, 1, \dots$ ,



1.25  $p_r(n, a)$

$$= \left[ (\mu n + \gamma) \sum_{k=0}^{m+1} a_k \right]^{-1} \left\{ \sum_{k=0}^m \mu n [a_k p_{r-e_{k+1}}(n-1, a+e_{k+1}) + \gamma a_k p_r(n, a-e_k)] \right. \\ \left. + \mu n a_{m+1} p_{r-e_{m+1}}(n-1, a+e_{m+1}) + \gamma a_{m+1} p_r(n, a-e_{m+1}) \right\}, \\ n = 1, 2, \dots, \quad a_0, a_1, \dots, a_{m+1} = 0, 1, \dots,$$

where any probability whose subscripts are either zero or whose sum exceeds  $n$  is defined to be zero, and

$$p_r(0, a) = \delta(r),$$

where

$$\delta(\alpha) = \begin{cases} 1 & \text{if } \alpha = 0, \\ 0 & \text{if } \alpha \neq 0. \end{cases}$$

#### THE DETERMINISTIC MODEL

Let  $x$  and  $y_g$ ,  $g = 0, 1, \dots$ , be the deterministic equivalents of  $X$  and  $Y_g$  and  $z_g$ ,  $g = 0, 1, \dots$ , be the number of  $g$ th generation removed at time  $t$ . The deterministic model corresponding to the stochastic model is defined by the equations:

$$1.26a) \quad \dot{x} = -\mu xy,$$

$$1.26b) \quad \dot{y}_g = \mu xy_{g-1} - \gamma y_g, \quad g = 0, 1, \dots,$$

$$1.26c) \quad \dot{z}_g = \gamma y_g, \quad g = 0, 1, \dots,$$

where  $y = \sum_{g=0}^{\infty} y_g$  and  $y_{-1}$  is defined to be zero, and where the initial conditions are  $(x(0), y_0(0), y_1(0), \dots) = (n, a, 0, \dots)$ , and

$$z_g(0) = 0, \quad g = 0, 1, \dots$$

Daley (1967) showed that

$$1.27 \quad z_g(t) = \frac{\rho}{g!} \int_{x(t)}^n \left[ \int_u^n \frac{dv}{\psi(v)} \right]^g \exp \left[ - \int_u^n \frac{dv}{\psi(v)} \right] \frac{du}{u},$$

where

$$1.28 \quad \psi(v) = n + a - v + \rho \ln \frac{v}{n}.$$

## 1.7 The general epidemic in a stratified population

This is an important extension of the general epidemic model which attempts to make a more realistic assumption about the mixing of the individuals in the population than that made by the general epidemic model. The population is assumed to consist of  $m$  distinct groups in which homogeneous mixing occurs but between which mixing is restricted. Thus in the time interval  $(t, t+\delta t)$  an infected individual of the  $j$ th group,  $j = 1, \dots, m$ , has probability  $\mu_{ji}\delta t + o(\delta t)$ , as  $\delta t \rightarrow 0$ , of infecting any susceptible in the  $i$ th group,  $i = 1, \dots, m$ , where in general  $\mu_{ii} > \mu_{ji}$ ,  $i \neq j$ . The idea of considering the population as stratified goes back to Rushton and Mautner (1955) and Haskey (1957). The following formulation of both the deterministic and stochastic models is due to Watson (1972).

### THE STOCHASTIC MODEL

Let  $X_i, Y_i$ ,  $i = 1, \dots, m$ , be the number of susceptibles and infectives in the  $i$ th group at time  $t$ . Let  $X = (X_1, \dots, X_m)$ ,  $Y = (Y_1, \dots, Y_m)$ ,  $\mu_i$  be the  $i$ th column of the matrix  $\{\mu_{ji}\}$  and  $e_i$

be the  $i$ th row of the  $m \times m$  identity matrix.

The infinitesimal transition probability rates for the model are given by

$$1.29 \quad (X, Y) \rightarrow \begin{cases} (X-e_i, Y+e_i) & \text{at rate } X_i \mu_i^T \cdot Y, \\ (X, Y-e_i) & \text{at rate } \gamma_i Y_i, \end{cases} \quad i = 1, \dots, m,$$

where as in section 1.6 we understand  $(X, Y)$  to mean

$$(X_1, \dots, X_m, Y_1, \dots, Y_m).$$

The initial conditions are  $(X(0), Y(0)) = (n, a)$ , where  $n = (n_1, \dots, n_m)$  and  $a = (a_1, \dots, a_m)$ .

Let

$$p_{(n,a)}(r, s, t) = \Pr\{(X, Y) = (r, s) \mid (X(0), Y(0)) = (n, a)\},$$

where  $r = (r_1, \dots, r_m)$  and  $s = (s_1, \dots, s_m)$ .

It follows from the forward equation that this function satisfies

$$1.30 \quad \dot{p}_{(n,a)}(r, s, t) = \sum_{i=1}^m \left[ -\left( \gamma_i a_i + n_i \mu_i^T \cdot a \right) p_{(n,a)}(r, s, t) \right. \\ \left. + n_i \mu_i^T \cdot a p_{(n-e_i, a+e_i)}(r, s, t) + \gamma_i a_i p_{(n, a-e_i)}(r, s, t) \right],$$

$$n_i, a_i = 0, 1, \dots, \quad r_i = 0, 1, \dots, n_i,$$

$$s_i = 0, 1, \dots, n_i + a_i - r_i, \quad i = 1, \dots, m,$$

where any  $p_{(n,a)}(r, s, t)$  having subscripts for which some  $r_i > n_i$ ,  $i = 1, \dots, m$ , is defined to be zero, and

$$p_{(n,a)}(r, s, 0) = \delta(n-r, a-s).$$

An equation equivalent to 1.30 was first stated by Billard (1976) where the stochastic model was presented in a form which would enable the application of her method of solution for the general stochastic epidemic model (see Billard (1973)).

#### THE DETERMINISTIC MODEL

Let  $x_i, y_i, z_i$ ,  $i = 1, \dots, m$ , be the numbers of susceptibles, infectives and removed in the  $i$ th group at time  $t$  in the deterministic model. The model is described by the equations

$$1.31a) \quad \dot{x}_i = -x_i \sum_{j=1}^m \mu_{ji} y_j, \quad i = 1, \dots, m,$$

$$1.31b) \quad \dot{y}_i = x_i \sum_{j=1}^m \mu_{ji} y_j - \gamma_i y_i, \quad i = 1, \dots, m,$$

$$1.31c) \quad \dot{z}_i = \gamma_i y_i, \quad i = 1, \dots, m.$$

The initial conditions are  $(x_i(0), y_i(0), z_i(0)) = (n_i, a_i, 0)$ ,  $i = 1, \dots, m$ .

Watson (1972) combines 1.31a) and 1.31c) to give

$$1.32 \quad -\gamma_i \ln \frac{x_i}{n_i} = \sum_{j=1}^m \mu_{ji} (n_j + a_j - x_j - y_j), \quad i = 1, \dots, m.$$

As  $t \rightarrow \infty$ ,  $y_i \rightarrow 0$ ,  $i = 1, \dots, m$ , so 1.32 becomes

$$1.33 \quad -\gamma_i \ln \frac{\theta_i}{n_i} = \sum_{j=1}^m \mu_{ji} (n_j + a_j - \theta_j), \quad i = 1, \dots, m,$$

where  $\theta_i = x_i(\infty)$ ,  $i = 1, \dots, m$ .

## CHAPTER 2

## SOME THEORETICAL RESULTS ON THE GENERAL STOCHASTIC EPIDEMIC MODEL

## 2.0 Introduction

This chapter presents some theoretical results on the general stochastic epidemic model formulated as a continuous time Markov chain on a finite state space. With the exception of the first section these results are asymptotic results valid as the size of the initial susceptible population increases with other parameters remaining fixed.

In the first section we obtain a solution for the state probabilities at any time. The solution arises by writing the process in the form of a one dimensional finite Markov chain in continuous time and then using theorems from the general theory of linear differential equations. This method is simpler than existing methods for obtaining either the state probabilities or the joint p.g.f. (see Gani (1965), Siskind (1965), Billard (1973)) and the solution is in simpler form. Inspection of the form of the solution makes it difficult to imagine that it could be simplified further. Nevertheless it is still quite complicated.

Because the process is Markovian, simple recursive equations for many quantities of interest may be found using arguments involving backward equations. Some of these are well known (e.g. 1.9 and 1.14). We establish a lemma which enables us to work with such equations to find asymptotic expansions of the moments of the final size of the process (see Dunstan (1980)) the probability of its early extinction, and the probability that none escape infection. In this last case, while the proof is incomplete, the truth of the conjecture is supported by computer calculations. These asymptotic expansions are particularly informative when the bimodal nature

of the process is taken into account.

Although simple recursive equations may also be found for the mean duration time of the epidemic, it was not possible to use the same technique to find the asymptotic form. We are able to use a heuristic argument which may also be applied to more complicated models. For this purpose we define here a modification of the general epidemic model which allows for an arbitrary latent period between an individual's becoming infected and becoming infectious. We find the asymptotic form of the mean duration time in this model and we also show that the distribution of the final size is the same as that for the usual general epidemic model.

The next section presents a process which is the limit of the general epidemic process under certain conditions. This process arose out of an attempt to put on a rigorous basis Kendall's idea of using a birth and death process to approximate the general epidemic process in its early stages. Another limiting process which results when a different sequence of initial conditions is assumed is presented in the last section.

## 2.1 The state probabilities

Any ordered pair  $(r, s)$  where  $r = 0, 1, \dots, n$  and  $s = 0, 1, \dots, n+a-r$ , represents a possible state of the system with  $r$  denoting the number of susceptibles and  $s$  the number of infectives. The process is a two dimensional finite Markov chain on these states. By enumerating the possible states uniquely we can regard the process as a one dimensional Markov chain. Hence it may be described by the equation

$$2.1 \quad \dot{p}(t) = Ap(t) ,$$

where  $p(t)$  is a column vector whose  $i$ th element corresponds to one (and

only one)  $p_{rs}(t)$  and  $A$  is the matrix of infinitesimal transition probability rates. The theory of such a system is well known.

The following theorem gives the solution for the state probabilities in our particular case under a mild restriction on the parameter  $\rho$ .

**THEOREM 2.1.** *If  $\rho$  is such that*

$$j(i+\rho) \neq j'(i'+\rho)$$

*when  $(i, j) \neq (i', j')$  for all integer pairs representing a possible state of the system, then the eigenvalues of  $A$  are distinct and*

$$p_{rs}(t) = \sum_{i=1}^n \sum_{j=1}^{n+a-i} e^{\lambda_{ij} t} K_{rs}(\lambda_{ij}),$$

$$r = 0, 1, \dots, n, \quad s = 0, 1, \dots, n+a-r,$$

where

$$\lambda_{ij} = -j(i+\rho), \quad i = 0, 1, \dots, n, \quad j = 0, 1, \dots, n+a-i,$$

and the  $K_{rs}(\lambda_{ij})$  are determined by the recurrence relation

$$\rho(s+1)K_{r,s+1}(\lambda_{ij}) - [\lambda_{ij} + s(n+\rho)]K_{rs}(\lambda_{ij}) + (r+1)(s-1)K_{r+1,s-1}(\lambda_{ij}) = 0,$$

where  $K_{rs}(\lambda_{ij}) = 0$  if  $r > n$ ,  $s+r > n+a$ , or  $s < 0$ , and by the initial condition

$$p_{rs}(0) = \begin{cases} 1 & \text{if } r = n, \quad s = a, \\ 0 & \text{otherwise.} \end{cases}$$

**Proof.** See Appendix A.  $\square$

## 2.2 The mean final size

The following theorem establishes the first term of an asymptotic series expansion for  $C(n, a)$ .

**THEOREM 2.2.** For  $\rho$  a positive constant and  $a$  a positive integer,

$$n - C(n, a) = o(n^{-a+2}), \text{ as } n \rightarrow \infty.$$

**Proof.** We shall need a lemma, which shall be proved below, giving uniform convergence of the terms of the series in equation 1.16.

Another result is needed to prove the theorem, namely that the  $a_k$ , defined in 1.17, are uniformly bounded. This follows from the result of Gani and Shanbhag (1974) that the  $a_k$  are all positive and hence writing 1.17 in the form

$$a_k = 1 - \sum_{j=1}^{k-1} \binom{k-1}{j-1} a_j \left( \frac{\rho}{j+\rho} \right)^{k-j},$$

we see that they are all less than or equal to one.

From 1.16 we have

$$\begin{aligned} n^{\alpha-2} [n - C(n, a)] &= n^{\alpha-2} \sum_{k=1}^n \binom{n}{k} k a_k \left( \frac{\rho}{k+\rho} \right)^{n+\alpha-k} \\ &= n^{\alpha-2} \sum_{k=1}^n \binom{n}{k} \left( \frac{\rho}{k+\rho} \right)^{n+\alpha-k-1} \frac{k a_k \rho}{k+\rho} \\ &< n^{\alpha-2} \rho \left[ \sum_{k=1}^{n-[\sqrt{n}]} + \sum_{k=n-[\sqrt{n}]+1}^n \right] \binom{n}{k} \left( \frac{\rho}{k+\rho} \right)^{n+\alpha-k-1} \end{aligned}$$

where  $[\alpha]$  means the greatest integer not greater than  $\alpha$

$$= o(1) + O(n^{-\frac{1}{2}}), \text{ by Lemma 2.3. } \quad \square$$



LEMMA 2.3. For  $\rho$  a positive constant and  $a$  a positive integer,

$$\binom{n}{k} \left( \frac{\rho}{k+\rho} \right)^{n+a-k} = \begin{cases} o(n^{-a}) & \text{if } k \leq n-\sqrt{n}, \\ O(n^{-a}) & \text{if } n-\sqrt{n} < k \leq n, \end{cases}$$

as  $n \rightarrow \infty$ .

**Proof.** By Stirling's inequalities (see e.g. Feller Vol. I, p. 54) we have for  $k = 1, \dots, n-1$ ,

$$\begin{aligned} 2.2 \quad n^a \binom{n}{k} \left( \frac{\rho}{k+\rho} \right)^{n+a-k} &< \frac{1}{\sqrt{(2\pi)}} \left( \frac{\rho}{k+\rho} \right)^{n+a-k} n^a \frac{n^{n+\frac{1}{2}}}{k^{k+\frac{1}{2}}(n-k)^{n-k+\frac{1}{2}}} \exp\left(\frac{1}{12n} - \frac{1}{12k+1} - \frac{1}{12(n-k)+1}\right) \\ &< \frac{1}{\sqrt{\pi}} \left( \frac{\rho n}{k+\rho} \right)^a \left\{ \binom{n}{k} \frac{k/(n-k)}{k(n-k)} \right\}^{n-k} \\ &< \frac{1}{\sqrt{\pi}} \left( \frac{\rho n}{k+\rho} \right)^a \left\{ \frac{\rho e n}{k(n-k)} \right\}^{n-k}. \end{aligned}$$

Consider now the 4 cases

- (i)  $k \leq 3\rho e$ ,
- (ii)  $3\rho e < k \leq n-\sqrt{n}$ ,
- (iii)  $n-\sqrt{n} < k \leq n-2\rho e$ ,
- (iv)  $n-2\rho e < k \leq n$ .

The lemma is trivial for cases (i) and (iv). For case (ii) we have from 2.2, taking  $\sqrt{n} \geq 3\rho e$ ,

$$\begin{aligned} \sqrt{\pi n}^a \binom{n}{k} \left( \frac{\rho}{k+\rho} \right)^{n+a-k} &< \left( \frac{\rho n}{k+\rho} \right)^a \left\{ \frac{\rho e n}{3\rho e(n-3\rho e)} \right\}^{n-k} \\ &< n^a \left( \frac{1}{2} \right)^{\sqrt{n}}, \quad n > 9\rho e. \end{aligned}$$

For case (iii), from 2.2,

$$\begin{aligned} \sqrt{\pi n} \binom{n}{k} \left( \frac{\rho}{k+\rho} \right)^{n+a-k} &< \left( \frac{\rho n}{n-\sqrt{n+\rho}} \right)^\alpha \left\{ \frac{\rho e n}{2\rho e(n-2\rho e)} \right\}^{n-k} \\ &< \rho^\alpha \left( \frac{1}{2} \right)^{2\rho e} + 1, \quad n > N, \text{ some } N. \quad \square \end{aligned}$$

We note that in the Kendall approximating process discussed in section 1.4 the mean final size is given by 1.22. From 1.8 we would expect that as  $n \rightarrow \infty$ ,

$$n - C(n, 1) = \rho + o(1).$$

This was also conjectured in Abakuks (1973). The next theorem extends the asymptotic expansion of  $C(n, \alpha)$  and establishes the truth of this conjecture.

**THEOREM 2.4.** *Under the conditions of Theorem 2.2,*

$$C(n, \alpha) = n - \rho \left( \frac{\rho}{n} \right)^{\alpha-1} + o(n^{-\alpha+1}), \text{ as } n \rightarrow \infty.$$

**Proof.** From Theorem 2.2 we may write

$$2.3 \quad C(n, \alpha) = n - \alpha_n(\alpha),$$

where

$$\alpha_n(\alpha) = o(n^{-\alpha+2}), \text{ as } n \rightarrow \infty.$$

Now

$$C(n, 1) = [1 + C(n-1, 2)] \left( \frac{n}{n+\rho} \right), \text{ from 1.14.}$$

Substituting from 2.3 gives

$$n - \alpha_n(1) = [n + \alpha_{n-1}(2)] \left( \frac{n}{n+\rho} \right).$$

Therefore

$$2.4 \quad \alpha_n(1) = \rho + o(1), \text{ as } n \rightarrow \infty.$$

Substituting 2.3 in 1.14 for  $a > 1$  gives

$$n - \alpha_n(a) = [n - \alpha_{n-1}(a+1)] \left( \frac{n}{n+\rho} \right) + [n - \alpha_n(a-1)] \left( \frac{\rho}{n+\rho} \right).$$

Therefore

$$\begin{aligned} \alpha_n(a) &= \alpha_n(a-1) \left( \frac{\rho}{n} \right) + o(n^{-a+1}) \\ &= \rho \left( \frac{\rho}{n} \right)^{a-1} + o(n^{-a+1}), \text{ as } n \rightarrow \infty, \end{aligned}$$

from 2.4.  $\square$

In principle it is possible by the method of establishing Theorem 2.4 to find the expansion of  $C(n, a)$  up to terms of any order. However the algebra quickly becomes tedious and we assert without proof the further refinement

$$\begin{aligned} 2.5 \quad C(n, a) &= n - \rho \left( \frac{\rho}{n} \right)^{a-1} - \frac{a(a+1)}{2} \left( \frac{\rho}{n} \right)^{a+1} \\ &\quad - \frac{a}{\rho} [(a+3)(a+3\rho)+2] \left( \frac{\rho}{n} \right)^{a+2} + o(n^{-a-2}), \text{ as } n \rightarrow \infty. \end{aligned}$$

The expected final size was calculated using equation 1.14 for various values of the parameters  $\rho, a, n$ . The following tables compare the true values of  $n - C(n, a)$  with the approximations calculated from equation 2.5 (shown in brackets). The approximation seems fairly insensitive to variation in the parameter  $a$ . As we would expect it is useless for  $\rho/n \approx 1$  but surprisingly good for values of  $\rho/n$  as large as .5, even for small values of  $n$ .

$\rho = 1$ 

$\begin{matrix} a \\ n \end{matrix}$	1	2	3
5	1.12 (1.84)	0.29 (0.31)	0.09 (0.09)
10	1.03 (1.03)	0.11 (0.11)	0.01 (0.01)
25	0.00 (1.00)	0.04 (0.04)	0.00 (0.00)

 $\rho = 2$ 

$\begin{matrix} a \\ n \end{matrix}$	1	2	3
5	2.16 (3.12)	1.03 (2.07)	0.53 (1.33)
10	2.22 (2.16)	0.57 (0.49)	0.19 (0.12)
25	2.01 (2.01)	0.16 (0.16)	0.01 (0.01)

 $\rho = 5$ 

$\begin{matrix} a \\ n \end{matrix}$	1	2	3
5	3.69 (19.2)	2.77 (42.8)	2.12 (.77)
10	5.67 (6.9)	3.48 (5.05)	2.31 (3.69)
25	5.31 (5.15)	1.28 (1.08)	0.42 (0.23)

We note that the approximation for  $C(n, a)$  given by 1.22 may be written

$$C'(n, a) = n - \rho \left(\frac{\rho}{n}\right)^{\alpha-1} + a \left(\frac{\rho}{n}\right)^{\alpha+1} + o(n^{-\alpha-1}), \text{ as } n \rightarrow \infty,$$

which agrees with 2.5 as far as the term in  $n^{-\alpha-1}$ .

### 2.3 The second moment of the final size

Let

$$D(n, a) = E(W^2 \mid (X(0), Y(0)) = (n, a)) = \sum_{r=0}^n r^2 p_r(n, a) .$$

Multiplying equation 1.9 by  $r^2$  and summing over  $r = 0, 1, \dots, n$ , we obtain

$$2.6 \quad D(n, a) = \frac{2n}{n+\rho} C(n-1, a+1) + \frac{n}{n+\rho} [1+D(n-1, a+1)] + \frac{\rho}{n+\rho} D(n, a-1) ,$$

$$n, a = 1, 2, \dots .$$

Substituting successively for the final term gives

$$2.7 \quad D(n, a) = \frac{n}{n+\rho} \sum_{k=0}^{a-1} \left( \frac{\rho}{n+\rho} \right)^k D(n-1, a+1-k) + 2C(n, a) - 1 + \left( \frac{\rho}{n+\rho} \right)^a .$$

From 2.7 we may readily prove by induction that

$$2.8 \quad D(n, a) = 2nC(n, a) - n^2 + \sum_{k=1}^n \binom{n}{k} b_k \left( \frac{\rho}{k+\rho} \right)^{n+a-k} ,$$

where the  $b_k$  are defined by

$$2.9 \quad \sum_{k=1}^n \binom{n}{k} b_k \left( \frac{\rho}{k+\rho} \right)^{n-k} = n^2 , \quad n = 1, 2, \dots .$$

We now need the following lemma which gives the order of magnitude of the  $b_k$ .

LEMMA 2.5. For  $n = 1, 2, \dots$ ,

$$n \binom{n+\rho}{1+\rho} \leq b_n \leq n^2 .$$

**Proof.** From 2.9 we have  $b_1 = 1$  and  $b_2 = 2(2+\rho)/(1+\rho)$  so that the lower bound holds for  $n = 1, 2$ . Assume that the lower bound holds for  $n = m - 1$ ,  $m > 1$ , then from 2.9,

$$\begin{aligned}
2.10 \quad b_m &= m^2 - \sum_{k=1}^{m-1} \binom{m}{k} b_k \left( \frac{\rho}{k+\rho} \right)^{m-k} \\
&= m^2 - \sum_{k=1}^{m-1} \binom{m-1}{k} b_k \left( \frac{\rho}{k+\rho} \right)^{m-1-k} \frac{m\rho}{(m-k)(k+\rho)}.
\end{aligned}$$

Now  $(m-k)(k+\rho)$  for  $k = 1, \dots, m-1$ , has its minimum at  $(m-1)(1+\rho)$ . By the induction hypothesis all the  $b_1, \dots, b_{m-1}$  are positive, therefore

$$\begin{aligned}
b_m &\geq m^2 - \frac{\rho m(m-1)}{1+\rho} \\
&= \frac{m(m+\rho)}{1+\rho}.
\end{aligned}$$

Hence by induction  $b_n \geq n(n+\rho)/(1+\rho)$  for all positive integers  $n$ . It

now follows trivially from 2.10 that  $b_n \leq n^2$  for all integers  $n$ .  $\square$

**COROLLARY.** Under the conditions of Theorem 2.2,

$$2.11 \quad (i) \quad \sum_{k=1}^n \binom{n}{k} b_k \left( \frac{\rho}{k+\rho} \right)^{n+a-k} = o(n^{-a+3}), \text{ as } n \rightarrow \infty,$$

$$2.12 \quad (ii) \quad D(n, a) = n^2 - \rho^2 \left( \frac{\rho}{n} \right)^{a-2} + \rho^2 (a-1) \left( \frac{\rho}{n} \right)^{a-1} + o(n^{-a+1}),$$

as  $n \rightarrow \infty$ ,

$$2.13 \quad (iii) \quad V(n, a) = \rho^2 \left( \frac{\rho}{n} \right)^{a-2} + \rho^2 (a-1) \left( \frac{\rho}{n} \right)^{a-1} + o(n^{-a+1}), \text{ as } n \rightarrow \infty,$$

where  $V(n, a) = \text{Var}\{W \mid (X(0), Y(0)) = (n, a)\}$ .

**Proof.** The proof of (i) is exactly the same as that of Theorem 2.2.

(ii) is arrived at by using (i) together with 2.5 and 2.8 to show that

$$n^2 - D(n, \alpha) = o(n^{-\alpha+3}), \text{ as } n \rightarrow \infty,$$

and then extending the expansion using the same method as in Theorem 2.4.

(iii) is a trivial extension of (ii).

## 2.4 The moments conditional on a major outbreak

As stated in section 1.2 an important feature of the distribution of the final size is that it is bimodal. The first mode of behaviour corresponds to early extinction of the process in which only a small proportion of susceptibles are infected and the second to a major outbreak affecting a large proportion of the susceptible population. The discussion in section 1.4 shows that in the case  $n > \rho$ , we can approximate the probability of early extinction by  $(\rho/n)^\alpha$  (see also section 2.6) and the process conditional on this eventuality by a birth and death process having birth rate  $\gamma$  and death rate  $\mu n$ . Hence, if we let  $W$  be the final size,  $W'$  the final size conditional on early extinction and  $W''$  the final size conditional on a major outbreak we have

$$\begin{aligned} 2.14 \quad E(W'') &= \frac{E(W) - E(W') \Pr\{\text{early extinction}\}}{1 - \Pr\{\text{early extinction}\}} \\ &\approx \left[ E(W) - \left(\frac{\rho}{n}\right)^\alpha \frac{\alpha \rho}{n - \rho} \right] \left(1 - \left(\frac{\rho}{n}\right)^\alpha\right)^{-1} \\ &= n - \frac{\alpha(\alpha+3)}{2} \left(\frac{\rho}{n}\right)^{\alpha+1} - \rho \left(\frac{\rho}{n}\right)^{2\alpha-1} - \dots, \end{aligned}$$

using 2.5.

Hence we see that the term  $\rho(\rho/n)^{\alpha-1}$  appearing in 2.5 is the result of the probability mass of the first mode of the bimodal distribution of  $W$ . Similarly, working with the second moments we find

$$2.15 \quad \text{Var}(W''') = \rho^2(\alpha-1) \left(\frac{\rho}{n}\right)^{\alpha-1} + \rho^2 \left(\frac{\rho}{n}\right)^{2\alpha-2} + \dots$$

Comparing this with 2.13 we again conclude that the dominant term of the variance arises from the bimodal nature of the distribution.

## 2.5 The distribution of the final size

We may readily apply the methods of the previous section to other recurrence relations. Substituting successively for the final term in equation 1.9 leads to

$$2.16 \quad p_r(n, \alpha) = \frac{n}{n+\rho} \sum_{k=0}^{\alpha-1} \left(\frac{\rho}{n+\rho}\right)^k p_{r-1}(n-1, \alpha+1-k) + \left(\frac{\rho}{n+\rho}\right)^\alpha \delta(r),$$

which gives

$$p_0(n, \alpha) = \left(\frac{\rho}{n+\rho}\right)^\alpha,$$

$$p_1(n, \alpha) = n \left[ \left(\frac{\rho}{n-1+\rho}\right)^{\alpha+1} - \frac{\rho}{n-1+\rho} \left(\frac{\rho}{n+\rho}\right)^\alpha \right],$$

and so on. Rearranging this latter equation we have

$$n \left(\frac{n-1+\rho}{\rho}\right)^\alpha p_0(n, \alpha) + \left(\frac{n-1+\rho}{\rho}\right)^{\alpha+1} p_1(n, \alpha) = \alpha,$$

which is equation 1.12 for  $m = 1$ , and in fact 1.12 follows easily from 2.16 by induction on  $r$ .

We now consider equation 1.10. The quantity  $p_n(n, \alpha)$  is of interest and it is conjectured that  $p_n(n, \alpha) \rightarrow 1$  as  $n \rightarrow \infty$ . To justify this conjecture, first let  $c_k = -A_k(\rho/(\rho+k))^k$ , so that with  $r = 0$  equations



1.10 and 1.11 become

$$p_n(n, a) = 1 - \sum_{k=1}^n \binom{n}{k} c_k \left( \frac{\rho}{\rho+k} \right)^{n+a-k}, \quad n = 1, 2, \dots, \quad a = 0, 1, \dots,$$

where the  $c_k$  are defined recursively for  $k = 1, 2, \dots$ , by

$$2.17 \quad \sum_{k=1}^n \binom{n}{k} c_k \left( \frac{\rho}{\rho+k} \right)^{n-k} = 1, \quad n = 1, 2, \dots.$$

Now if it can be shown that the  $c_k$  are uniformly bounded then Lemma 2.3

guarantees that the sum appearing in 2.17 is  $o(n^{-a+1})$  as  $n \rightarrow \infty$ . In the case  $\rho \leq 1$  we may show by induction (proceeding as in Lemma 2.5) that all the  $c_k$  are between 0 and 1. For  $\rho > 1$  a heuristic argument and computer calculations suggest that this is also true.

The result is readily established however by arguing as follows. (We are indebted to Dr. M. Faddy for suggesting this approach.)

Equation 4.3 of Daniels (1967) states that

$$p_{n-k}(n, a, \rho) = \binom{n}{k} \left( \frac{\rho}{\rho+k} \right)^{n+a-k} p_n(n-k, a, \rho+k),$$

where the extra parameter  $\rho$  for the relative removal rate of the process has been introduced into the function  $p_n(n, a)$ .

$$\begin{aligned} \therefore p_n(n, a, \rho) &= 1 - \sum_{k=1}^n p_k(n, a, \rho) \\ &= 1 - \sum_{k=1}^n \binom{n}{k} \left( \frac{\rho}{\rho+k} \right)^{n+a-k} p_n(n-k, a, \rho+k) \end{aligned}$$

Now since the  $p_n(n-k, a, \rho+k)$  are uniformly bounded the result follows.

Hence we may use the recurrence relation 1.9 and the method of Theorem 2.4 to establish that

$$2.18 \quad p_n(n, a) = 1 - \left(\frac{\rho}{n}\right)^a + o(n^{-a}), \text{ as } n \rightarrow \infty.$$

## 2.6 The probability of early extinction

It has long been accepted, following the arguments of Kendall (see section 1.4), that the probability of early extinction in a general epidemic with  $\rho < n$  is  $(\rho/n)^a$ . Exactly what is meant by "early extinction" or its opposite "major outbreak" has yet to be defined. The above-mentioned result is obtained by arguing that early extinction occurs if the birth and death process with birth rate  $n$  and death rate  $\rho$  becomes extinct. This criterion is chosen because such a process approximates the general epidemic process in its early stages, since in the early stages we may ignore the effect on the contact rate of the small depletion in the number of susceptibles. It would be more appropriate that the final size be the sole criterion for deciding whether a major outbreak has occurred. Here we discuss the probability of early extinction under such criteria.

Let

$$q_r(n, a) = \Pr\{W < r \mid (X(0), Y(0)) = (n, a)\}.$$

By the usual argument

$$2.19 \quad q_r(n, a) = \frac{n}{n+\rho} q_{r-1}(n-1, a+1) + \frac{\rho}{n+\rho} q_r(n, a-1),$$

$$n, a = 1, 2, \dots, \quad r = 1, \dots, n,$$

and

$$q_r(0, a) = q_r(n, 0) = 1 - \delta(r).$$

These probabilities may easily be calculated from these equations.

Referring to equation 1.21 we see that as long as  $r = o(n)$  as  $n \rightarrow \infty$ ,

$$q_r(n, a) \sim \left(\frac{\rho}{n}\right)^a, \text{ as } n \rightarrow \infty.$$

It seems very difficult to obtain this result under more general conditions on  $r$ . Equation 2.18 suggests that it is true even for  $r = n$ .

As in Theorem 2.4 we may use the recurrence relation 2.19 to find further terms in the series for  $q_r(n, a)$ . Thus we may show that

$$2.20 \quad q_r(n, a) = \left(\frac{\rho}{n}\right)^a + \frac{a(a+3)}{2\rho} \left(\frac{\rho}{n}\right)^{a+2} + o(n^{-a-2}), \text{ as } n \rightarrow \infty.$$

## 2.7 The mean duration time

Equation 1.19 is of the same form as equations 1.9 and 1.14.

Proceeding in the same manner we find that

$$2.21 \quad M(n, a) = \frac{1}{n+\rho} \sum_{k=0}^{a-1} \left[ \frac{1}{a-k} + nM(n-1, a+1-k) \right].$$

It was expected that expressions of the form of 1.10 and 1.16 could be obtained from 2.21 and the asymptotic result of Ridler-Rowe (1967) that

$$M(n, a) \sim \frac{1}{\gamma} \ln(n+a), \text{ as } n \rightarrow \infty,$$

could be obtained using the algebraic methods of sections 2.2 and 2.3.

Unfortunately this has not been possible, but the following heuristic argument may be applied.

From the conjecture of section 2.5 we may reasonably assume that if  $n$

is large enough no member of the population escapes infection. Lemma 4.2 indicates that this mass infection takes place in a time interval which is arbitrarily small as  $n$  becomes larger. If everyone were to be infected at time zero the duration of the process would be the maximum of  $n + a$  exponential variates with parameter  $\gamma$ . Hence we would expect such a random variate to have the same limiting form as  $T$  and it is a simple matter to show that its mean is

$$\frac{1}{\gamma} \sum_{k=1}^{n+a} \frac{1}{k} \sim \frac{1}{\gamma} \ln(n+a), \text{ as } n \rightarrow \infty.$$

## 2.8 The general epidemic model with a latent period before infectiousness

In many diseases a newly infected individual passes through a latent period before becoming infectious. If we modify the general epidemic model to incorporate this feature the resulting model is of course much more complicated. Nevertheless some interesting conclusions may be drawn from it.

We will assume that the population is composed of individuals who are either susceptible, latent infectives, infectives or removed and we will denote the number of such individuals at any time  $t$  by  $X, L, Y$  and  $Z$  respectively. In the time interval  $(t, t+\delta t)$  an infective may become removed with probability  $\gamma Y \delta t + o(\delta t)$ , as  $\delta t \rightarrow 0$  and a susceptible may become a latent infective with probability  $\mu X Y \delta t + o(\delta t)$ , as  $\delta t \rightarrow 0$ . A latent infective becomes an infective after a time period  $W$ , where  $W$  is an arbitrary random variable independent of the state of the system.

### THE DISTRIBUTION OF THE FINAL SIZE

The final size distribution is not affected by this modification. This is easily seen by considering the embedded random walk process defined by

the transitions in which either a susceptible or an infective is changed.

The two possible transitions at time  $t$  have probabilities

$$\Pr\{(X, Y, L) \rightarrow (X-1, Y, L+1)\} = \begin{cases} \frac{X}{X+\rho} & \text{if } Y+L > 0, \\ 0 & \text{if } Y+L = 0, \end{cases}$$

$$\Pr\{(X, Y, L) \rightarrow (X, Y-1, L)\} = \begin{cases} \frac{\rho}{X+\rho} & \text{if } Y+L > 0, \\ 0 & \text{if } Y+L = 0. \end{cases}$$

These are the same transition probabilities as in the same embedded random walk process for the general epidemic model with zero latent period. The fact that some of the infectives are now called latents has made no difference.

#### AN EXPONENTIAL LATENT PERIOD

The simplest way to incorporate a non-zero latent period into the general epidemic model is to make the distribution of the latent period independent of the state of the system and exponential with parameter  $\lambda$  say. This distribution for the latent period will preserve the Markovian nature of the process, i.e. at any time  $t$  the behaviour of the process is dependent only on its state at time  $t$ . At any time  $t$  the model has infinitesimal transition probability rates given by

$$2.22 \quad (X, Y, L) \rightarrow \begin{cases} (X-1, Y, L+1) & \text{at rate } XY, \\ (X, Y+1, L-1) & \text{at rate } \lambda L, \\ (X, Y-1, L) & \text{at rate } \rho Y, \end{cases}$$

where  $(X(0), Y(0), L(0)) = (n, 0, b)$ .

The corresponding deterministic model is

$$\begin{aligned}\dot{x} &= -xy, \\ \dot{y} &= \lambda l - \rho y, \\ \dot{l} &= xy - \lambda l,\end{aligned}$$

where  $(x(0), y(0), l(0)) = (n, 0, b)$ .

Equations similar to 1.2 and 1.3 may easily be found for this model. While these would be of little use in practice, approximations of the same form as those of chapter 3 are readily derived.

#### THE MEAN DURATION TIME OF THE EPIDEMIC

Let  $M(n, a, b)$  be the expected time to extinction of the general epidemic with exponentially distributed latent period and initial conditions  $(X(0), Y(0), L(0)) = (n, a, b)$ . Then by the usual argument we have that  $M(n, a, b)$  satisfies the recurrence relation

$$2.23 \quad M(n, a, b) = \frac{1}{na + \rho a + \lambda b} [naM(n-1, a, b+1) + \rho aM(n, a-1, b) + \lambda bM(n, a+1, b-1)], \quad n, a, b = 0, 1, \dots,$$

$$M(n, 0, 0) = 0, \quad n = 0, 1, \dots$$

Using the heuristic argument of section 2.7 we may infer the asymptotic form of  $M(n, a, b)$  as  $n \rightarrow \infty$ . Every individual once infected will stay infected until its removal after a random period of time equal to  $J + I$ , where  $J$  and  $I$  are independent exponential variates with parameters  $\lambda$  and  $\rho$  respectively. If everyone becomes infected at time zero, the duration  $T$  of the epidemic will be equal to  $\max_{1 < i < n+b} (J_i + I_i)$ , where initially we assume  $(X(0), Y(0), L(0)) = (n, 0, b)$ .

Let

$$T' = \max_{1 < i < n+b} (J_i + I_i).$$

$T'$  has distribution function

$$F_{T'}(t) = \left[ 1 - \frac{1}{\lambda - \rho} (\lambda e^{-\rho t} - \rho e^{-\lambda t}) \right]^{n+b},$$

where we assume that  $\lambda \neq \rho$ .

$$ET' = \int_0^{\infty} \left[ 1 - \left( 1 - \frac{1}{\lambda - \rho} (\lambda e^{-\rho t} - \rho e^{-\lambda t}) \right)^{n+b} \right] dt.$$

Substitute  $u = vt / (\ln(n+b))$ , where  $v = \min(\lambda, \rho)$ .

$$\begin{aligned} & \frac{vET'}{\ln(n+b)} \\ &= \int_0^{\infty} \left[ 1 - \left( 1 - \frac{1}{\lambda - \rho} (\lambda(n+b)^{-(\rho/v)u} - \rho(n+b)^{-(\lambda/v)u}) \right)^{n+b} \right] du \\ &= \left[ \int_0^1 + \int_1^{\infty} \right] \left[ 1 - \left( 1 - \frac{(n+b)^{-u}}{\lambda - \rho} (\lambda(n+b)^{-((\rho/v)-1)u} - \rho(n+b)^{-((\lambda/v)-1)u}) \right)^{n+b} \right] du. \end{aligned}$$

Using l'Hôpital's rule we see that for fixed  $u$  the integrand converges to  $G(u)$  where

$$G(u) = \begin{cases} 1, & u < 1, \\ 1 - e^{-1/(|\rho-\lambda|)}, & u = 1, \\ 0, & u > 1. \end{cases}$$

Therefore

$$\lim_{n \rightarrow \infty} \frac{vET'}{\ln(n+b)} = 1 + \lim_{n \rightarrow \infty} \lim_{m \rightarrow \infty} f(m, n),$$

where

$f(m, n)$

$$= \int_1^m \left[ 1 - \left( 1 - \frac{(n+b)^{-u}}{\lambda - \rho} (\lambda(n+b)^{-((\rho/v)-1)u} - \rho(n+b)^{-((\lambda/v)-1)u}) \right)^{n+b} \right] du.$$

It may be verified by straightforward (though messy) algebra that  $f(m, n)$  converges uniformly to 0 as  $n \rightarrow \infty$ . Hence

$$\lim_{n \rightarrow \infty} \frac{\sqrt{ET'}}{\ln(n+b)} = 1 ,$$

and so the conjecture is that

$$M(n, 0, b) \sim \frac{\ln(n+b)}{\min(\lambda, \rho)} , \text{ as } n \rightarrow \infty .$$

Note that it is not necessary to assume that  $b$  is a constant for this result.

## 2.9 The birth and death process limit

In section 1.4 we discussed an approximating process due to Kendall which is based on the idea that the initial behaviour of the number of infectives in the general epidemic process is approximately the same as a birth and death process with birth rate  $\mu n$  and death rate  $\gamma$ . In this section we show that with a plausible modification of the contact rate parameter we can put this idea on a rigorous basis. We consider the general epidemic model as defined in section 1.1 but with  $\mu$  replaced by  $\mu/n$ , i.e. the infinitesimal transition probability rates are

$$2.24 \quad (X, Y) \rightarrow \begin{cases} (X-1, Y+1) & \text{at rate } \frac{\mu}{n} XY , \\ (X, Y-1) & \text{at rate } \gamma Y , \end{cases}$$

and the initial conditions are  $(X(0), Y(0)) = (n, a)$ .

This modification represents a restriction in the mixing of the population where, as the population size increases, the contact rate of any individual stays the same. In large populations this is a more realistic



assumption to make.

The following theorem gives the limit of this modified process as  $n \rightarrow \infty$  with the other parameters constant.

**THEOREM 2.6.** For  $\mu$  and  $\gamma$  positive constants and  $a$  a positive integer, as  $n \rightarrow \infty$  the process  $Y$  defined at 2.24 converges weakly to a birth and death process with birth rate  $\mu$  and death rate  $\gamma$  on  $t \in (0, \tau)$  for any fixed  $\tau$ .

**Proof.** Let

$M$  be the event  $\{n - X(\tau) > \sqrt{n}\}$ ,

$Y'$  be the birth and death process with birth rate  $\mu$ , death rate  $\gamma$  and initial condition  $Y'(0) = a$ , and

$Y''$  be the birth and death process with birth rate  $\mu \left(1 - \frac{1}{\sqrt{n}}\right)$ , death rate  $\gamma$  and initial condition  $Y''(0) = a$ .

Further let  $P_a(z, t)$ ,  $P'_a(z, t)$  and  $P''_a(z, t)$  be the p.g.f.'s of  $Y$ ,  $Y'$  and  $Y''$  respectively.

Now choose any finite number of time points  $0 \leq t_1 < t_2 \dots < t_m \leq \tau$ . Let

$\underline{y} = (Y(t_1), \dots, Y(t_m))$ , defining  $\underline{y}'$  and  $\underline{y}''$  similarly. Denote their p.g.f.'s by  $P_a(\underline{z}; \underline{t}) (= P_a(z_1, \dots, z_m; t_1, \dots, t_m))$ ,  $P'_a(\underline{z}; \underline{t})$  and  $P''_a(\underline{z}; \underline{t})$  respectively.

Now

$$\underline{y} <_d \underline{y}' ,$$

where  $<_d$  means less than in distribution (see Theorem 4.2.10 of Stoyan (1977))

Hence

$$2.25 \quad P_a(\underline{z}, \underline{t}) > P'_a(\underline{z}, \underline{t}) ,$$

(see e.g. Barlow and Proschan (1975)).

Also  $\underline{y}'' <_d \underline{y}$  except on a set of probability less than  $\Pr\{M\}$ . Hence

$$\begin{aligned}
2.26 \quad P''_a(z, t) &> E_{M^c} \left\{ \prod_{i=1}^m z_i Y''(t_i) \right\} \\
&> E_{M^c} \left\{ \prod_{i=1}^m z_i Y(t_i) \right\} \\
&> P_a(z, t) - \Pr\{M\} .
\end{aligned}$$

Let the random variable  $T_i$  be the time between the  $(i-1)$ th and  $i$ th infection,  $i = 1, \dots, n$ .  $T_i$  is stochastically greater than or equal to an exponential variate with parameter less than or equal to

$$\mu \left( \frac{n-i+1}{n} \right) Y \left( \sum_{k=1}^{i-1} T_k \right) < \mu(a+i) .$$

So  $T_i \stackrel{d}{\geq} T'_i$ , where  $T'_i$  is exponential with parameter  $\mu(a+i)$ . Therefore

$$2.27 \quad \Pr\{M\} = \Pr\{T_1 + \dots + T_{[Vn]+1} < \tau\}$$

where  $[\alpha]$  means the greatest integer less than or equal to  $\alpha$

$$< \Pr\{T'_1 + \dots + T'_{[Vn]+1} < \tau\} .$$

Now

$$E \left( \sum_{k=1}^{[Vn]+1} T'_k \right) = \frac{1}{\mu} \sum_{k=1}^{[Vn]+1} \frac{1}{a+k} = O(\ln n) \text{ as } n \rightarrow \infty ,$$

and

$$\text{Var} \left( \sum_{k=1}^{[Vn]+1} T'_k \right) = \frac{1}{\mu^2} \sum_{k=1}^{[Vn]+1} \frac{1}{(a+k)^2} = O(1) \text{ as } n \rightarrow \infty .$$

Hence from 2.27, using Chebychev's inequality we have

$$2.28 \quad \Pr\{M\} = O((\ln n)^{-2}) , \text{ as } n \rightarrow \infty .$$

Now it is well known that

$$2.29 \quad P'(z, t) = \left[ \frac{\gamma(1-z) - (\gamma - \mu z)e^{-(\mu - \gamma)t}}{\mu(1-z) - (\gamma - \mu z)e^{-(\mu - \gamma)t}} \right]^\alpha,$$

and it is easily shown that

$$P'_{\alpha \sim} (z; t) = P'_{\alpha} (z_1 P'_{\alpha} (z_2 P'_{\alpha} \dots (z_{m-1} P'_{\alpha} (z_m; t_{m-1} - t_{m-1} - t_{m-2}) \dots); t_1).$$

Now it follows that  $P''_{\alpha \sim} (z; t) = P'_{\alpha \sim} (z; t) + o(1)$ , as  $n \rightarrow \infty$ .

Hence equations 2.25, 2.26 and 2.28 show that

$$2.30 \quad |P(z, t) - P'(z, t)| = o(1), \text{ as } n \rightarrow \infty. \quad \square$$

## 2.10 The diffusion limit

We consider the process defined at 2.24 but with the initial condition  $(X(0), Y(0)) = (n, nh)$ , where  $h$  is a constant. This modification in the initial condition ensures that the probability of early extinction is arbitrarily small as  $n \rightarrow \infty$  and a different limiting process results. In this form the process is a special case of a general class of processes discussed in Barbour (1974) from which the following result is directly obtainable.

Let

$$2.31 \quad (U_n, V_n) = \left( \frac{X - n\xi}{\sqrt{n}}, \frac{Y - n\eta}{\sqrt{n}} \right),$$

where  $\xi$  and  $\eta$  satisfy the equations

$$\dot{\xi} = -\mu\xi\eta,$$

$$\dot{\eta} = \mu\xi\eta - \gamma\eta,$$

with initial conditions  $(\xi(0), \eta(0)) = (1, h)$ . The variables  $\xi$  and  $\eta$  are the deterministic analogues of the stochastic proportions  $X/n$  and

$$P_n(u, v; t) = E(u^n v^n) .$$

Then  $P = \lim_{n \rightarrow \infty} P_n$  satisfies the equation

$$2.32 \quad \frac{\partial P}{\partial t} - \mu \ln \frac{v}{u} \left[ u\eta \frac{\partial P}{\partial u} + v\xi \frac{\partial P}{\partial v} \right] + \gamma v \ln v \frac{\partial P}{\partial v} - \frac{1}{2} \left[ \mu\xi\eta \left( \ln \frac{v}{u} \right)^2 + \gamma\eta (\ln v)^2 \right] P = 0 ,$$

where  $P(u, v; 0) = 1$  .

From 2.32 we may easily show that the means  $EU$  and  $EV$  are identically zero and that the second moments satisfy the following system of differential equations

$$2.33a) \quad \frac{dEU^2}{dt} + 2\mu(\eta EU^2 + \xi EUV) - \mu\xi\eta = 0 ,$$

$$2.33b) \quad \frac{dEUV}{dt} + \mu[\eta(EUV - EU^2) - \xi(EUV - EV^2)] + \gamma EUV + \mu\xi\eta = 0 ,$$

$$2.33c) \quad \frac{dEV^2}{dt} - 2\mu\eta EUV - 2(\mu\xi - \gamma)EV^2 - (\mu\xi + \gamma)\eta = 0 .$$

We shall use equations 2.33 in chapter 3 to construct an approximating process for the general epidemic.

## CHAPTER 3

## APPROXIMATING PROCESSES

## 3.0 Introduction

The general stochastic epidemic model presents great mathematical difficulties. Explicit solutions for the state probabilities associated with the process are available (see section 2.1) but unfortunately these solutions are so complicated that they are useless in practice. Hence we must look for good approximations to the process.

The approximating procedures used here make use of the well-known fact that the general epidemic exhibits two distinct modes of behaviour: either the process becomes extinct early or there is a major outbreak. Thus we look for approximations to each of these modes. This approach was first exploited by Kendall (see section 1.4) who used a birth and death process for the first mode and the deterministic solution for the second mode. In section 3.1 we derive a different approximation for the second mode of the process which in most cases enables good approximations to be found for the means of the variables  $X(t)$  and  $Y(t)$ , the distribution of the final size and the distribution of the duration time of the process.

In the case of the general epidemic being near critical (i.e.  $\rho \approx n$ ), this approach is not useful. We suggest a way to deal with this situation and support the idea by heuristic arguments and numerical comparisons.

## 3.1 A quasi-deterministic model

In this section we consider a model which arises by replacing the stochastic variable  $Y$  appearing in the contact probability rate by its

deterministic analogue  $y$ . The use of a deterministic variable as the contact rate is a reasonable modification for the following reason: for many diseases it is difficult to ascertain the role played by infected individuals in the spreading of the disease. In general it may be nearer to the truth to assume that new infections are caused by the presence of susceptibles in an infected environment of which infected individuals are only a part. Thus we could regard  $Y$  as an indicator of the level of infection in the environment whose true value is a continuous function like  $y(t)$ .

If we let  $X'$  and  $Y'$  be the number of susceptibles and infectives at time  $t$  for this model, the infinitesimal transition probability rates are given by

$$3.1 \quad (X', Y') \rightarrow \begin{cases} (X'-1, Y'+1) & \text{at rate } X'y, \\ (X', Y'-1) & \text{at rate } \rho Y', \end{cases}$$

where  $(X'(0), Y'(0)) = (n, a)$ , and where  $y$  is defined by equations 1.4.

The forward equation for  $p_{rs}(t)$ , the joint relative frequency function (the state probability function) of  $X'$  and  $Y'$  yields for  $r = 0, 1, \dots, n$  and  $s = 0, 1, \dots, n+a-r$ ,

$$3.2 \quad \dot{p}_{rs}(t) = -(ry + \rho s)p_{rs}(t) + (r+1)y p_{r+1, s-1}(t) + \rho(s+1)p_{r, s+1}(t),$$

where we define  $p_{rs}(t) = 0$  if either  $s = -1$ ,  $r > n$  or  $s > n+a-r$ .

Multiplying 3.2 by  $w^r z^s$  and summing over  $r = 0, 1, \dots, n$  and  $s = 0, 1, \dots, n+a-r$ , we find that  $P(w, z; t)$ , the joint p.g.f. of  $X'$  and  $Y'$  satisfies the partial differential equation

$$3.3 \quad \frac{\partial P}{\partial t} = y(z-w) \frac{\partial P}{\partial w} + \rho(1-z) \frac{\partial P}{\partial z},$$

where  $P(w, z; 0) = w^n z^a$ .

The characteristic equations of 3.3 are

$$-\frac{dt}{1} = \frac{dw}{y(z-w)} = \frac{dz}{\rho(1-z)},$$

yielding the integrals

$$3.4 \quad (1-z)e^{-\rho t} = k_1 = \text{const},$$

and

$$3.5 \quad w \exp\left[-\int_0^t y(s)ds\right] + \int_0^t y(u) \left[1 - k_1 e^{\rho u}\right] \exp\left[-\int_0^u y(s)ds\right] du = k_2 = \text{const}.$$

From equation 1.4a) we note that  $e^{-\int_0^u y(s)ds} = x(u)/n$ . Thus with some elementary algebra we may write 3.5 as

$$3.6 \quad 1 - (1-w) \frac{x}{n} + k_1 \left[ \frac{a}{n} - \frac{y}{n} e^{\rho t} \right] = k_2.$$

Hence the general solution of 3.3 is of the form

$$\pi\left\{(1-z)e^{-\rho t}, 1 - (1-w) \frac{x}{n} - \frac{1}{n} (1-z)(y - ae^{-\rho t})\right\},$$

where  $\pi(\cdot, \cdot)$  is an arbitrary function.

Using the initial condition we find that

$$3.7 \quad P(w, z; t) = [1 - (1-z)e^{-\rho t}]^a \left[ 1 - (1-w) \frac{x}{n} - \frac{1}{n} (1-z)(y - ae^{-\rho t}) \right]^n.$$

We note that this result may also be derived using the different approach of Faddy (1978) (see section 1.5).

The moments  $EX'$  and  $EY'$  are easily obtained from 3.7 or directly from 3.3 and are, as expected,

$$3.8a) \quad EX' = x ,$$

and

$$3.8b) \quad EY' = y .$$

Similarly, for the second factorial moments we obtain

$$3.8c) \quad EX'(X'-1) = \left(1 - \frac{1}{n}\right)x^2 ,$$

$$3.8d) \quad EX'Y' = \left(1 - \frac{1}{n}\right)xy + \frac{a}{n}xe^{-\rho t} ,$$

and

$$3.8e) \quad EY'(Y'-1) = ae^{-\rho t}[2y - (a+1)e^{-\rho t}] + \left(1 - \frac{1}{n}\right)(y - ae^{-\rho t})^2 .$$

Numerical results given in Faddy (1977) indicate that this process is a good approximation to the general epidemic model as long as the probability of early extinction,  $(\approx (\rho/n)^a)$  is small. However, the process shows systematic variation from true values which increases as  $(\rho/n)^a$  increases. The reason for this is that this modified process has very little chance of early extinction. The way to correct this shortcoming would be to use the birth and death process approximation (obtained by holding  $X$  constant) conditional on early extinction of the general epidemic process and use the quasi-deterministic process conditional on a major outbreak. The resulting process is discussed in the next section.

Note: We could also have formed an approximation by replacing  $X$  by  $x$  in the contact rate. This results in a generalised birth and death process (see Kendall (1948)). It is easily shown that  $EX' = x$  and  $EY' = y$ .

However, the other quantities of interest are not obtainable in such simple form



### 3.2 The approximating process

In the subcritical case ( $\rho > n$ ) the approximating process uses a birth and death process with birth rate  $n$  and death rate  $\rho$  for the number of infectives  $Y$ . If the population is supercritical ( $\rho < n$ ) with probability  $(\rho/n)^\alpha$  we use a birth and death process with birth rate  $\rho$  and death rate  $n$  for  $Y$ , and with probability  $1 - (\rho/n)^\alpha$  we use the quasi-deterministic process defined in section 3.1.

If we are using a birth and death process with birth rate  $\alpha$  and death rate  $\beta$  to approximate  $Y$  then  $n - X$  is the number of births in this process by  $t$ . The joint p.g.f.  $Q(w, z; t) = E(w^{n-X} z^Y)$  is given by

$$3.9 \quad Q(w, z; t) = \left\{ r_1 - (r_1 - r_2) \left[ 1 - \frac{z - r_2}{z - r_1} \exp(-\alpha(r_1 - r_2)t) \right] \right\}^{-1\alpha},$$

where  $r_1(w)$  and  $r_2(w)$  are the larger and smaller roots respectively of the equation

$$\alpha w r^2 - (\alpha + \beta)r + \beta = 0$$

(see Kendall (1948)).

Making use of equations 3.8 and 3.9, the first two factorial moments for the approximating process  $Y'$  are easily found to be as follows.

#### (i) THE SUBCRITICAL CASE

$$3.10a) \quad EY' = \alpha e^{-(\rho-n)t},$$

$$3.10b) \quad EX' = n \left[ 1 - \frac{\alpha}{\rho-n} (1 - e^{-(\rho-n)t}) \right],$$

$$3.10c) \quad EY'(Y'-1) = \alpha e^{-(\rho-n)t} \left[ \left( \alpha - \frac{\rho+n}{\rho-n} \right) e^{-(\rho-n)t} + \frac{2n}{\rho-n} \right],$$

$$3.10d) \quad EX'Y' = \frac{na}{\rho-n} e^{-(\rho-n)t} \left[ \left( a - \frac{\rho+n}{\rho-n} \right) (1-e^{-(\rho-n)t})^{-2\rho t} \right],$$

and

$$3.10e) \quad EX'(X'-1) = (n-1) \left[ n + \frac{2an}{\rho-n} (e^{-(\rho-n)t} - 1) \right] \\ + \frac{an^2}{(\rho-n)^2} \left\{ \left( a - \frac{\rho+n}{\rho-n} \right) (e^{-(\rho-n)t} - 1)^{2-4n} \left[ e^{-(\rho-n)t} \left( t + \frac{1}{\rho-n} \right) - \frac{1}{\rho-n} \right] \right\}.$$

(ii) THE SUPERCRITICAL CASE

$$3.11a) \quad EY' = \left( \frac{\rho}{n} \right)^\alpha a e^{-(n-\rho)t} + \left( 1 - \left( \frac{\rho}{n} \right)^\alpha \right) y,$$

$$3.11b) \quad EX' = \left( \frac{\rho}{n} \right)^\alpha \left[ n - \frac{a\rho}{n-\rho} (1-e^{-(n-\rho)t}) \right] + \left( 1 - \left( \frac{\rho}{n} \right)^\alpha \right) x,$$

$$3.11c) \quad EY'(Y'-1) = \left( \frac{\rho}{n} \right)^\alpha a \left[ \left( a - \frac{n+\rho}{n-\rho} \right) e^{-(n-\rho)t} + \frac{2\rho}{n-\rho} \right] e^{-(n-\rho)t} \\ + \left( 1 - \left( \frac{\rho}{n} \right)^\alpha \right) \left\{ a e^{-\rho t} [2y - (a+1)e^{-\rho t}] + \left( 1 - \frac{1}{n} \right) (y - a e^{-\rho t})^2 \right\},$$

$$3.11d) \quad EX'Y' = \left( \frac{\rho}{n} \right)^\alpha \frac{\rho a}{n-\rho} e^{-(n-\rho)t} \left[ \left( a - \frac{n+\rho}{n-\rho} \right) (1-e^{-(n-\rho)t})^{-2nt} \right] \\ + \left( 1 - \left( \frac{\rho}{n} \right)^\alpha \right) \left[ \left( 1 - \frac{1}{n} \right) xy + \frac{a}{n} x e^{-\rho t} \right],$$

and

$$3.11e) \quad EX'(X'-1) = \left( \frac{\rho}{n} \right)^\alpha \left\{ (n-1) \left[ n + \frac{2a\rho}{n-\rho} (e^{-(n-\rho)t} - 1) \right] \right. \\ \left. + \frac{a\rho^2}{(n-\rho)^2} \left[ \left( a - \frac{n+\rho}{n-\rho} \right) (e^{-(n-\rho)t} - 1)^{2-4n} \left[ e^{-(n-\rho)t} \left( t + \frac{1}{n-\rho} \right) - \frac{1}{n-\rho} \right] \right] \right\} \\ + \left( 1 - \left( \frac{\rho}{n} \right)^\alpha \right) \left( 1 - \frac{1}{n} \right) x^2.$$

Also in the supercritical case conditional on a major outbreak occurring, we may find approximations for the second moments of  $X$  and  $Y$  by using the diffusion limit. We assume that  $n$  is large enough so that

$$(U_n, V_n) \approx (U, V),$$

(see section 2.10), and then use equations 2.31 and 2.33.

### THE DISTRIBUTION OF THE FINAL SIZE

Letting  $t \rightarrow \infty$  in equations 3.7 and 3.9 we find the distribution of the final size for the quasi-deterministic process and the approximating birth and death process respectively. Thus we may readily find the distribution of  $Z'$ , the final size for the approximating process of this section, as follows.

(i) The subcritical case

Let  $P_{Z'}(w) = E(w^{Z'})$  be the p.g.f. of  $Z'$ . From 3.9 we have

$$3.12 \quad P_{Z'}(w) = \left[ \frac{n+\rho - \sqrt{(n+\rho)^2 - 4\rho w}}{2wn} \right]^a.$$

It can be shown from this expression (see Bailey (1975), p. 102) that

$$3.13 \quad \Pr\{Z' = r\} = \frac{a(2r+a-1)!}{r!(r+a)!} \frac{n^r \rho^{r+a}}{(n+\rho)^{2r+a}}.$$

Here we are neglecting the event that for this approximation  $Z'$  may be greater than  $n$ . For some cases, for instance when  $a$  is large compared with  $n$ , this event is not negligible (see figures 6a) and 7a) of Appendix B).

(ii) The supercritical case

From equation 3.7 we have that conditional on a major outbreak the number of susceptibles left after the process has become extinct,  $n - Z'$ , has p.g.f.

$$\left[ 1 - (1-w) \frac{\theta}{n} \right]^n .$$

Hence  $n - Z'$  has the binomial distribution with mean  $\theta$ , which is to say that as  $n \rightarrow \infty$  it has the Poisson distribution with mean  $\theta$ .

Recalling from 1.8 that

$$\theta \sim ne^{-(n+a)/\rho} , \text{ as } n \rightarrow \infty ,$$

we have agreement with Daniels' heuristic result given by equation 1.13. (For this result Daniels assumes that  $a/\rho$  is negligible.)

The binomial distribution of the number of susceptibles left has a simple interpretation. It is the distribution obtained by assuming that at the beginning of the epidemic and conditional on a major outbreak, each susceptible independently has probability  $\theta/n$  of escaping infection.

Hence for the p.g.f. of  $Z'$  we have

$$\begin{aligned} 3.14 \quad P_{Z'}(w) &= \left( \frac{\rho}{n} \right)^\alpha \left[ \frac{n+\rho - \sqrt{(n+\rho)^2 - 4n\rho w}}{2w\rho} \right]^\alpha + \left[ 1 - \left( \frac{\rho}{n} \right)^\alpha \right] w^n \left[ 1 - \left( 1 - \frac{1}{w} \right) \frac{\theta}{n} \right]^n \\ &= \left[ \frac{n+\rho - \sqrt{(n+\rho)^2 - 4n\rho w}}{2wn} \right]^\alpha + \left[ 1 - \left( \frac{\rho}{n} \right)^\alpha \right] \left[ w^{-(w-1)} \frac{\theta}{n} \right]^n . \end{aligned}$$

Thus using 3.13,

$$3.15 \quad \Pr\{Z' = r\} = \frac{a(2r+a-1)!}{r!(n+a)!} \frac{n^r \rho^{r+a}}{(n+\rho)^{2r+a}} + \left\{1 - \left(\frac{\rho}{n}\right)^a\right\} \binom{n}{r} \left(1 - \frac{\theta}{n}\right)^r \left(\frac{\theta}{n}\right)^{n-r}.$$

### THE DISTRIBUTION OF THE TIME TO EXTINCTION

Let  $T'$  be the time to extinction of the approximating process of this section. The distribution function of  $T'$  is given by

$F_{T'}(t) = P(1, 0; t)$ . Hence from 3.7 and 3.9 we obtain the following expressions.

(i) The subcritical case

$$3.16 \quad F_{T'}(t) = \left( \frac{\rho - \rho e^{-(\rho-n)t}}{\rho - n e^{-(\rho-n)t}} \right)^a.$$

(ii) The supercritical case

$$3.17 \quad F_{T'}(t) = \left(\frac{\rho}{n}\right)^a \left( \frac{n - n e^{-(n-\rho)t}}{n - \rho e^{-(n-\rho)t}} \right)^a + \left\{1 - \left(\frac{\rho}{n}\right)^a\right\} (1 - e^{-\rho t})^a \left[1 - \frac{1}{n} (y - a e^{-\rho t})\right]^n$$

$$= \left( \frac{\rho - \rho e^{-(n-\rho)t}}{n - \rho e^{-(n-\rho)t}} \right)^a + \left\{1 - \left(\frac{\rho}{n}\right)^a\right\} (1 - e^{-\rho t})^a \left[1 - \frac{1}{n} (y - a e^{-\rho t})\right]^n.$$

By the following theorem we establish that the asymptotic form of the mean of the approximation  $T'$  is the same as the asymptotic form of  $ET$  (see equation 1.20).

**THEOREM 3.1.** For  $\rho$  a positive constant,

$$ET' \sim \frac{1}{\rho} \ln(n+a), \text{ as } n \rightarrow \infty.$$

Proof. For  $n > \rho$  we have

$$ET' = \int_0^\infty \left\{ 1 - \left[ \frac{\rho}{n} \right]^\alpha \left( 1 + \frac{n-\rho}{\rho-ne^{(n-\rho)t}} \right)^\alpha + \left[ 1 - \left( \frac{\rho}{n} \right)^\alpha \right] \left[ 1 - e^{-\rho t} \right]^\alpha \left[ 1 - \frac{1}{n} (y - \rho e^{-\rho t}) \right]^n \right\} dt .$$

Let  $t_\epsilon$  ( $\epsilon > 0$ ) be the time for the deterministic process to reach  $x = \epsilon$ . By Lemma 4.2,  $t_\epsilon = o(1)$  as  $n \rightarrow \infty$ . Now for  $t > t_\epsilon$  by making use of equations 1.5 and 1.4b) we have that

$$3.18 \quad \left( n + \alpha - \epsilon + \rho \ln \frac{\epsilon}{n} \right) e^{-\rho t} < y(t) < \left( n + \alpha - \epsilon + \rho \ln \frac{\epsilon}{n} \right) e^{(\epsilon - \rho)t} .$$

Letting  $t = (u \ln(n + \alpha)) / \rho$  we may write the first inequality as

$$y \left( \frac{u \ln(n + \alpha)}{\rho} \right) > \left( n + \alpha - \epsilon + \rho \ln \frac{\epsilon}{n} \right) \frac{1}{(n + \alpha)^u} ,$$

as long as  $u > (\rho t_\epsilon) / \ln(n + \alpha)$ .

Making the change of variable to  $u$  in the integration and letting

$$g_n(u) = 1 - \left( \frac{\rho}{n} \right)^\alpha \left\{ 1 + (n - \rho) \left[ \rho - n(n + \alpha)^{(n - \rho)u / \rho} \right]^{-1} \right\}^\alpha + \left[ 1 - \left( \frac{\rho}{n} \right)^\alpha \right] \left( 1 - \frac{1}{(n + \alpha)^u} \right)^\alpha \left( 1 - \frac{n - \epsilon + \rho \ln(\epsilon / n)}{n(n + \alpha)^u} \right)^n ,$$

we have

$$\frac{\rho ET'}{\ln(n + \alpha)} > \int_0^{\rho t_\epsilon / \ln(n + \alpha)} \left[ 1 - F_{T'} \left( \frac{\ln(n + \alpha)}{\rho} \right) \right] du + \left\{ \int_{\rho t_\epsilon / \ln(n + \alpha)}^1 + \int_1^\infty \right\} g_n(u) du .$$

Using l'Hôpital's rule we may show that

$$\lim_{n \rightarrow \infty} g_n(u) = \begin{cases} 1 & , u < 1 , \\ 1 - e^{-1} & , u = 1 , \\ 0 & , u > 1 . \end{cases}$$

Therefore,

$$\lim_{n \rightarrow \infty} \frac{\rho ET'}{\ln(n+a)} > 1 + \lim_{n \rightarrow \infty} \lim_{m \rightarrow \infty} f(m, n) ,$$

where

$$f(m, n) = \int_1^m g_n(u) du .$$

The uniform convergence of  $f(m, n)$  to 0 as  $n \rightarrow \infty$  may be established by straightforward though tedious algebra. Hence the order of taking limits may be reversed and we have

$$\lim_{n \rightarrow \infty} \frac{\rho ET'}{\ln(n+a)} > 1 .$$

Similarly by using the second inequality in 3.18 we may show that

$$\lim_{n \rightarrow \infty} \frac{(\rho - \epsilon) ET'}{\ln(n+a)} < 1 .$$

Since  $\epsilon$  is an arbitrary number greater than  $\theta$  and  $\theta \rightarrow 0$  as  $n \rightarrow \infty$ , the result follows.  $\square$

### 3.3 Numerical results and discussion

In Appendix B we show comparisons of true values of  $EX$ ,  $\text{Var } X$ ,  $EY$ ,  $\text{Var } Y$ ,  $F_T(t)$  and the final size distribution with the corresponding

approximating functions calculated from the formulae given in the last section. The true values were calculated from 10,000 computer simulations of each epidemic. The initial number of susceptibles,  $n$ , takes the values 5, 10, 20, 40 and 80. The initial number of infectives,  $a$ , takes the values 1 and 5. In all cases the relative removal rate,  $\rho$ , is 9.

The quantities shown with a prime are the approximations. The variances shown with a double prime which appear in the graphs where  $n = 20, 40$  and  $80$  are derived from the diffusion approximation (i.e. using equations 2.31 and 2.33).

Another approximation which has been put forward is that of Ludwig (1973). This approximation gives excellent results for  $EX$ ,  $EY$  and  $F(t)$ , which, for the cases shown, are almost indistinguishable from the real values. However the approximate solution is itself quite complicated, involving the solution of  $2(n+a+1)$  recursive D.E.'s. When this method was applied even to the case  $(n,a) = (5,5)$  and  $\rho = 9$ , standard double precision library subroutines using either Runge-Kutta or Hamings modified predictor corrector method were unable to guarantee accuracy of .01 for  $t > .2$ .

The main advantage of the approximation presented here is its simplicity. A simple expression for the p.g.f. of the process is available, enabling closed form expressions for quantities of interest to be found. Evaluating these expressions involves only one numerical integration.

The use of the approximation results in an enormous saving in computer time. On the Univac 1100/42 the total computer time involved in the simulations was 2,300 seconds whereas the total time involved in calculating the approximations was 7.0 seconds.



## THE BEHAVIOUR OF THE EPIDEMIC PROCESS GIVEN EARLY EXTINCTION

Figures 1, 2, 6 and 7 of Appendix B show cases in which early extinction occurs with high probability so that the birth and death process part of the approximation is dominant. The approximate means  $EX'$  and  $EY'$  are seen to deviate wildly from the true values except for the case of figure 1 where  $(n, a) = (5, 1)$ . This has occurred because the assumption that conditional on early extinction  $X$  does not vary much from its initial value is not true in these cases. Quite clearly we need something other than  $n$  with which to estimate the mean of the approximating birth and death process. The expected final size in a birth and death process with birth rate  $\mu$ , death rate  $\gamma$  and  $a$  initial individuals is  $\frac{a\mu}{\gamma-\mu}$ , so if we choose  $\gamma = \rho$  and  $\mu = \frac{\rho C_{\rho}(n,a)}{a + C_{\rho}(n,a)}$ , this process will have the same final size as the epidemic process. The resulting approximations are shown with a double prime on figures 1, 2, 6 and 7. This results in a considerable improvement, although the approximation to  $Var X$  is still poor.

## THE EXPECTED FINAL SIZE IN A NEAR CRITICAL EPIDEMIC

It is the near critical (i.e.  $\rho \approx n$ ) epidemics whose behaviour is most difficult to describe. In the following we consider the asymptotic properties of  $C_n(n,a)$ .

We know that

$$3.19 \quad C_n(n,a) = \frac{1}{2}[1 + C_n(n-1,a+1)] + \frac{1}{2}C_n(n,a-1) .$$

It is readily shown that

$$3.20 \quad C_n(n,a) < a C_n(n,1) \quad a = 2,3,\dots ,$$

and that

$$3.21 \quad C_n(n-1,a) < C_n(n,a) .$$

Putting  $a = 1$  in 3.19 we get

$$C_n(n,1) = \frac{1}{2} + \frac{1}{2}C_n(n-1,2) ,$$

which with 3.20 and 3.21 gives

$$\frac{C_n(n, 2)}{2} < C_n(n, 1) < \frac{C_n(n, 2) + 1}{2} .$$

This may easily be extended by induction to give

$$3.22 \quad \frac{C_n(n, a)}{a} < C_n(n, 1) < \frac{C_n(n, a) + 2^{a-1} - 1}{a} , \quad a = 2, 3, \dots .$$

Since  $C_n(n, a) < n$  we have

$$\frac{C_n(n, 1)}{n} < \frac{1}{a} + \frac{1}{n} \cdot \frac{2^{a-1} - 1}{a} , \quad a = 2, 3, \dots .$$

This implies that  $C_n(n, 1)$  (and hence  $C_n(n, a)$ ,  $a = 2, 3, \dots$ ), is  $o(n)$  as  $n \rightarrow \infty$ .

We would expect that  $C_n(n-1, a)$  and  $C_n(n, a)$  are of the same order of magnitude as  $n \rightarrow \infty$  (with  $a = o(n)$ ). Hence from 3.19 we get

$$C_n(n, a) \sim a C_n(n, 1) - 2^{a-1} + 1 .$$

Now  $C_n(n, 1)$  must be unbounded as  $n \rightarrow \infty$ , otherwise we could choose  $a$  so that the R.H.S. is negative.

#### SOME NUMERICAL RESULTS

$n$	$C_n(n, 1)$	$\log_e n$	$\frac{1}{2}\sqrt{n}$
1	.5	0	.5
5	1.31	1.61	1.12
10	1.89	2.30	1.59
20	2.62	3.00	2.24
50	3.95	3.91	3.54
100	5.29	4.61	5.00
500	9.98	6.21	11.12
1000	12.95	6.91	15.81

These results show  $C_n(n, 1)$  to be increasing very slowly with  $n$ .

The function does not seem to follow a power or logarithm law.

#### APPLICATION TO OTHER MODELS

The idea behind the quasi-deterministic model of section 3.1 would also be useful in constructing approximations for other processes which like the general epidemic process have transition probability rates which are non-linear in stochastic variables. One such model is the predatory-prey model (see e.g. Bharucha Reid (1960)). In Appendix C we present a brief study of the application of a quasi-deterministic approximation to this model.

## CHAPTER 4

## THE GENERATION-WISE SPREAD OF INFECTION

## 4.0 Introduction

In some applications of epidemic models it is important to consider the individual generations of infection (see e.g. Becker (1976), (1980)). In particular this is useful when applying the model to the spread of rumours (see section 1.6) in which case we would expect that the rumour becomes more distorted as the "generation distance" of the hearer from the source increases. By the source we mean the initial or "zeroth generation" infectives.

In section 4.1 we find recursive expressions for the mean final sizes of the individual generations. These expressions would be useful only for the case of fairly small population sizes and consequently we turn to the deterministic model, deriving a simple formula for each generation size at any time and also an asymptotic result for its final size.

The approximating process of chapter 3 is applied to this situation in section 4.2. The limiting process analogous to that of section 2.10 is presented in the final section.

## 4.1 The mean generation size

Let

$$C_g(n, \mathbf{a}) = E \left\{ W_g \mid \left[ X(0), Y_0(0), \dots, \sum_{k=m+1}^{\infty} Y_k(0) \right] = (n, \mathbf{a}) \right\},$$

$$g = 0, 1, \dots, m,$$

where  $(n, \mathbf{a}) \equiv (n, a_0, \dots, a_{m+1})$ .

Multiplying equation 1.25 by  $r_g$  and summing over  $r_g = 0, 1, \dots, n$ , we obtain for  $g = 1, 2, \dots, m$ ,

$$4.1 \quad C_g(n, a) = \left[ (\mu n + \gamma) \sum_{k=0}^{m+1} a_k \right]^{-1} \left\{ \mu n \sum_{k=1}^{m+1} a_{k-1} [\delta(k-g) + C_g(n-1, a + e_k)] \right. \\ \left. + \mu n a_{m+1} C_g(n-1, a + e_{m+1}) + \gamma \sum_{k=0}^m a_k C_g(n, a - e_k) \right\}, \\ n = 1, 2, \dots, \quad a_0, \dots, a_{m+1} = 0, 1, \dots,$$

where  $e_k$  is the  $(k+1)$ th row of the  $(m+2) \times (m+2)$  identity matrix, and

$$C_g(0, a) = 0, \quad a_0, \dots, a_{m+1} = 0, 1, \dots$$

Any  $C_g(\cdot, \cdot)$  may be found from 4.1 using a recursive procedure.

(Section 5.4 describes explicitly a similar procedure.) We note that for realistic initial conditions we would have  $a_1 = a_2 = \dots = a_{m+1} = 0$  but in order to find  $C_g(n, a_0, 0, \dots, 0)$  we must also compute the  $C_g(\cdot, \cdot)$  for more general initial conditions.

Equation 4.1, though similar in form to 1.14, is sufficiently more complicated to be useless for the development of expressions analogous to 1.16 and 1.17 from which asymptotic results like Theorem 2.2 were derived. We turn therefore to the deterministic model to examine the behaviour of the generation sizes as  $n \rightarrow \infty$ . In section 2.2 we saw that asymptotically the expected final size in the stochastic model and the final size in the quasi-deterministic model were very close and we expect the same to be true with regard to the final generation sizes.

Before looking at this asymptotic behaviour we obtain some useful expressions from equation 1.6.

From 1.6 we have

$$4.2 \quad t(u) = \int_u^n \frac{dv}{\mu v \psi(v)},$$

where

$$\psi(v) = n + a - v + \frac{\gamma}{\mu} \ln \frac{v}{n}.$$

Also

$$4.3 \quad \frac{d\psi}{dv} = -1 + \frac{\gamma}{\mu v}.$$

Using 4.2 and 4.3 we obtain

$$4.4 \quad \int_u^n \frac{dv}{\psi(v)} = \gamma t + \ln \frac{y(t)}{a}.$$

Substituting 4.4 in 1.27 and using 4.2 yields

$$z_g(t) = \frac{\alpha \gamma}{g!} \int_0^t \left( \gamma \tau + \ln \frac{y(\tau)}{a} \right)^g e^{-\gamma \tau} d\tau.$$

Hence from 1.26c) we have

$$4.5 \quad y_g(t) = \frac{a}{g!} \left( \gamma t + \ln \frac{y(t)}{a} \right)^g e^{-\gamma t},$$

$$4.6 \quad = \frac{a}{g!} \left[ \mu \int_0^t x(\tau) d\tau \right]^g e^{-\gamma t}, \text{ using 1.4b).}$$

Equation 4.5 is particularly useful because it shows that since  $y = \psi(x)$ , it is only necessary to compute  $x(t)$  to find all the  $y_g(t)$ ,  $g = 0, 1, \dots$ .

The asymptotic behaviour (as  $n \rightarrow \infty$ ) of the final generation sizes in the deterministic model is described in the following theorem.

**THEOREM 4.1.** *In the deterministic model defined in section 1.6, if  $\mu$  and  $\gamma$  are positive constants and  $a$  a positive integer,*

$$4.7 \quad z_g^{(\infty)} \sim \frac{a}{g!} (\ln n)^g, \text{ as } n \rightarrow \infty, \quad g = 0, 1, \dots$$

**Proof.** We shall make use of two lemmas which we shall prove below.

Let  $t_\epsilon$  be the time for  $x$  to reach  $\epsilon$ , where  $\epsilon > \theta$ . (Note that since  $\theta \rightarrow 0$  as  $n \rightarrow \infty$ ,  $\epsilon$  can be arbitrarily small.) Now

$$z_g(t_1) + y_g(t_1) \leq z_g^{(\infty)} \leq z_g(t_1) + y_g(t_1) + 1$$

Hence

$$z_g^{(\infty)} = o(1) + \frac{a}{g!} \left[ \gamma t_1 + \ln \left( \frac{n+a-1-\rho \ln n}{a} \right) \right]^g e^{-\gamma t_1}$$

using Lemma 4.3 and equation 4.5

$$\sim \frac{a}{g!} (\ln n)^g, \text{ as } n \rightarrow \infty,$$

from Lemma 4.2.  $\square$

We note that this result is the same as that of Daley (1967) for the final generation sizes in the simple epidemic ( $\gamma = 0$ ).

**LEMMA 4.2.** *Under the conditions of Theorem 4.1 and where  $\epsilon$  is a positive constant,*

$$t_\epsilon \rightarrow 0, \text{ as } n \rightarrow \infty.$$

Proof.

$$t_{\varepsilon} = \int_{\varepsilon}^n \frac{dv}{\mu v \psi(v)}$$

$$= \left( \int_{n-\sqrt{n}}^n + \int_{\sqrt{n}}^{n-\sqrt{n}} + \int_{\varepsilon}^{\sqrt{n}} \right) \frac{dv}{\mu v (n+a-v+\rho \ln(v/n))}.$$

Therefore,

$$\mu t_{\varepsilon} \leq \int_{n-\sqrt{n}}^n \frac{dv}{v (n+a-v+\rho \ln(1-(1/\sqrt{n})))} + \int_{\sqrt{n}}^{n-\sqrt{n}} \frac{dv}{v (n+a-v-(\rho/2) \ln n)}$$

$$+ \int_{\varepsilon}^{\sqrt{n}} \frac{dv}{v (n+a-v-\rho \ln(n/\varepsilon))},$$

as long as  $n$  is large enough so that each integrand is positive over its range of integration.

Under this condition,

$$\mu t_{\varepsilon} \leq \frac{1}{n-\sqrt{n}} \ln \left( \frac{\sqrt{n}+a+\rho \ln(1-(1/\sqrt{n}))}{a+\rho \ln(1-(1/\sqrt{n}))} \right) + \frac{1}{\sqrt{n}} \ln \left( \frac{n-\sqrt{n}+a-(\rho/2) \ln n}{\sqrt{n}+a-(\rho/2) \ln n} \right)$$

$$+ \frac{1}{n+a-\rho \ln(n/\varepsilon)} \ln \left( \frac{\sqrt{n}(n-\varepsilon+a-\rho \ln(n/\varepsilon))}{n-\sqrt{n}+a-\rho \ln(n/\varepsilon)} \right),$$

$\rightarrow 0$ , as  $n \rightarrow \infty$ .  $\square$

LEMMA 4.3. Under the conditions of Theorem 4.1,

$$z_g(t_1) \rightarrow 0, \text{ as } n \rightarrow \infty.$$

Proof. If  $u \in [n-\sqrt{n}, n]$  then

$$\int_u^n \frac{dv}{\psi(v)} \leq \int_u^n \frac{dv}{n+a-v+\rho \ln(1-(1/\sqrt{n}))}$$

as long as  $n$  is large enough so that the integrand is positive over its range of integration

$$= \ln \left( \frac{n+a-u}{a} \right) + o(1), \text{ as } n \rightarrow \infty.$$

Similarly, by partitioning the interval  $[u, n]$  as in Lemma 4.2 we have for  $n$  large enough,

$$u \in [\sqrt{n}, n-\sqrt{n}] \Rightarrow \int_u^n \frac{dv}{\psi(v)} \leq \ln \left( \frac{n+a-u-(\rho/2)\ln n}{a} \right) + o(1)$$

and

$$u \in [1, \sqrt{n}] \Rightarrow \int_u^n \frac{dv}{\psi(v)} \leq \ln \left( \frac{n+a-u-\rho \ln n}{a} \right) + o(1), \text{ as } n \rightarrow \infty.$$

Hence 1.27 gives for  $n$  large enough,

$$\begin{aligned} z_g(t_1) &\leq \int_{n-\sqrt{n}}^n \left[ \ln \left( \frac{n+a-u}{a} \right) + \alpha_1 \right]^g \frac{ae^{\alpha_2}}{(n+a-u)u} du \\ &\quad + \int_{\sqrt{n}}^{n-\sqrt{n}} \left[ \ln \left( \frac{n+a-u-(\rho/2)\ln n}{a} \right) + \alpha_3 \right]^g \frac{ae^{\alpha_4}}{(n+a-u)u} du \\ &\quad + \int_1^{\sqrt{n}} \left[ \ln \left( \frac{n+a-u-\rho \ln n}{a} \right) + \alpha_5 \right]^g \frac{ae^{\alpha_6}}{(n+a-u)u} du \end{aligned}$$

where  $\alpha_i = o(1)$  as  $n \rightarrow \infty$ ,  $i = 1, \dots, 6$

$\rightarrow 0$ , as  $n \rightarrow \infty$ .  $\square$

We note that this result means that although when  $x = 1$  all except 1 of the possible infectives has already been "born" this has happened so fast that none has yet "died".



## 4.2 An approximating process

Using the same method as used in the proof of Theorem 2.1 it may be possible to find an expression for the joint p.g.f. of  $(X, Y_0, Y_1, \dots)$  which is of similar form. This expression would however be so complicated that it would be useless for any practical purpose. Hence we turn to the methods of chapter 3 for a process which will provide workable approximations to quantities of interest.

### (i) THE SUBCRITICAL CASE

In the subcritical case the bounding birth and death process  $Y'$  will become extinct with probability one. In this eventuality we form the approximating process by letting  $X$  be constant at its initial value  $n$ . Thus the process has the following infinitesimal transition probability rates:

$$(X', Y') \rightarrow \begin{cases} (X'-1, Y'+\epsilon_{g+1}) & \text{at rate } \mu n Y'_g, \\ (X', Y'-\epsilon_g) & \text{at rate } \gamma Y'_g, \end{cases} \quad g = 0, 1, \dots,$$

where  $\epsilon_g$ ,  $g = 0, 1, \dots$ , is the vector with 1 in the  $(g+1)$ th position and zero elsewhere.

In the usual way we find that the p.g.f.,

$$P'(z_0, z_1, \dots; t) = E \left\{ z_0^{Y_0} z_1^{Y_1} \dots \right\}$$

satisfies

$$4.8 \quad \frac{\partial P'}{\partial t} = \sum_{k=0}^{\infty} [\gamma(1-z_k) + \mu n z_k (z_{k+1} - 1)] \frac{\partial P'}{\partial z_k}.$$

From 4.8 we obtain

$$4.9 \quad \frac{dEY'_g}{dt} = -\gamma EY'_g + \mu n EY'_{g-1}, \quad g = 0, 1, \dots,$$

where  $EY'_{-1} \equiv 0$ .

It follows that

$$4.10 \quad EY'_g = a \frac{(\mu n t)^g}{g!} e^{-\gamma t}, \quad g = 0, 1, \dots,$$

and it is easily shown that the expected final size of the  $g$ th generation is given by

$$4.11 \quad E(W'_g(\infty)) = a \left( \frac{\mu n}{\gamma} \right)^g.$$

#### (ii) THE SUPERCRITICAL CASE

In the supercritical case  $Y'$  will become extinct with probability  $(\rho/n)^\alpha$  in which case it behaves like a birth and death process with birth rate  $\gamma$  and death rate  $\mu n$ . Thus we assume that with probability  $(\rho/n)^\alpha$  the epidemic process will become extinct early and in this eventuality we use  $Y'$  as the approximation for  $Y$ . It follows from the above equations that

$$E(Y'_g \mid \text{early extinction}) = a \frac{(\gamma t)^g}{g!} e^{-\mu n t}, \quad g = 0, 1, \dots,$$

and

$$E(W'_g(\infty) \mid \text{early extinction}) = a \left( \frac{\gamma}{\mu n} \right)^g.$$

The epidemic process will become a major outbreak with probability approximately  $1 - (\rho/n)^\alpha$  and in this eventuality the approximating process has infinitesimal transition probability rates given by

$$(X', Y') \rightarrow \begin{cases} (X'-1, Y'+\epsilon_{g+1}) & \text{at rate } \mu X' y_g, \\ (X', Y'-\epsilon_g) & \text{at rate } \gamma Y'_g. \end{cases}$$

The joint p.g.f.,  $P'(w, z_0, z_1, \dots; t)$  satisfies

$$4.12 \quad \frac{\partial P'}{\partial t} = \sum_{k=0}^{\infty} \left[ u(z_{k+1}-w) y_k(t) \frac{\partial P'}{\partial w} + \gamma(1-z_k) \frac{\partial P'}{\partial z_k} \right].$$

The characteristic equations of 4.12 are

$$-\frac{dt}{1} = dw / \left( \sum_{k=0}^{\infty} u y_k(z_{k+1}-w) \right) = \frac{dz}{\gamma(1-z_g)}, \quad g = 0, 1, \dots,$$

which yield the integrals

$$(1-z_g) e^{-\gamma t} = k_g = \text{const}, \quad g = 0, 1, \dots,$$

and

$$\sum_{k=1}^{\infty} \frac{y_k(t)}{n} (1-z_k) + \frac{x(t)}{n} (1-w) - 1 = k = \text{const},$$

from which we obtain, with the use of the initial condition

$$P'(w, z_0, z_1, \dots; 0) = w^n z_0^a,$$

$$4.13 \quad P'(w, z_0, z_1, \dots; t)$$

$$= \left[ 1 - (1-z_0) e^{-\gamma t} \right]^a \left[ 1 - (1-w) \frac{x(t)}{n} - \sum_{k=1}^{\infty} (1-z_k) \frac{y_k(t)}{n} \right]^n.$$

We easily obtain the following factorial moments from 4.13:

$$4.14a) \quad EX' = x(t),$$

$$4.14b) \quad EY'_g = y_g(t), \quad g = 0, 1, \dots,$$

$$4.14c) \quad EX'(X'-1) = \left( 1 - \frac{1}{n} \right) (x(t))^2,$$

$$4.14d) \quad EY'_0(Y'_0-1) = a(a-1) e^{-2\gamma t},$$

$$4.14e) \quad EY'_g(Y'_g-1) = \left(1 - \frac{1}{n}\right) (y_g(t))^2, \quad g = 1, 2, \dots$$

Further we have

$$4.15 \quad E\{W_g(\infty)\} = \gamma \int_0^\infty y_g(t) dt = z_g(\infty).$$

### 4.3 A limiting process

We present the limiting process which is analogous to that of section 2.10 and follows directly from Barbour (1974).

Let  $X(0) = n$  and  $Y_g(0) = nh\delta(g)$ , where  $h$  is a constant,  $g = 0, 1, \dots$ . Further, let  $\xi(t) = x(t)/n$  and  $\eta_g(t) = y_g(t)/n$ ,  $g = 0, 1, \dots$ , where  $x(t)$  and  $y_g(t)$  are defined by equation 1.26 with  $\mu$  replaced by  $\mu/n$ . Then on any fixed time interval  $(0, \tau)$ , the random vector

$$\left( U^{(n)}, V_0^{(n)}, V_1^{(n)}, \dots \right) = \left( \frac{X-n\xi}{\sqrt{n}}, \frac{Y_0-n\eta_0}{\sqrt{n}}, \frac{Y_1-n\eta_1}{\sqrt{n}}, \dots \right)$$

converges weakly as  $n \rightarrow \infty$  to the diffusion  $(U, V_0, V_1, \dots)$  whose joint p.g.f.  $P(u, v_0, \dots; t)$  satisfies

$$4.16 \quad \frac{\partial P}{\partial t} - \sum_{i=1}^{\infty} \left\{ \mu \left( \ln \frac{v_i}{u} \right) \left[ \eta_{i-1} u \frac{\partial P}{\partial u} + \xi v_{i-1} \frac{\partial P}{\partial v_{i-1}} \right] \right. \\ \left. - \gamma v_i \ln v_i \frac{\partial P}{\partial v_i} + \frac{1}{2} P \left[ \mu \xi \eta_{i-1} \left( \ln \frac{v_i}{u} \right)^2 + \gamma \eta_i (\ln v_i)^2 \right] \right\} = 0,$$

where  $\eta_{-1} \equiv 0$  and  $v_{-1} = 0$ .

From 4.16 we may readily show that the means  $EU, EV_i$ ,  $i = 0, 1, \dots$ , are all identically zero and the second moments satisfy the equations

$$4.17a) \quad \frac{dEU^2}{dt} + \mu \left( \sum_{i=1}^{\infty} \eta_{i-1} \right) (2EU^2 - \xi) + 2\mu\xi \sum_{i=1}^{\infty} EUV_{i-1} = 0,$$

$$4.17b) \quad \frac{dEUV_j}{dt} + \left( \gamma + \mu \sum_{i=1}^{\infty} \eta_{i-1} \right) EUV_j + \mu\xi \sum_{i=1}^{\infty} EV_{i-1} V_j \\ - \mu \left( \eta_{j-1} EU^2 + \xi EUV_{j-1} \right) + \mu\xi \eta_{j-1} = 0, \quad j = 0, 1, \dots,$$

$$4.17c) \quad \frac{dEV_j V_k}{dt} - \mu \left( \eta_{k-1} EUV_j + \eta_{j-1} EUV_k + \xi [EV_{k-1} V_j + EV_k V_{j-1}] \right) \\ - (\mu\xi \eta_{j-1} + \gamma \eta_j) \delta(k-j) + 2\gamma EV_k V_j = 0, \quad j, k = 0, 1, \dots$$

Assuming that  $n$  is large enough to take

$$\left( U^{(n)}, V_0^{(n)}, \dots \right) \approx (U, V_0, \dots),$$

we may use equations 4.17 to find an approximation to  $\text{Var}(X)$  and  $\text{Var}(Y_g)$ ,  $g = 0, 1, \dots$ , that would be useful in the event of a major outbreak.

## CHAPTER 5

## THE GENERAL EPIDEMIC IN A STRATIFIED POPULATION

## 5.0 Introduction

One of the assumptions made in the general epidemic model is that the individuals in a population (except for those that are removed) mix uniformly, i.e., in any given time interval each pair of individuals has an equal chance of meeting. In the case of a human population of any size this is certainly not true. In general any member of the population meets the same people each day. A population can be considered as stratified with people mixing within their particular strata or group and with much more restricted contact between groups. In this chapter we study a model which incorporates this feature.

The first section deals with the effect of the stratification on the important threshold theorem. In the stochastic case we may apply known results of general linear processes to find the threshold condition which arises from making a simplifying assumption that is analogous to one which is reasonable in the case of the general epidemic in a homogeneous population. Equations for the probability of early extinction (under this assumption) are found and solved in a simple case. We also find an approximate expression for the probability that infection initially introduced into one subpopulation will not spread to other subgroups.

In the usual way we use renewal arguments to find recursive expressions for the mean final sizes of the epidemic in each subgroup and also for the mean duration time of the process.

The final section presents the limiting process analogous to that of section 2.10.

## 5.1 The threshold theorem

The threshold theorem for the general epidemic in a homogeneous population does not have a simple analogue for the case of a general epidemic in a stratified population. In the latter model a greater range of behaviour is possible. Thus in the case of the deterministic model an initial decrease in the number of infectives in a particular group does not guarantee that the infectives will always be decreasing. However, the usual thresholds  $n_i \mu_{ii} = \gamma_i$ ,  $i = 1, \dots, m$ , which we would have if the groups were to be isolated ( $\mu_{ji} = 0$ ,  $i, j = 1, \dots, m$ ,  $i \neq j$ ) do have a big effect on the size of the epidemic. This will be demonstrated for both the deterministic and stochastic models.

### THE DETERMINISTIC MODEL

We consider the case when  $m = 2$ . Let  $\theta_i = x_i^{(\infty)}$ ,  $i = 1, 2$ .

Equations 1.32 become

$$5.1 \quad -\gamma_1 \ln \frac{\theta_1}{n_1} = \mu_{11}(n_1 + a_1 - \theta_1) + \mu_{21}(n_2 + a_2 - \theta_2),$$

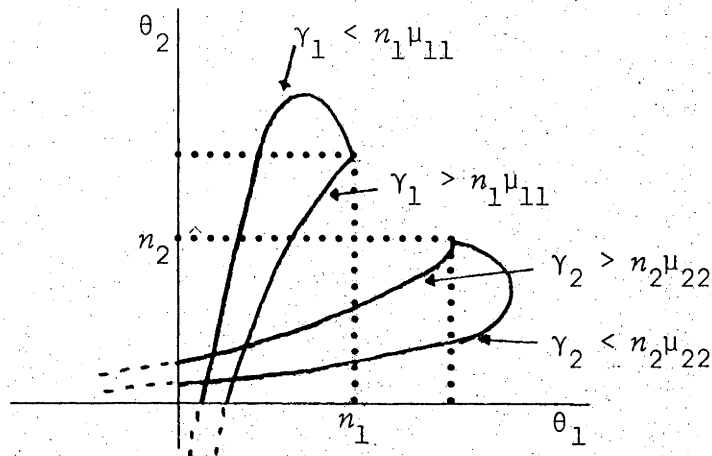
and

$$5.2 \quad -\gamma_2 \ln \frac{\theta_2}{n_2} = \mu_{22}(n_2 + a_2 - \theta_2) + \mu_{12}(n_1 + a_1 - \theta_1).$$

From 5.1 we have

$$\begin{aligned} \frac{d\theta_2}{d\theta_1} &= \frac{1}{\mu_{21}} \left( -\mu_{11} + \frac{\gamma_1}{\theta_1} \right) \\ &= 0 \quad \text{when} \quad \theta_1 = \frac{\gamma_1}{\mu_{11}}. \end{aligned}$$

Since  $0 \leq \theta_1 \leq n_1$  there can be no turning point if  $\gamma_1 > n_1 \mu_{11}$ . Treating equation 5.2 similarly we may draw the curves defined by 5.1 and 5.2 as follows.



The solutions to 5.2 and 5.3 are the points of intersection of the curves with horizontal and vertical asymptotes. The effect of the thresholds  $(n_i \mu_{ii} = \gamma_i, i = 1, 2)$  on these points is plainly seen.

#### THE STOCHASTIC MODEL

In the case of the general epidemic process in a homogeneous population the early behaviour can be approximated by assuming that the number of susceptibles in the population remains constant at its initial value and considering the behaviour of the birth and death process which results from this assumption. We expect this to be true for the general epidemic process in a stratified population. Letting  $X_i = n_i, i = 1, \dots, m$ , the process becomes a linear multivariate birth and death process which we shall call  $Y'$ . The necessary and sufficient condition for the extinction with probability 1 of  $Y'$  is well known (see e.g. Griffiths (1973)) to be that the characteristic roots of the matrix  $M = A - B$  have negative real parts, where in our case

$$A = \{\alpha_{ij}\} = \{n_i \mu_{ji}\},$$



and

$$B = \{\beta_{ij}\} ,$$

where

$$\beta_{ij} = \begin{cases} \gamma_i & \text{if } i = j , \\ 0 & \text{otherwise.} \end{cases}$$

We take this condition to be the threshold condition, no major outbreak being possible if it is satisfied.

For the case  $m = 2$  the characteristic roots are

$$\frac{1}{2} \left\{ n_1 \mu_{11} - \gamma_1 + n_2 \mu_{22} - \gamma_2 \pm \left[ (n_1 \mu_{11} - \gamma_1 - n_2 \mu_{22} + \gamma_2)^2 + 4 n_1 n_2 \mu_{21} \mu_{12} \right]^{\frac{1}{2}} \right\} .$$

The roots are both real and in order that they both be negative it is necessary and sufficient that all of

$$5.3 \quad n_1 \mu_{11} - \gamma_1 < 0 ,$$

$$5.4 \quad n_2 \mu_{22} - \gamma_2 < 0 ,$$

and

$$5.5 \quad (n_1 \mu_{11} - \gamma_1) (n_2 \mu_{22} - \gamma_2) > n_1 n_2 \mu_{21} \mu_{12} ,$$

should be satisfied.

Equations 5.3 and 5.4 are the familiar threshold conditions for the case of isolated populations.

When we have two populations interacting in this fashion we might expect that to a good approximation,  $\mu_{11} = \mu_{22} = \mu$ ,  $\mu_{12} = \mu_{21} = q\mu$ ,

where  $0 < q < 1$ , and  $\gamma_1 = \gamma_2 = \gamma$ . Hence equation 5.5 shows that even for two subpopulations which are individually subcritical a major outbreak may occur if

$$5.6 \quad \left(1 - \frac{\gamma}{n_1 \mu}\right) \left(1 - \frac{\gamma}{n_2 \mu}\right) < q^2.$$

We conclude by noting that for  $Y'$  to become extinct with probability 1 it is obviously necessary that  $\mu_{ii} n_i \leq \gamma_i$ ,  $i = 1, \dots, m$ , because otherwise

$$\frac{dEY_i}{dt} \geq (\mu_{ii} n_i - \gamma_i) EY_i \text{ for some } i.$$

## 5.2 The probability of early extinction

We approximate the probability of early extinction of the general epidemic process in a stratified population by the probability of eventual extinction of the initial approximating multivariate birth and death process  $Y'$ .

If the characteristic roots of  $M$  do not all have negative real parts  $Y'$  may become extinct with probability less than 1. In this case let

$$p_i = \Pr\{\text{eventual extinction of } Y' \mid Y'(0) = e_i\}, \quad i = 1, \dots, m,$$

where  $e_i$  is the  $i$ th row of the  $m \times m$  identity matrix.

Because each infective acts independently of the others we have

$$5.7 \quad \Pr\{\text{eventual extinction of } Y' \mid Y'(0) = (a_1, \dots, a_m)\} = \prod_{i=1}^m p_i^{a_i}.$$

By considering the possible transitions of the embedded random walk process we have that the  $p_i$  satisfy the set of equations

$$-\left(\gamma_i + \sum_{j=1}^m n_i \mu_{ji}\right) p_i + \gamma_i + \sum_{j=1}^m n_i \mu_{ji} p_j p_i = 0, \quad i = 1, \dots, m,$$

which may also be written in the form

$$5.8 \quad (n_i \mu_{ii} p_i - \gamma_i) (p_i - 1) + \sum_{\substack{j=1 \\ j \neq i}}^m n_i \mu_{ji} p_i (p_j - 1) = 0, \quad i = 1, \dots, m,$$

(this result is essentially contained in Griffiths (1973)).

From 5.8 we see that (as expected) for isolated population groups (i.e.  $\mu_{ij} = 0, \quad i \neq j$ ) we have

$$p_i = \min\left(\frac{\gamma_i}{n_i \mu_{ii}}, 1\right), \quad i = 1, \dots, m.$$

In the simple case  $m = 2$ ,  $\mu_{11} = \mu_{22} = \mu$ ,  $\mu_{12} = \mu_{21} = q\mu$ ,  $\gamma_1 = \gamma_2 = \gamma$  and  $n_1 = n_2 = n$ , we obtain

$$5.9 \quad p_1 = p_2 = \frac{\gamma}{n\mu(1+q)},$$

so that

$$\Pr\{\text{early extinction}\} \approx \left(\frac{\gamma}{n\mu(1+q)}\right)^{a_1 + a_2}.$$

### 5.3 The probability that initial infection does not spread

In section 5.1 it was shown that the individual thresholds still exerted a strong influence on the behaviour of the epidemic. Any group  $i$  may be classified as subcritical or supercritical depending on whether  $n_i \mu_{ii} < \gamma_i$  or  $n_i \mu_{ii} > \gamma_i$  and we note that a group which is subcritical

can never subsequently become supercritical. Any infection arising in a subcritical group will die out quickly in that group. If a major outbreak were to occur in a subcritical group it must be mainly due to the action of infectives from other groups rather than from its own infectives. The major influence of subcritical groups in causing major outbreaks is thus in infecting supercritical groups.

Suppose that initially we have infection in one subcritical group which we shall call group 1. We have seen that the behaviour of subcritical populations can be approximated by regarding the number of susceptibles in that population to be constant at its initial value. Hence we assume that  $X_1 = n_1$ . Further, let

$$q(a) = \Pr\{\text{no infection occurs outside group 1} \mid Y_1(0) = a\}.$$

Since each infective acts independently under this assumption we have

$$q(a) = (q(1))^a, \quad a = 1, 2, \dots,$$

and

$$q(0) = 1.$$

Now the backwards equation yields

$$q(1) = \left[ \sum_{j=1}^m \mu_{1j} n_j^{+\gamma_1} \right]^{-1} \{ \mu_{11} n_1 q(2) + \gamma_1 q(0) \},$$

which gives us a quadratic equation for  $q(1)$ . It is easily seen that the roots of this equation are real and positive and that it is the smaller root which is required. Hence

$$5.10 \quad q(1) = \frac{\left[ \sum_{j=1}^m \mu_{1j} n_j^{+\gamma_1} - \left[ \left( \sum_{j=1}^m \mu_{1j} n_j^{+\gamma_1} \right)^2 - 4\mu_{11} n_1 \gamma_1 \right]^{\frac{1}{2}} \right]}{2\mu_{11} n_1}.$$

Now suppose that initially all infected individuals are contained solely in a supercritical group which we shall now for convenience call group 1. We may expect that if a major outbreak occurs in this group the infection will spread with probability close to 1. However, we know that with probability approximately  $(\gamma_1/\mu_{11}n_1)^a$  a supercritical group will behave like a subcritical group with contact rate  $\gamma_1$  and removal rate  $\mu_{11}n_1$ . Hence in this case the infection will not spread with probability approximately

$$q'(a) = (p'(1))^a \left( \frac{\gamma_1}{\mu_{11}n_1} \right)^a,$$

where  $q'(1)$  is the same as  $q(1)$  in equation 5.10 with  $\gamma_1$  and  $\mu_{11}n_1$  interchanged. Thus we see that the expressions for  $q'(a)$  and  $q(a)$  are identical.

#### 5.4 The final sizes

Let  $W_i$ ,  $i = 1, \dots, m$ , be the final size of the epidemic in the  $i$ th group and

$$p_r(n, a) = \Pr\{W_i = r_i, i = 1, \dots, m \mid (X, Y) = (n, a)\},$$

where  $(n, a) = (n_1, \dots, n_m, a_1, \dots, a_m)$ ,  $r = (r_1, \dots, r_m)$  and  $(X, Y) = (X_1, \dots, X_m, Y_1, \dots, Y_m)$ .

We consider the embedded random walk process with transitions

$$5.11 \quad (n, a) \rightarrow \begin{cases} (n-e_i, a+e_i) & \text{with probability } \left( n_i \mu_i^T \cdot a \right) \left[ \sum_{i=1}^m \left( \gamma_i a_i + n_i \mu_i^T \cdot a \right) \right]^{-1}, \\ (n, a-e_i) & \text{with probability } \gamma_i a_i \left[ \sum_{i=1}^m \left( \gamma_i a_i + n_i \mu_i^T \cdot a \right) \right]^{-1}, \\ n_i, a_i = 0, 1, \dots, \quad i = 1, \dots, m, \end{cases}$$

where  $\mu_i$  is the  $i$ th column of the matrix  $\{\mu_{ji}\}$ ,  $e_i$  is the  $i$ th row of the  $m \times m$  identity matrix, and where no transition is possible if  $a_i = 0$ ,  $i = 1, \dots, m$ .

The backwards equation yields for  $r_i = 0, 1, \dots, n_i$ ,

$i = 1, \dots, m$ ,

$$5.12 \quad p_r(n, a) = \left[ \sum_{i=1}^m \left( \gamma_i a_i + n_i \mu_i^T \cdot a \right) \right]^{-1} \sum_{i=1}^m \left[ \gamma_i a_i p_r(n, a-e_i) + n_i \mu_i^T \cdot a p_{r-e_i}(n-e_i, a+e_i) \right], \quad n_i, a_i = 0, 1, \dots,$$

and

$$p_r(0, a) = \delta(r), \quad a_i = 0, 1, \dots, \quad i = 1, \dots, m.$$

Let

$$C_h(n, a) = E(W_h \mid (X(0), Y(0)) = (n, a)).$$

Multiplying 5.12 by  $r_h$  and summing over  $r_k = 0, \dots, n_k$ ,

$k = 1, \dots, m$ , we obtain for  $h = 1, \dots, m$ ,

$$5.13 \quad C_h(n, a) = \left[ \sum_{i=1}^m \left( \gamma_i a_i + n_i \mu_i^T \cdot a \right) \right]^{-1} \sum_{i=1}^m \left[ \gamma_i a_i C_h(n, a - e_i) \right. \\ \left. + n_i \mu_i^T \cdot a (C_h(n - e_i, a + e_i) + \delta(h-i)) \right], \\ n_i, a_i = 0, 1, \dots, \quad i = 1, \dots, m,$$

and

$$C_h(0, a) = 0, \quad a_i = 0, 1, \dots, \quad i = 1, \dots, m.$$

The recursive equations 5.12 and 5.13 enable the joint distribution of the final sizes or the individual mean final sizes to be found for any initial conditions. The equations are complicated and the procedure to follow is not at all obvious. We outline the method for finding any  $C_h(\cdot, \cdot)$ .

Suppose we wish to find  $C_h(N_1, \dots, N_m, A_1, \dots, A_m)$ . We consider the  $(N)$ -hyperplanes defined by  $n_1 + \dots + n_m = r$ ,  $r = 0, 1, \dots$ . For each successive value of  $r$  we take each point on the  $(N)$ -hyperplane and determine  $C_h(\cdot, \cdot)$  at each point on the  $(A)$ -hyperplane defined by

$a_1 + \dots + a_m = s$ ,  $s = 0, 1, \dots, \sum_{i=1}^m A_i + r + 1$ . It is easily seen that for the first  $(N)$ -hyperplane ( $r = 0$ ),  $C_h(\cdot, \cdot) = 0$  for each point on each of the  $(A)$ -hyperplanes. We continue in this manner until the point  $(N_1, \dots, N_m, A_1, \dots, A_m)$  is reached.

## 5.5 Expected time to extinction

The epidemic is defined to be extinct when there are no more infectives

left in the population. As in the previous section we consider the embedded random walk process.

Let  $M(n, a)$  be the expected time to reach extinction from the state  $(n, a)$ . The expected time spent in this state is

$$\left[ \sum_{i=1}^m \left( \gamma_i a_i + n_i \mu_i^T \cdot a \right) \right]^{-1}.$$

The transition probabilities from this state are given by 5.11 and the usual argument gives us

$$5.14 \quad M(n, a) = \left[ \sum_{i=1}^m \left( \gamma_i a_i + n_i \mu_i^T \cdot a \right) \right]^{-1} \left\{ 1 + \sum_{i=1}^m \left[ \gamma_i a_i M(n, a - e_i) + n_i \mu_i^T \cdot a M(n - e_i, a + e_i) \right] \right\}.$$

This expression may be used to compute the expected time to extinction from any initial state by using the procedure outlined in the previous section.

## 5.6 An approximating process

Let  $P(w_1, \dots, w_m, z_1, \dots, z_m; t)$  be the joint probability generating function of  $(X_1, \dots, X_m, Y_1, \dots, Y_m)$ . It is readily shown from 1.30 that  $P$  satisfies the partial differential equation

$$5.15 \quad \frac{\partial P}{\partial t} = \sum_{i=1}^m \left[ \gamma_i (1 - z_i) \frac{\partial P}{\partial z_i} + \sum_{j=1}^m \mu_j z_j (z_i - w_i) \frac{\partial^2 P}{\partial w_i \partial z_j} \right].$$



This equation could be solved by the same method as was used in section 2.1 to solve the corresponding equation for the general stochastic epidemic model. The solution would be even more complicated and thus completely useless for any practical purposes. Because of this we will consider an approximating process analogous to that used in chapter 3.

#### MAJOR OUTBREAK

In the event that a major outbreak occurs (see section 5.2) we form an approximating process by replacing in the contact probability rate the stochastic variables  $Y_i$ ,  $i = 1, \dots, m$ , by their deterministic analogues  $y_i$ . Thus the infinitesimal transition probability rates are given by

$$5.16 \quad (X', Y') \rightarrow \begin{cases} (X' - e_i, Y' + e_i) & \text{at rate } X'_i \sum_{j=1}^m \mu_{ji} y_j, \\ (X', Y' - e_i) & \text{at rate } \gamma_i Y'_i. \end{cases} \quad i = 1, \dots, m.$$

In the usual way we have that  $P'(w_1, \dots, w_m, z_1, \dots, z_m; t)$ , the joint p.g.f. of  $(X'_1, \dots, X'_m, Y'_1, \dots, Y'_m)$  satisfies the equation

$$5.17 \quad \frac{\partial P'}{\partial t} = \sum_{i=1}^m \left[ \gamma_i (1 - z_i) \frac{\partial P'}{\partial z_i} + (z_i - w_i) \frac{\partial P'}{\partial w_i} \sum_{j=1}^m \mu_{ji} y_j \right].$$

This may be solved in the same way as equation 3.3, but the result follows more easily by noting from 5.16 the independence of the process in each group. Hence we obtain

$$5.18 \quad P'(w_1, \dots, w_m, z_1, \dots, z_m; t) = \prod_{i=1}^m \left[ 1 - (1-z_i) e^{-\gamma_i t} \right]^{a_i} \left[ 1 - (1-w_i) \frac{x_i}{n_i} - \frac{1}{n_i} (1-z_i) \left( y_i - a_i e^{-\gamma_i t} \right) \right]^{n_i}.$$

Factorial moments are easily found from 5.18 to be for  $i = 1, \dots, m$ ,

$$5.19 \quad EX'_i = x_i,$$

$$5.20 \quad EY'_i = y_i,$$

$$5.21 \quad EX'_i(X'_i - 1) = \left( 1 - \frac{1}{n_i} \right) x_i^2,$$

$$5.22 \quad EY'_i(Y'_i - 1) = a_i(a_i - 1)e^{-2\gamma_i t} + 2a_i \left( y_i - a_i e^{-\gamma_i t} \right) + \left( 1 - \frac{1}{n_i} \right) \left( y_i - a_i e^{-\gamma_i t} \right)^2,$$

$$5.23 \quad EX'_i Y'_i = \left( 1 - \frac{1}{n_i} \right) x_i y_i + \frac{a_i}{n_i} x_i e^{-\gamma_i t}.$$

The distribution of the time to extinction,  $T'$ , is given by

$$5.24 \quad F_{T'}(t) = P'(1, \dots, 1, 0, \dots, 0; t) \\ = \prod_{i=1}^m (1 - e^{-\gamma_i t})^{a_i} \left( 1 - \frac{1}{n_i} \left( y_i - a_i e^{-\gamma_i t} \right) \right)^{n_i},$$

and the joint p.g.f. of the distribution of the number of susceptibles left after the epidemic has become extinct by

$$5.25 \quad Q(w_1, \dots, w_m) = P'(w_1, \dots, w_m, 1, \dots, 1; \infty) \\ = \prod_{i=1}^m \left( 1 - (1-w_i) \frac{\theta_i}{n_i} \right)^{n_i},$$

which shows that for this approximation process the number left after the epidemic in the  $i$ th population is an independent binomial variate with parameter  $\theta_i$ .

#### EARLY EXTINCTION IN THE SUBCRITICAL CASE

In the event that the multivariate birth and death process  $Y'$  becomes extinct with probability 1 (see section 5.1) we use it as our approximation to  $Y$ . Here we are assuming that if the process becomes extinct early then each  $X_i$  will not decrease much from its initial value  $n_i$ .

The moments of  $Y'$  are given by

$$5.26 \quad \frac{dEY'}{dt} = MEY',$$

where  $EY'(0) = \mathbf{a}^T = (a_1, \dots, a_m)^T$ , (see e.g. Mode (1962)).

The joint p.g.f. of the distribution of the final size (see Appendix D) is given by

$$P_{\mathbf{a}}(w_1, \dots, w_m) = \prod_{i=1}^m (P_{\mathbf{e}_i}(w_1, \dots, w_m))^{a_i},$$

where  $\mathbf{e}_i$  is the  $i$ th row of the identity matrix and the  $P_{\mathbf{e}_i}(\cdot)$  satisfy

the set of equations

$$P_{\mathbf{e}_i}(w_1, \dots, w_m) = \left[ \gamma_i + \sum_{j=1}^m n_j \mu_{ij} \right]^{-1} \left\{ \gamma_i + P_{\mathbf{e}_i}(w_1, \dots, w_m) \left( \sum_{j=1}^m n_j \mu_{ij} w_j P_{\mathbf{e}_j}(w_1, \dots, w_m) \right) \right\},$$

$i = 1, \dots, m.$

## 5.7 The diffusion limit

We consider the general epidemic in a stratified population as defined in section 1.7 but with the following modifications. The initial condition is  $(X_i(0), Y_i(0)) = (n_i, n_i h_i)$ ,  $i = 1, \dots, m$ , where each  $h_i$  is a constant. The parameters  $\mu_{ji}$ ,  $i, j = 1, \dots, m$ , are replaced by  $\mu_{ji}/n_j$  where  $n_j = n\lambda_j$ ,  $j = 1, \dots, m$ .

As was the case in sections 2.10 and 4.3 this process is a member of a general class of processes discussed in Barbour (1974) from which it follows that on any fixed time interval  $(0, \tau)$  the random vector

$$\begin{aligned} & \left( U_1^{(n)}, \dots, U_m^{(n)}, V_1^{(n)}, \dots, V_m^{(n)} \right) \\ &= \left( \frac{X_1 - n\xi_1}{\sqrt{n}}, \dots, \frac{X_m - n\xi_m}{\sqrt{n}}, \frac{Y_1 - n\eta_1}{\sqrt{n}}, \dots, \frac{Y_m - n\eta_m}{\sqrt{n}} \right), \end{aligned}$$

where  $(\xi_i, \eta_i) = \left( \frac{x_i}{n_i}, \frac{y_i}{n_i} \right)$ ,  $i = 1, \dots, m$ , converges weakly as  $n \rightarrow \infty$  to the diffusion  $(U_1, \dots, U_m, V_1, \dots, V_m)$  whose joint p.g.f.

$P(u_1, \dots, u_m, v_1, \dots, v_m)$  satisfies

$$\begin{aligned} 5.27 \quad \frac{\partial P}{\partial t} - \sum_{i=1}^m \left\{ \left( \ln \frac{v_i}{u_i} \right) \left[ u_i \frac{\partial P}{\partial u_i} \sum_{j=1}^m \mu_{ji} \eta_j + \xi_i \sum_{j=1}^m \mu_{ji} v_j \frac{\partial P}{\partial v_j} \right] \right. \\ \left. - \gamma_i v_i \ln v_i \frac{\partial P}{\partial v_i} + \frac{1}{2\lambda_i} P \left[ \left( \ln \frac{v_i}{u_i} \right)^2 \xi_i \sum_{j=1}^m \mu_{ji} \eta_j + (\ln v_i)^2 \gamma_i \eta_i \right] \right\} = 0. \end{aligned}$$

From 5.27 it follows easily that  $EU_i$ ,  $EV_i$ ,  $i = 1, \dots, m$ , are identically zero and the second moments satisfy the equations

$$5.28a) \quad \frac{dEU_k U_l}{dt} + EU_l U_k \sum_{j=1}^m (\mu_{jl} + \mu_{jk}) \eta_j + \xi_l \sum_{j=1}^m (\mu_{jl} EU_k V_j + \mu_{jk} EU_l V_j) \\ - \frac{1}{\lambda_k} \xi_k \delta(k-l) \sum_{j=1}^m \mu_{jk} \eta_j = 0, \quad k, l = 1, \dots, m,$$

$$5.28b) \quad \frac{dEU_k V_l}{dt} + EU_k V_l \left( \gamma_l + \sum_{j=1}^m \mu_{jl} \eta_j \right) - EU_l U_k \sum_{j=1}^m \mu_{jl} \eta_j - \xi_l \sum_{j=1}^m \mu_{jl} EU_k V_j \\ + \xi_k \sum_{j=1}^m \mu_{jk} EV_j V_k + \frac{1}{\lambda_k} \xi_k \delta(k-l) \sum_{j=1}^m \mu_{jk} \eta_j = 0, \quad k, l = 1, \dots, m,$$

$$5.28c) \quad \frac{dEV_k V_l}{dt} + (\gamma_k + \gamma_l) EV_k V_l - \left( \xi_l \sum_{j=1}^m \mu_{jl} EV_j V_k + \xi_k \sum_{j=1}^m \mu_{jk} EV_j V_l \right) \\ - \left( EU_l V_k \sum_{j=1}^m \mu_{jl} \eta_j + EU_k V_l \sum_{j=1}^m \mu_{jk} \eta_j \right) \\ - \frac{1}{\lambda_k} \left( \gamma_k \eta_k + \xi_k \sum_{j=1}^m \mu_{jk} \eta_j \right) \delta(k-l) = 0, \quad k, l = 1, \dots, m.$$

These equations are useful in approximating  $\text{Var}(X_i)$  and  $\text{Var}(Y_i)$ ,

$i = 1, \dots, m$ , conditional on a major outbreak occurring.

## CHAPTER 6

## SOME OTHER MODELS FOR EPIDEMICS

## 6.0 Introduction

In the introduction to chapter 5 we discussed the assumption of uniform mixing of the population. This is perhaps the weakest assumption of the general epidemic model and chapter 5 studies a model in which the assumption is modified. In this chapter we introduce and study two models in which a completely different mixing behaviour is assumed.

The first of these is a model for a population with very restricted mobility. We formulate the model and find expressions for the mean number of infectives at any time. The probability of eventual extinction of the process is also found.

In the second of the models we make assumptions about the mixing of the population that are based on the family structure of human populations. The process which arises is a two-type branching process. We discuss the probability of early extinction of the process, find recurrence relations for the mean numbers of the various types of infective and finally we discuss the estimation of the parameters of the model.

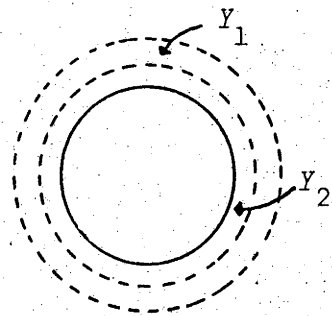
## 6.1. A model for an epidemic in a community with very restricted mobility

This model would be applicable to a population with little or no mobility such as a population of trees in a forest. (In this case we might imagine the epidemic to be the spread of a parasitic growth for example.)

Infection is assumed to be spread by those infectives on or next to the

boundary of the infected area.

We shall call those infectives that actually form the boundary of the infected area the primary boundary infectives and those that are adjacent to the boundary shall be called secondary boundary infectives. Their numbers at any time  $t$  shall be denoted by  $Y_1$  and  $Y_2$  respectively.



In the time interval  $(t, t+\delta t)$  the following transitions may occur: each of the  $Y_1$  primary boundary infectives may produce a new primary boundary infective with probability  $\mu_1\delta t$  and become itself a secondary boundary infective (i.e. the boundary is now at the new infective); each of the  $Y_2$  secondary infectives may produce a primary infective with probability  $\mu_2\delta t$  and become itself a non-boundary infective; each infective may become removed with probability  $\gamma\delta t$  regardless of type. Non-boundary and removed individuals are assumed to have no influence on the behaviour of the boundary infectives. We are interested primarily in the spread of infection so the removed and non-boundary individuals will be ignored.

Thus the infinitesimal transition probability rates for the model are given by

$$(Y_1, Y_2) \rightarrow \begin{cases} (Y_1, Y_2+1) & \text{at rate } \mu_1 Y_1, \\ (Y_1+1, Y_2-1) & \text{at rate } \mu_2 Y_2, \\ (Y_1-1, Y_2) & \text{at rate } \gamma Y_1, \\ (Y_1, Y_2-1) & \text{at rate } \gamma Y_2, \end{cases}$$

and the initial conditions are  $(Y_1(0), Y_2(0)) = (a, 0)$ .

The model may readily be generalised to include more types of infectives characterised by their distance from the boundary although the mathematics rapidly becomes tedious.

#### THE MEANS

Let  $P(v_1, v_2; t)$  be the joint p.g.f. of  $Y_1$  and  $Y_2$ . In the usual way we may show that  $P$  satisfies the partial differential equation

$$6.1 \quad \frac{\partial P}{\partial t} = [\mu_1 v_1 (v_2 - 1) + \gamma (1 - v_1)] \frac{\partial P}{\partial v_1} + [\mu_2 (v_1 - v_2) + \gamma (1 - v_2)] \frac{\partial P}{\partial v_2},$$

where  $P(v_1, v_2; 0) = v_1^a$ .

An explicit solution for  $P$  appears very difficult because of the non-linearity of the characteristic equations of 6.1. However, putting  $y_1 = EY_1$  and  $y_2 = EY_2$ , it follows easily from 6.1 that the means satisfy the equations

$$6.2a) \quad \dot{y}_1 = \mu_2 y_2 - \gamma y_1,$$

$$6.2b) \quad \dot{y}_2 = -(\gamma + \mu_2) y_2 + \mu_1 y_1,$$

where  $(y_1(0), y_2(0)) = (a, 0)$ .

Since the process is a linear one, equations 6.2 also define the corresponding deterministic model. The solutions to these equations are readily found by standard methods to be

$$6.3 \quad y_1(t) = ae^{-t(\gamma + \mu_2/2)} [\cosh(\frac{1}{2}\Delta t) + (\mu_2/\Delta) \sinh(\frac{1}{2}\Delta t)],$$



and

$$6.4 \quad y_2(t) = \frac{2\mu_1 a}{\Delta} e^{-t(\gamma + \mu_2/2)} \sinh(\frac{1}{2}\Delta t),$$

where  $\Delta = \sqrt{\mu_2(\mu_2 + 4\mu_1)}$ . It follows from 6.3 and 6.4 that the epidemic will die out if

$$6.5 \quad \mu_1 \mu_2 \leq \gamma(\gamma + \mu_2).$$

#### THE PROBABILITY OF EXTINCTION

Let

$$p(a, b) = \Pr\{\text{extinction of the process} \mid (Y_1(0), Y_2(0)) = (a, b)\}.$$

Since each infective acts independently we have

$$6.6 \quad p(a, b) = p(1, 0)^a p(0, 1)^b, \quad a, b = 0, 1, \dots$$

Also, a consideration of the embedded random walk process yields

$$6.7 \quad p(1, 0) = \frac{\mu_1}{\mu_1 + \gamma} p(1, 1) + \frac{\gamma}{\mu_1 + \gamma},$$

and

$$6.8 \quad p(0, 1) = \frac{\mu_2}{\mu_2 + \gamma} p(1, 0) + \frac{\gamma}{\mu_2 + \gamma}.$$

Equations 6.6, 6.7, 6.8 are easily solved to give

$$6.9 \quad p(a, b) = \begin{cases} 1 & \text{if } \gamma(\gamma + \mu_2) \geq \mu_1 \mu_2, \\ \left( \frac{\gamma(\gamma + \mu_2)}{\mu_1 \mu_2} \right)^a \left( \frac{\gamma(\mu_1 + \mu_2 + \gamma)}{\mu_1(\mu_2 + \gamma)} \right)^b & \text{otherwise,} \end{cases}$$

so that extinction is certain if  $\gamma(\gamma + \mu_2) \geq \mu_1 \mu_2$  (cf. 6.5).

## 6.2 A two-type branching process model

In this section we consider a branching process model for an epidemic. The theory of branching processes is well developed (see e.g. Harris (1963)). They are especially useful in modelling the spread of a disease which has a nearly constant latent period so that new "generations" of infection may be regarded as occurring at discrete time intervals. If we restrict ourselves to the early stages of the development of the epidemic before the depletion of the susceptible population becomes significant and we may take the distribution of the number of offspring (i.e. new infections caused by each infective) to be independent of the state of the system, the mathematics involved is tractable. This restriction still provides information of interest since it is the behaviour of the process during its early stages which determines if the outbreak will be minor or major.

The process we shall consider is a multitype branching process based on the family structure of a human population. We assume that, outside their family, every infected individual may pass on the disease to any other individual, but within a family only the first member to be infected may pass on the disease to other members of that family. This is a reasonable assumption when family units are quite small (e.g. in many middle and upper class urban societies). Thus we may classify infectives into two groups: type 1 are those infected by contacts outside their family; and type 2 are those infected within their family. We may also classify susceptibles into those from families which already have infected members and those from uninfected families.

Further, we regard the number of (both types of) susceptibles to be

approximately constant. Hence we may assume that each infective infects  $I_1$  type 1 infectives and each type 1 infective infects  $I_2$  type 2 infectives, where  $I_1$  and  $I_2$  are independent random variables with p.g.f.'s  $f(s)$  and  $g(s)$  respectively. In the special case where  $I_1$  has the Poisson distribution this model reduces to that of Bartoszyński (1972).

Let  $Y_{ij}^n$ ,  $i, j = 1, 2$ ,  $n = 0, 1, \dots$ , be the number of type  $j$  infectives in the  $n$ th generation given one initial type  $i$  infective, and let  $F_n^{(i)}(s, t)$ ,  $i = 1, 2$ ,  $n = 0, 1, \dots$ , be the joint p.g.f. of  $Y_{i1}^n$  and  $Y_{i2}^n$ . Then we have

$$6.10 \quad F_1^{(1)}(s, t) = f(s)g(t),$$

$$6.11 \quad F_1^{(2)}(s, t) = f(s),$$

and it is a well known result of branching process theory that

$$6.12 \quad F_{n+m}^{(i)}(s, t) = F_m^{(i)} \left( F_n^{(1)}(s, t), F_n^{(2)}(s, t) \right),$$

$$i = 1, 2, \quad n, m = 0, 1, 2, \dots$$

#### THE PROBABILITY OF EXTINCTION

We expect this model to be useful in describing the early behaviour of an epidemic in a population having family structure. If the branching process becomes extinct it is most likely to do so within a short period after its beginning. Therefore we expect that the probability of eventual extinction of the branching process will be a good approximation to the probability of early extinction of such an epidemic process.

Let  $f_1 = f'(1)$  and  $g_1 = g'(1)$  be the means of the non-family and

family offspring distributions, and let

$$\pi_i = \Pr\left\{Y_{ij}^k = 0, j = 1, 2, \text{ for some } k\right\}, \quad i = 1, 2,$$

be the probabilities of eventual extinction of the process. By another well known theorem,  $(\pi_1, \pi_2) = (1, 1)$  if the largest eigenvalue of the matrix

$$\begin{pmatrix} f_1 & f_1 \\ g_1 & 0 \end{pmatrix}$$

not greater than 1. This condition is easily shown to be equivalent to

$$6.13 \quad f_1(1+g_1) < 1.$$

If this condition is not satisfied then  $(\pi_1, \pi_2)$  is the smallest positive solution of

$$(\pi_1, \pi_2) = \left( F_1^{(1)}(\pi_1, \pi_2), F_1^{(2)}(\pi_1, \pi_2) \right).$$

Using 6.10 and 6.11 this condition becomes

$$6.14 \quad \pi_1 = f(\pi_1)g(f(\pi_1)),$$

and

$$6.15 \quad \pi_2 = f(\pi_2)g(\pi_2).$$

We shall consider 6.14 since it arises from the more realistic initial condition. The behaviour of the solution  $\pi_1$  when the process is only marginally supercritical is of interest.

Suppose the first 3 factorial moments of the distributions of which  $f$  and  $g$  are the p.g.f.'s are finite. Then making use of Taylor's theorem we may write

$$6.16 \quad f(s)g(f(s)) = 1 + (s-1)f_1(1+g_1) + (s-1)^2 \left[ f_2(1+g_1) + f_1^2(2g_1+g_2) \right] \\ + (s-1)^3 h(s) ,$$

where, since  $f(s)g(f(s))$  is a p.g.f.,

$$h(s) \left[ f_3(1+g_1) + 3f_1f_2(2g_1+g_2) + f_1^3(3g_2+g_3) \right]^{-1}$$

is a p.g.f. (see Daley and Narayan (1980)), and where  $f_i, g_i, i = 1, 2, 3$ , are the  $i$ th factorial moments of their respective distributions.

Using 6.14 and 6.16 we obtain

$$6.17 \quad 1 - \pi_1 = \frac{f_1(1+g_1)^{-1} + (1-\pi_1)^2 R(\pi_1)}{f_2(1+g_1) + f_1^2(2g_1+g_2)} ,$$

where  $R(s) \geq 0, 0 \leq s \leq 1$ .

If  $1 - \pi_1$  is close to zero we can neglect higher order terms and write

$$6.18 \quad 1 - \pi_1 \approx \frac{f_1(1+g_1)^{-1}}{f_2(1+g_1) + f_1^2(2g_1+g_2)} ,$$

and in fact we see from 6.17 that this approximation is a lower bound for  $1 - \pi_1$ .

#### THE MOMENTS OF THE GENERATION SIZES

Let

$$M_{ij}^n = EY_{ij}^n, \quad i = 1, 2, \quad n = 0, 1, \dots ,$$

and

$$N_{ij}^n = EY_{ij}^n \left( Y_{ij}^n - 1 \right), \quad i = 1, 2, \quad n = 0, 1, \dots$$

From equation 6.12 we obtain the sets of recurrence relations

$$6.19 \quad M_{ij}^{n+1} = m_{i1} M_{1j}^n + m_{i2} M_{2j}^n, \quad i, j = 1, 2, \quad n = 0, 1, \dots,$$

where

$$M_{11}^0 = M_{22}^0 = 1,$$

$$M_{12}^0 = M_{21}^0 = 0,$$

and

$$m_{11} = m_{21} = f_1,$$

$$m_{22} = 0,$$

$$m_{12} = g_1.$$

Similarly we find that

$$6.20 \quad N_{ij}^{n+1} = m_{i1} N_{1j}^n + n_{i1} \left( M_{1j}^n \right)^2 + 2o_{i1j} M_{1j}^n M_{2j}^n + m_{i2} N_{2j}^n + n_{i2} \left( M_{2j}^n \right)^2,$$

$$i, j = 1, 2, \quad n = 0, 1, \dots,$$

where

$$N_{11}^0 = N_{12}^0 = N_{21}^0 = N_{22}^0 = 0,$$

and where

$$n_{11} = n_{21} = f_2 ,$$

$$n_{22} = 0 ,$$

$$n_{12} = g_2 ,$$

$$o_1 = f_1 g_1 ,$$

$$o_2 = 0 .$$

### PARAMETER ESTIMATION

Here we use the technique of Harris (1948) who found the maximum likelihood estimator for the mean of the offspring distribution in the case of a "1-type" branching process (Galton-Watson process). This technique is easily extended to this case.

Let  $a_i, b_i, i = 0, 1, \dots, n$ , be the observed number of type 1 and type 2 infectives in the  $i$ th generation of infection and  $a_{i,k}, b_{i,k}, i = 0, 1, \dots, n, k = 0, 1, \dots$ , be the observed number of  $i$ th generation infectives that infect  $k$  type 1 and  $k$  type 2 individuals respectively. We note that

$$6.21 \quad \sum_{k=0}^{\infty} a_{i,k} = a_i + b_i ,$$

$$6.22 \quad \sum_{k=0}^{\infty} k a_{i,k} = a_{i+1} ,$$

$$6.23 \quad \sum_{k=0}^{\infty} b_{i,k} = a_i ,$$

and

$$\sum_{k=0}^{\infty} k b_{i,k} = b_{i+1} .$$

Let

$$f(s) = \sum_{i=0}^{\infty} p_i s^i \quad \text{and} \quad g_i(s) = \sum_{i=0}^{\infty} q_i s^i.$$

The conditional probability of  $a_{i0}, a_{i1}, \dots$ , given  $a_i, b_i$  has the multinomial form

$$(a_i + b_i)! \prod_{k=0}^{\infty} \frac{p_k^{a_{i,k}}}{(a_{i,k})!}.$$

Thus using 6.21-6.24 we have that the joint conditional likelihood of  $a_{i,k}$ ,  $i = 0, \dots, n$ ,  $k = 0, 1, \dots$ , is

$$L = \prod_{i=0}^n \left\{ (a_i + b_i)! \prod_{k=0}^{\infty} \frac{p_k^{a_{i,k}}}{(a_{i,k})!} \right\}.$$

Therefore

$$\ln L = \sum_{k=0}^{\infty} \left( \sum_{i=0}^n a_{i,k} \right) \ln p_k + \sum_{i=0}^n \ln(a_i + b_i)! + \sum_{k=0}^{\infty} \sum_{i=0}^n \ln a_{i,k}.$$

Using the method of Lagrange multipliers we find that the maximum likelihood estimators for the  $p_k$  are

$$\begin{aligned} 6.25 \quad \hat{p}_k &= \frac{\sum_{i=0}^n a_{i,k}}{\sum_{k=0}^{\infty} \sum_{i=0}^n a_{i,k}} \\ &= \frac{\sum_{i=0}^n a_{i,k}}{\sum_{i=0}^n (a_i + b_i)}. \end{aligned}$$

For  $f_1$  we have



6.26

$$\begin{aligned}\hat{f}_1 &= \sum_{k=0}^{\infty} k \hat{p}_k \\ &= \sum_{i=0}^n a_{i+1} / \sum_{i=0}^n (a_i + b_i) .\end{aligned}$$

Similarly

$$\hat{q}_k = \sum_{i=0}^n b_{i,k} / \sum_{i=0}^n a_i ,$$

and

$$\hat{g}_1 = \sum_{i=0}^n b_{i+1} / \sum_{i=0}^n a_i .$$

### 6.3 A MODEL FOR AN EPIDEMIC IN A STRATIFIED POPULATION

The model of Chapter 5 is very complicated mathematically and very little can be said about the qualitative behaviour of such processes. In this section we introduce a simplified model for an epidemic in a stratified population. We use this model in a heuristic discussion of the size of the epidemic based on assumptions about the social mixing of the population.

We will consider a population consisting of  $k$  household or "family" groups. We assume that the infection rates within households are much larger than the between household infection rates so that we can neglect reinfection of a group once it is infected.

The final size of an epidemic here shall mean the total number of individuals that become infected by the outbreak. Let the size of an epidemic in the  $i^{\text{th}}$  household group given one initial infective be  $W_i$ . We will assume that the  $W_i$  are pairwise independent. Let  $q_i$  be the probability that infection ever reaches the  $j^{\text{th}}$  household.

Let  $f_j(s) = E(s^{W_j})$ ,  $j = 1, \dots, k$ . Further, let  $W$  be the size of the epidemic in the whole population and  $f(s)$  be its p.g.f.

Then

$$\begin{aligned}
 6.27 \quad f(s) &= \sum_{i_1=0}^1 \dots \sum_{i_k=0}^1 \left[ \prod_{j=1}^k q_j^{i_j} (1-q_j)^{1-i_j} \right] \prod_{j=1}^k f_j^{i_j}(s) \\
 &= (1-q_1+q_1 f_1(s)) \sum_{i_2=0}^1 \dots \sum_{i_k=0}^1 \prod_{j=2}^k q_j^{i_j} (1-q_j)^{1-i_j} \prod_{j=2}^k f_j^{i_j}(s) \\
 &= \dots \\
 &= \prod_{j=1}^k (1-q_j+q_j f_j(s)) .
 \end{aligned}$$

The mean and variance of  $W$  are easily found to be

$$6.28 \quad EW = \sum_{j=1}^k q_j EW_j$$

and

$$\begin{aligned}
6.29 \quad \text{Var } W &= \sum_{j=1}^k q_j EW_j^2 + 2 \sum_{i \neq j} q_i q_j EW_i EW_j \\
&\quad - \left( \sum_{j=1}^k q_j EW_j \right)^2 \\
&= \sum_{j=1}^k q_j \left( EW_j^2 - q_j (EW_j)^2 \right) \\
&= \sum_{j=1}^k q_j \left( \text{Var } W_j + (1-q_j) (EW_j)^2 \right) .
\end{aligned}$$

Families are easily characterised by size. Suppose there are  $n_s$  households having  $s$  members,  $s = 1, \dots, m$ . We will assume that the final size of an epidemic in a household is a function of the size of the household. Let  $Z_s$  denote the final size of an epidemic in a household of size  $s$ . Then

$$EW = \sum_{s=1}^m n_s \bar{q}_s EZ_s, \quad \text{where } \bar{q}_s = \frac{1}{n_s} \sum^{(s)} q_j$$

and  $\sum^{(s)}$  denotes the sum over all households having  $s$  members. The parameters  $\bar{q}_s$  could be thought of as the average infection rate for a household of size  $s$ .

We would expect that as  $k \rightarrow \infty$ ,  $\frac{n_s}{k} \sim f_s$ , a constant. We would also expect that the  $\bar{q}_s$  are functions of  $k$  and that  $s$  plays little part in the asymptotic form of this function, so put  $\bar{q}_s = c_s q(k)$ , where  $c_s$  is a constant,  $s = 1, \dots, m$ .

Therefore

$$6.30 \quad EW \sim kq(k) \sum_{s=1}^m c_s f_s EZ_s.$$

We also have

$$6.31 \quad \text{Var } W = O(kq(k)).$$

Using the Chebychev inequality we can show that

$$6.32 \quad P\left\{\frac{1}{2}Ckq(k) < W < \frac{3}{2}Ckq(k)\right\} = 1 - O\left((kq(k))^{-1}\right),$$

where

$$C = \sum_{s=1}^m c_s f_s EZ_s.$$

Hence for any  $\epsilon > 0$ ,  $\text{Pr}\{W > \epsilon k\} \rightarrow 0$  as  $k \rightarrow \infty$ , unless  $q(k)$  is  $O(1)$ .

Thus it is the parameters  $q_i$  which play the dominant part in the qualitative behaviour of the process. In general they are functions of  $k$ , the size of the  $i^{\text{th}}$  households and the geographical and social "distance" between them.

We now introduce some assumptions about the mixing of the population in order to gain some insight about the parameters  $q_i$ . Suppose that infection spreads initially from the  $r^{\text{th}}$  household ( $q_r = 1$ ). Classify all house-

holds according to their social relations with the  $r^{\text{th}}$  household as follows :

Let  $S_r^{(1)}$  denote the set of those households having members with whom members of the  $r^{\text{th}}$  household mix regularly. Members of  $S_r^{(1)}$  will be said to have level 1 mixing with the  $r^{\text{th}}$  household. Households belonging to  $S_r^{(2)} = \cup_{i \in S_r^{(1)}} S_i/S_r$  (those who mix with those whom the  $r^{\text{th}}$  family mix with) have level 2 mixing with the  $r^{\text{th}}$  family, etc.

Assume that

$$q_j = p, \text{ for } j \in S_r^{(1)}$$

(for ease of notation here we are letting  $j$  stand for the  $j^{\text{th}}$  family)

From this assumption, and the classification of households follows the further assumption that

$$q_j = p^\ell, \text{ for } j \in S_r^{(\ell)}.$$

From 6.28 we may write

$$\begin{aligned} EW &= \sum_{\ell} p^\ell \sum_{i \in S_r^{(\ell)}} EW_i \\ &= \sum_{\ell} p^\ell n_\ell \sum_{i \in S_r^{(\ell)}} \frac{EW_i}{n_\ell}, \text{ where } n_\ell = n(S_r^{(\ell)}) \\ &\sim E\bar{W} \sum_{\ell} p^\ell n_\ell, \text{ where } E\bar{W} = \frac{1}{k} \sum_{i=1}^k EW_i. \end{aligned}$$

In order to find properties of the parameters  $n_\ell$  it would be necessary to make further assumptions about the connection between individuals or groups in the population. Little work appears to have been done along these lines, however a survey of material of some relevance may be found in Mollison (1977). It seems very difficult to make assumptions which are both realistic and lead to a model which is mathematically tractable.

If there is little "overlap" in the sets  $S_r$ ,  $r = 1, \dots, k$ , then we would expect that  $n_\ell \approx n_1^\ell$  and so major outbreaks would occur if  $qn_1 > 1$ . We will consider the following model, formulated geometrically, to demonstrate how overlap may effect the parameters  $n_\ell$ .

Let the households be distributed uniformly on the plane. Each household mixes regularly with other households within a radius  $R$ . Hence

$$n_1 \approx \rho \pi R^2, \quad \text{where } \rho \text{ is the household density.}$$

$$n_2 \approx 3\rho \pi R^2 = 3n_1,$$

and in general,

$$n_\ell \approx (2\ell - 1)n_1.$$

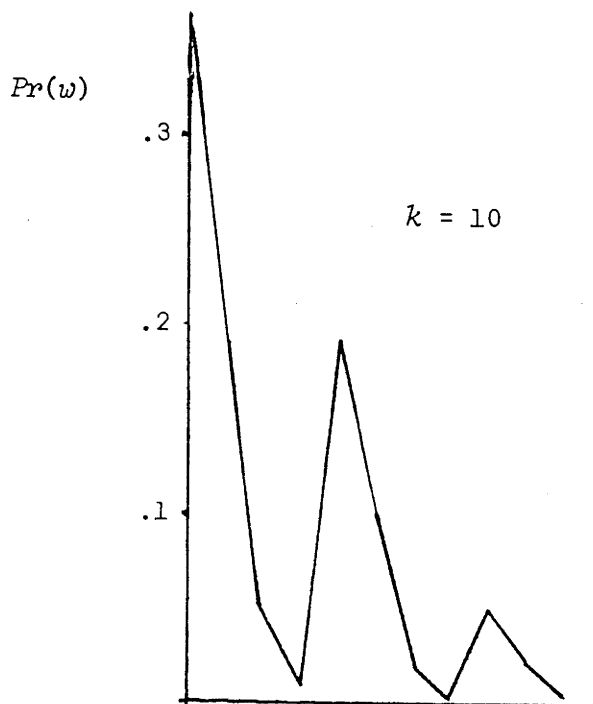
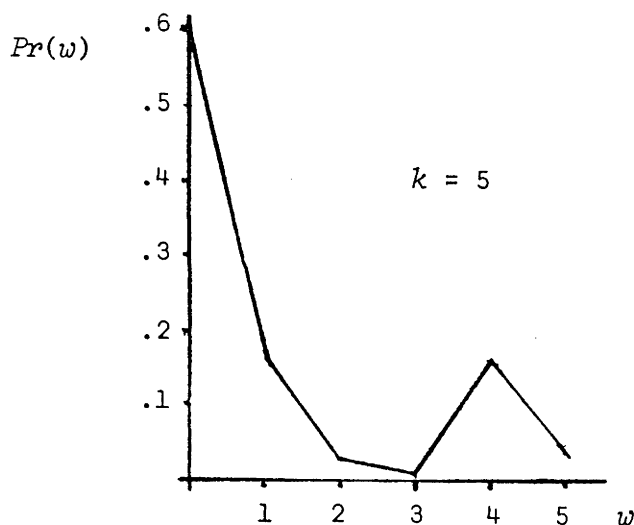
So (if  $k$  is large)  $\sum_{\ell} p^\ell n_\ell = O(1)$  and major outbreaks are impossible.

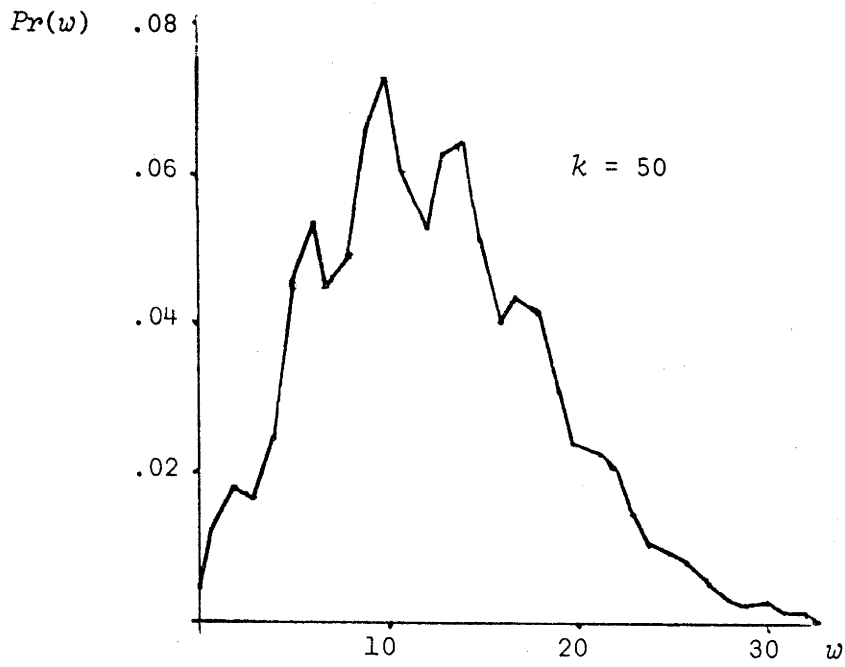
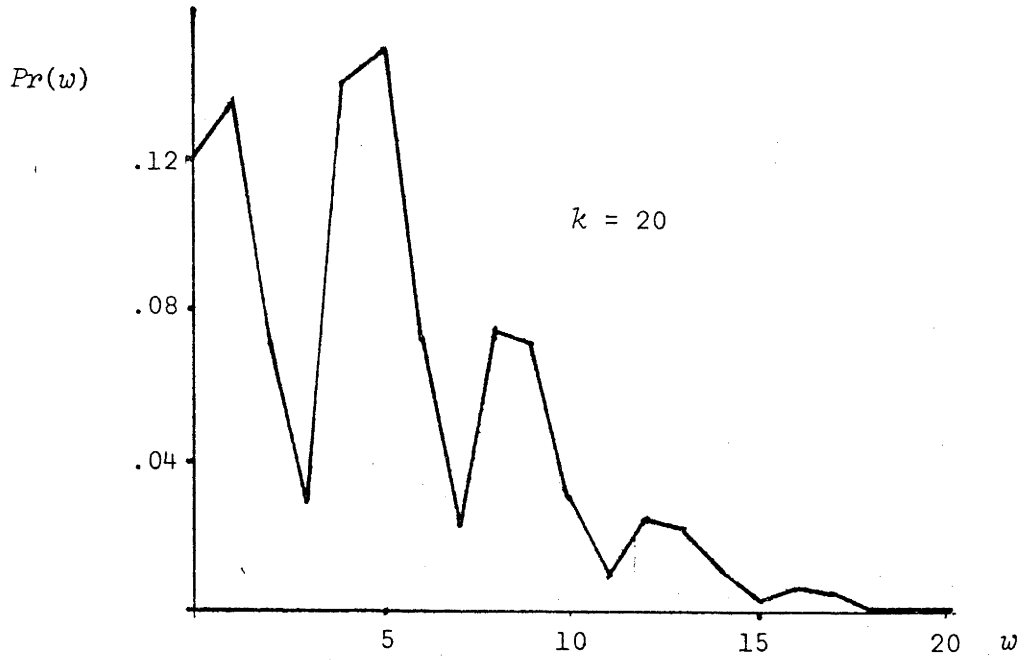
While neither of these two assumptions about the overlap of the sets  $S_r$  are realistic, the truth would lie somewhere between. It would be rather doubtful that  $\sum_{\ell} p^\ell n_\ell$  is  $O(k)$ . Hence the social mixing characteristics of human populations would have the effect of making epidemics of size  $O(k)$  impossible.

It is relevant to note here that the expected distance between two points uniformly distributed on many geometrical shapes of area  $A$  is proportional to  $\sqrt{A}$ . Hence, if geographical distance apart plays a major role and the population is fairly uniformly distributed, we might expect that  $q(k) = k^{-\frac{1}{2}}$ , so that epidemics of size  $O(\sqrt{k})$  would occur.

## THE EFFECT OF THE PROCESS WITHIN FAMILIES

We would imagine that members of a household mix uniformly so that the general epidemic model may be useful to describe the process within households. Family sizes are quite small so the threshold condition would not have a marked effect. However, even in small populations a distinct feature of the general epidemic model is that the distribution of the final size may be  $U$ -shaped. The effect of convoluting a number of such distributions will be to produce a multimodal distribution for  $W$ . This effect, however, will be quickly dissipated as  $k$  increases. This is shown by the following graphs of the distribution of  $W$  when  $q_j = q = .1$ ,  $f_j(s) = f_0 s + f_3 s^4$ ,  $j = 1, \dots, k$ .







## APPENDIX A

## PROOF OF THEOREM 2.1

Suppose  $A$  has  $m$  distinct eigenvalues  $\lambda_1, \dots, \lambda_m$  with multiplicities  $k_1, \dots, k_m$ . The set of independent solutions of equation 2.1 are given by

$$e^{\lambda_i t} [(D+t)^j K(\lambda)]|_{\lambda=\lambda_i}, \quad i = 1, \dots, m, \quad j = 0, \dots, k_i - 1,$$

where  $K(\lambda_i)$  is the eigenvector corresponding to  $\lambda_i$  and  $D$  is the differential operator  $\partial/\partial\lambda$  (see Bellman (1960), *Introduction to Matrix Theory*, p. 194).

Hence the general solution of equation 2.1 is

$$\text{A.1} \quad \sum_{i=1}^m e^{\lambda_i t} \sum_{j=0}^{k_i-1} a_{ij} [(D+t)^j K(\lambda)]|_{\lambda=\lambda_i},$$

where the  $a_{ij}$  are arbitrary.

Let  $K_{uv}(\lambda_i)$  be the element of the vector  $K(\lambda_i)$  which corresponds to the position of  $p_{uv}(t)$ . Then we have after rearranging A.1,

$$p_{uv}(t) = \sum_{i=1}^m e^{\lambda_i t} \sum_{j=0}^{k_i-1} a_{ij} [(D+t)^j K_{uv}(\lambda_i)],$$

so that

$$P(w, z; t) = \sum_{u=0}^n \sum_{v=0}^{n+a-u} \sum_{i=1}^m e^{\lambda_i t} \sum_{j=0}^{k_i-1} a_{ij} \left[ (D+t)^j K_{uv}(\lambda_i) \right].$$

Substituting this in 1.3 we get

$$\sum_{u=0}^n \sum_{v=0}^{n+a-u} \sum_{i=1}^m e^{\lambda_i t} \sum_{j=0}^{k_i-1} a_{ij} \left\{ \lambda_i^{(D+t)^j} K_{uv}(\lambda_i) w^u z^v + j^{(D+t)^{j-1}} K_{uv}(\lambda_i) w^u z^v - (D+t)^j K_{uv}(\lambda_i) (uvz(z-w)w^{u-1}z^{v-1} + \rho v(1-z)w^u z^{v-1}) \right\} = 0.$$

Changing the order of summation

$$\text{A.2} \quad \sum_{i=1}^m e^{\lambda_i t} \left\{ \sum_{j=0}^{k_i-1} a_{ij} \left\{ \sum_{u=0}^n \sum_{v=0}^{n+a-u} \left[ \left[ \lambda_i^{(D+t)^j} + j^{(D+t)^{j-1}} \right] K_{uv}(\lambda_i) w^u z^v - (D+t)^j K_{uv}(\lambda_i) [uvz(z-w)w^{u-1}z^{v-1} + \rho v(1-z)w^u z^{v-1}] \right] \right\} \right\} = 0,$$

where all terms having negative indices are understood to be zero.

Let  $\lambda$  be  $\max_i (\lambda_i)$  and  $k$  its multiplicity. Multiply the above equation by  $t^{-k+1} e^{-\lambda t}$  and let  $t \rightarrow \infty$ . All terms will vanish except the coefficient of  $e^{\lambda t} \cdot t^{k-1}$ . Hence

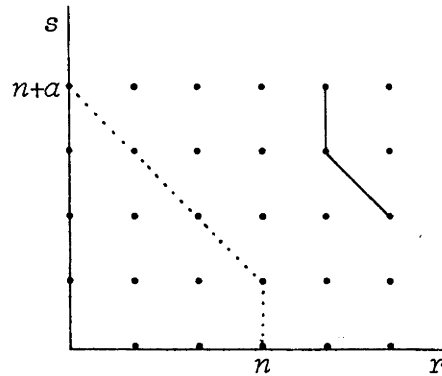
$$\sum_{u=0}^n \sum_{v=0}^{n+a-u} \left\{ \lambda K_{uv} w^u z^v - K_{uv} (uvz(z-w)w^{u-1}z^{v-1} + \rho v(1-z)w^u z^{v-1}) \right\} \equiv 0,$$

(for convenience  $K_{uv}(\lambda)$  is written  $K_{uv}$ ).

The coefficient of  $w^r z^s$  is

$$\text{A.3} \quad \rho(s+1)K_{r,s+1} - [\lambda + s(r+\rho)]K_{r,s} + (r+1)(s-1)K_{r+1,s-1} = 0,$$

where  $K_{rs} = 0$  if  $r > n$ ,  $s+r > n+a$ ,  $r < 0$  or  $s < 0$ .



Putting  $r = 0$ ,  $s = n + a$  we have

$$K_{1, n+a-1} = \frac{(n+a)\rho + \lambda}{n+a-1} \cdot K_{0, n+a}.$$

Continuing down the diagonal,

$$K_{na} = \left\{ \prod_{i=0}^{n-1} \frac{(n+a-i)(i+\rho) + \lambda}{(i+1)(n+a-[i+1])} \right\} \cdot K_{0, n+a}.$$

But putting  $r = n$ ,  $s = a$  we have

$$[\lambda + a(n+\rho)]K_{na} = 0.$$

So either  $\lambda = -(n+a-i)(i+\rho)$  for some  $i = 0, 1, \dots, n$ , or  $K_{0, n+a} = 0$ , in which case all the elements of the top diagonal are zero. Examining now each diagonal in turn we see that  $\lambda$  must take the value

$$\lambda = -s(r+\rho) \text{ for some } r = 0, \dots, n, \quad s+r = 1, \dots, n+a.$$

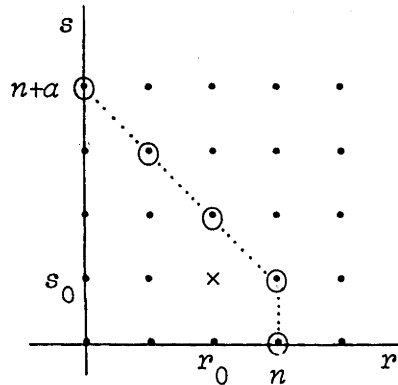
We note that  $\lambda = -s_0(r_0+\rho) \Rightarrow K_{rs} = 0$  for  $r > r_0$  and  $r+s > r_0+s_0$ , but  $K_{r_0, s_0} \neq 0$  otherwise the condition of Theorem 2.1 ensures that  $K$  is the zero vector.

Now suppose that  $k > 1$ . Multiply equation A.2 by  $t^{-k+2}e^{-\lambda t}$  and let  $t \rightarrow \infty$ . The coefficient of  $e^{\lambda t}t^{k-2}$  in A.2 will be the only term remaining. Hence

$$\sum_{u=0}^n \sum_{v=0}^{n+a-u} \left\{ [\lambda K'_{uv} + (k-1)K'_{uv}] w^u z^v - K'_{uv} [uvz(z-w)w^{u-1}z^{v-1} + \rho u(1-z)w^u z^v] \right\} \equiv 0.$$

The coefficient of  $w^r z^s$  is

$$A.4 \quad \rho(s+1)K'_{rs} - [\lambda + s(r+\rho)]K'_{rs} + (r+1)(s-1)K'_{r+1,s-1} + (k-1)K'_{rs} = 0.$$



Suppose  $\lambda = -s_0(r_0 + \rho)$ , then all  $K'_{rs}$  with  $r+s > r_0+s_0$  or  $r > r_0$  are zero (which implies from A.4 that the same is true for  $K'_{rs}$ ), but  $K'_{r_0, s_0} \neq 0$ . Putting  $r = r_0$ ,  $s = s_0$  in A.4 gives

$$K'_{r_0, s_0} = 0,$$

which is a contradiction.

If  $k = 1$ , take the next largest eigenvalue and repeat the procedure. Continuing in this way we see that all the  $k_i$  are 1.

Hence if the condition of Theorem 2.1 is satisfied we may write

$$p_{rs}(t) = \sum_{i=0}^n \sum_{j=1}^{n+a-i} e^{\lambda_{ij}t} K_{rs}(\lambda_{ij}), \quad r = 0, \dots, n, \quad s = 0, \dots, n+a-r,$$

where

$$\lambda_{ij} = -j(i+\rho), \quad i = 0, \dots, n, \quad j = 1, \dots, n+a-i,$$

and  $K_{rs}(\lambda_{ij})$  is the element of  $K(\lambda_{ij})$  corresponding to the position of  $p_{rs}(t)$  in  $p(t)$ . All the  $K_{rs}(\lambda_{ij})$  may be found from the recurrence relation A.3, which together with the initial conditions

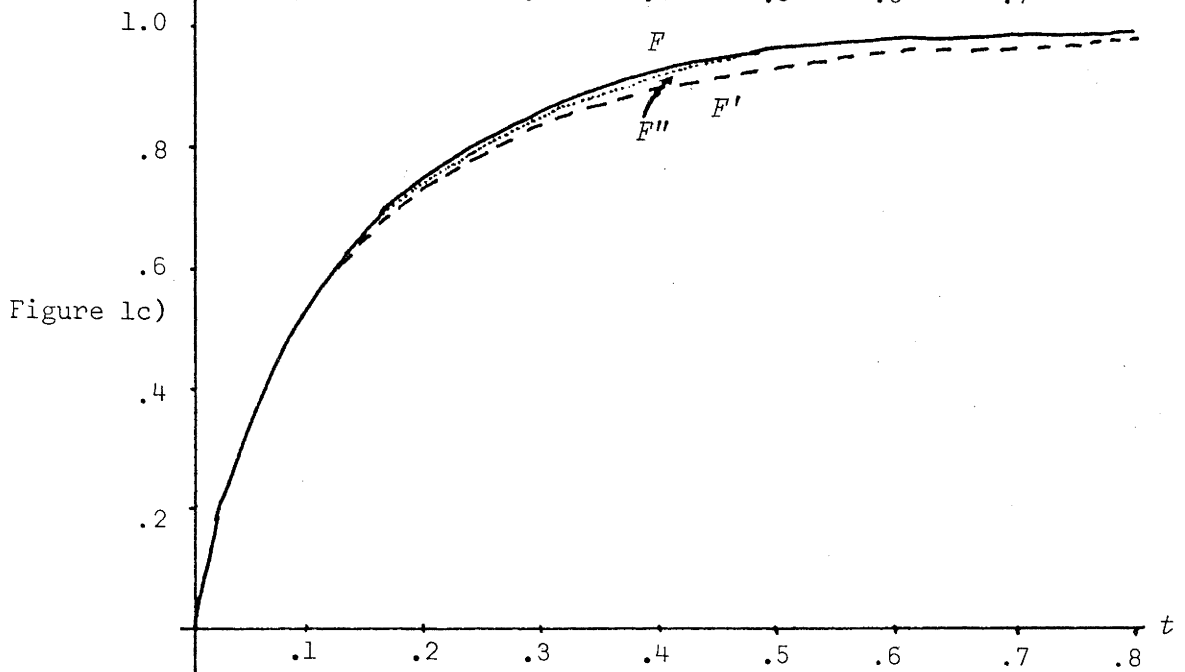
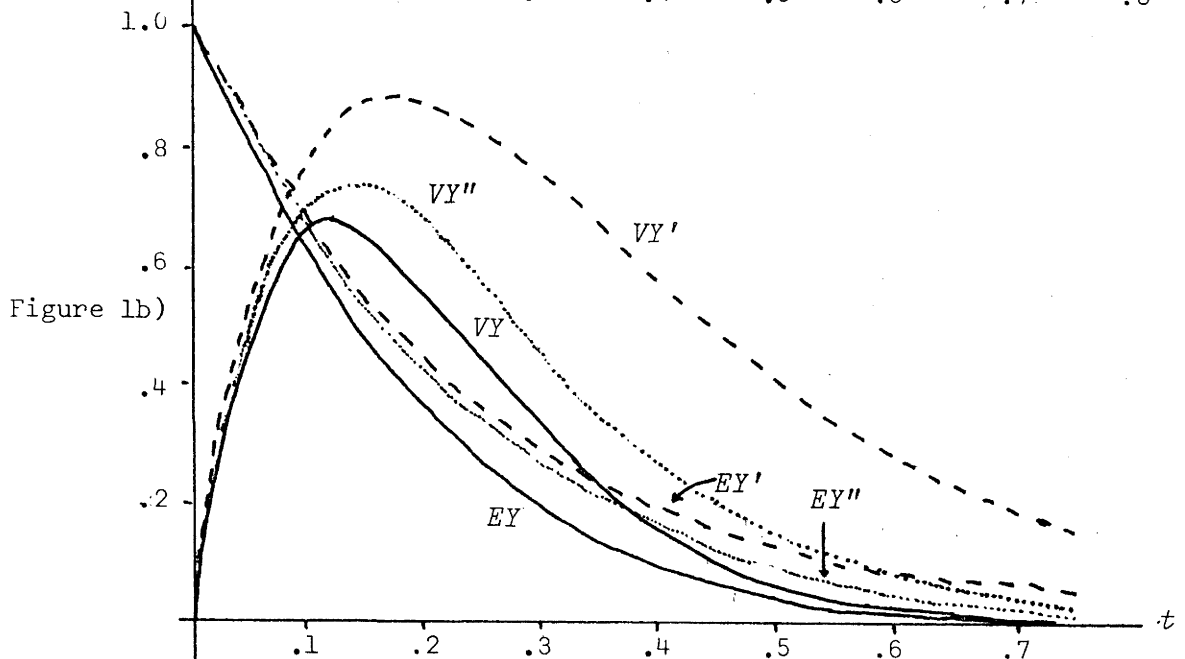
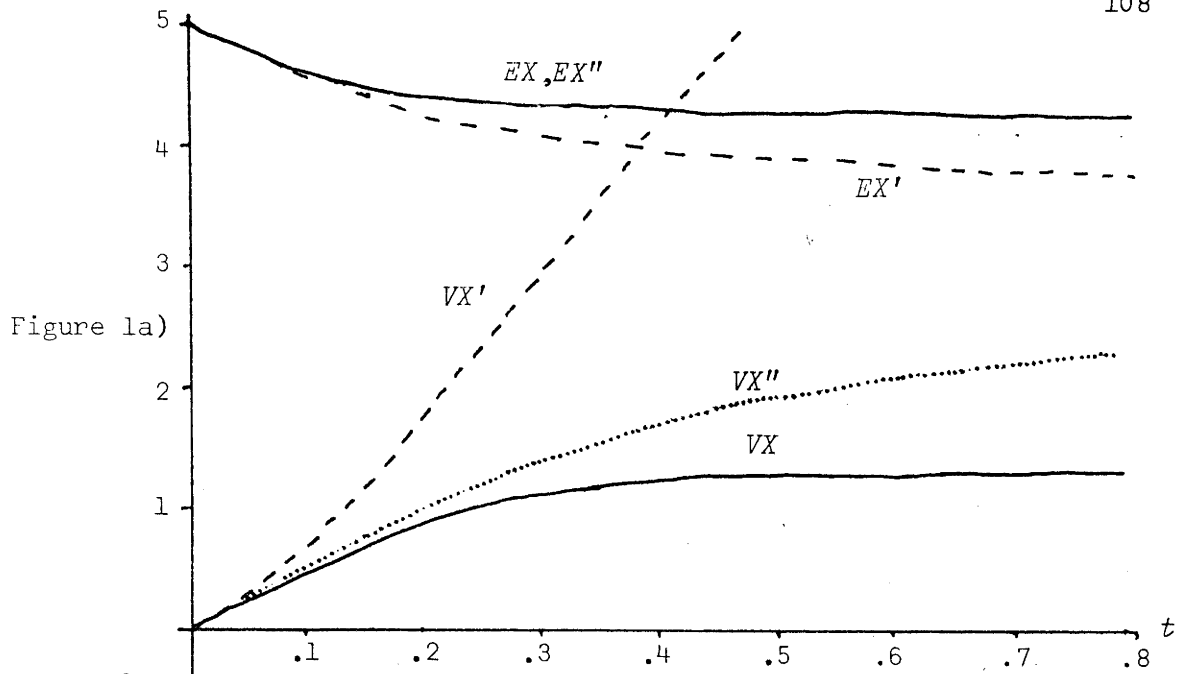
$$p_{rs}(0) = \begin{cases} 1 & \text{if } r = n, \quad s = a, \\ 0 & \text{otherwise,} \end{cases}$$

determine them uniquely.

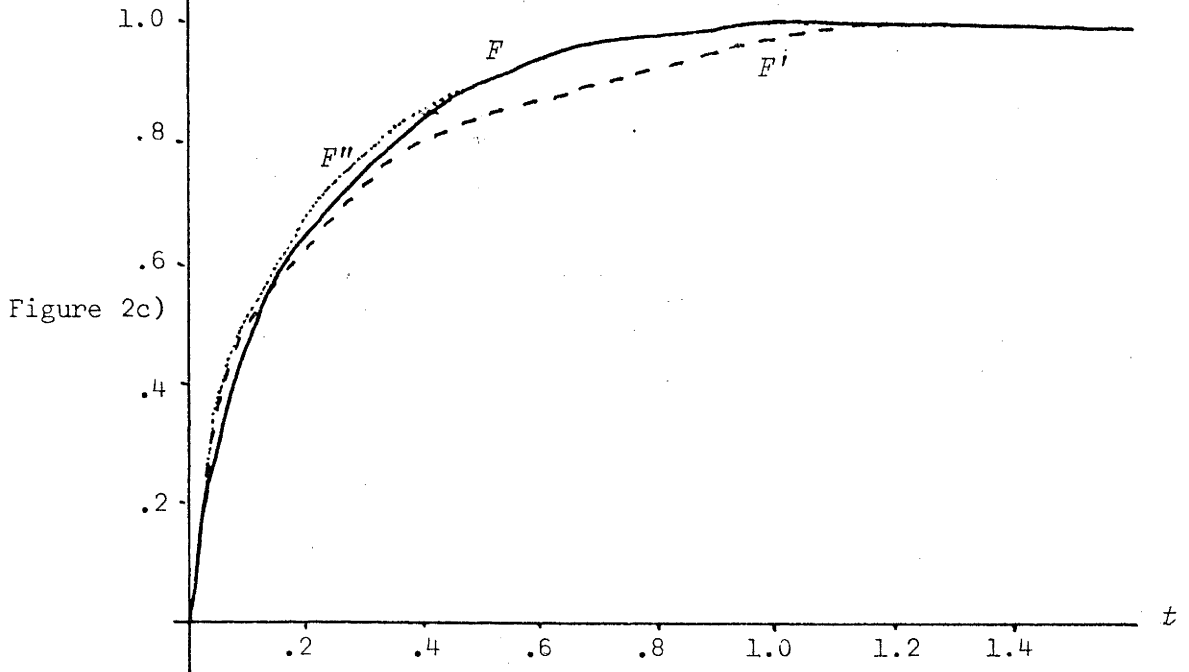
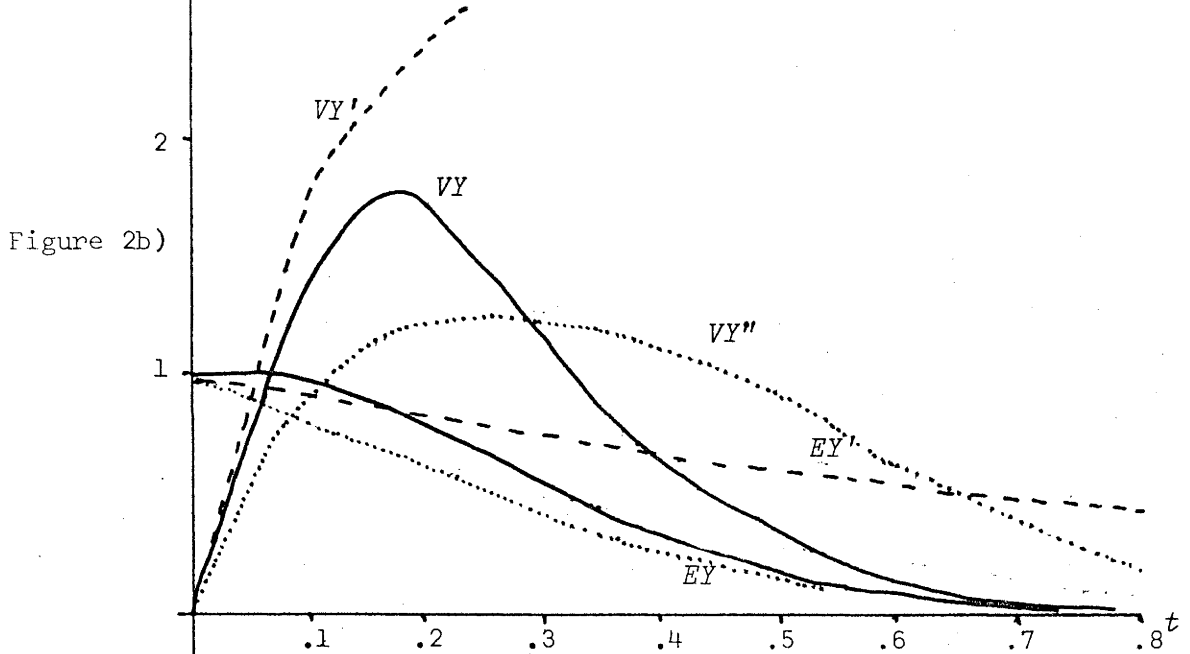
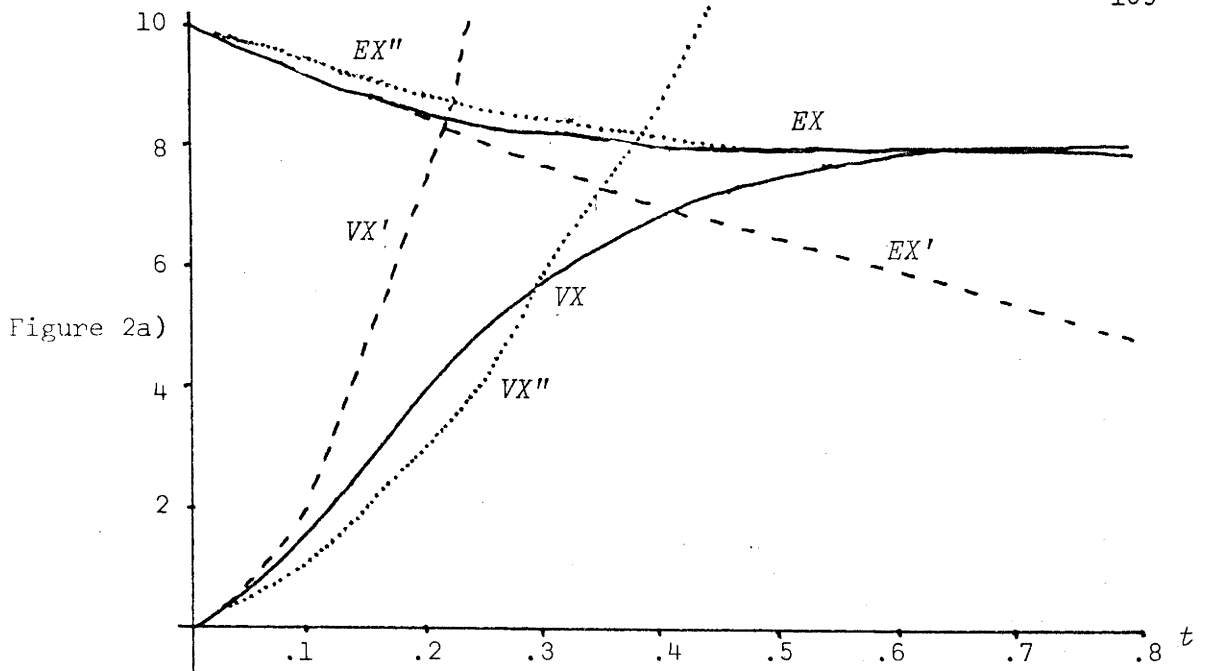
## APPENDIX B

COMPARISONS OF THE GENERAL EPIDEMIC MODEL  
TO THE APPROXIMATION OF CHAPTER THREE

The following pages of graphs compare the general stochastic epidemic model with the approximations derived in chapter 3. A description of the graphs and an explanation of the notation is given in section 3.3.

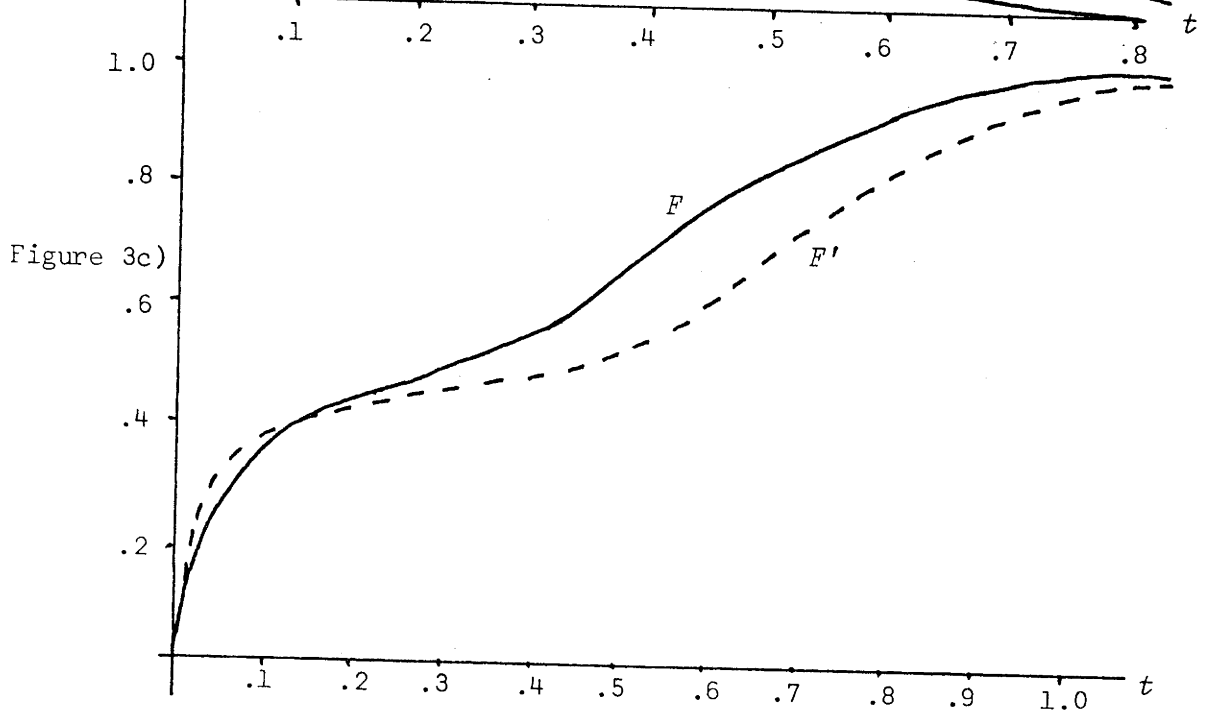
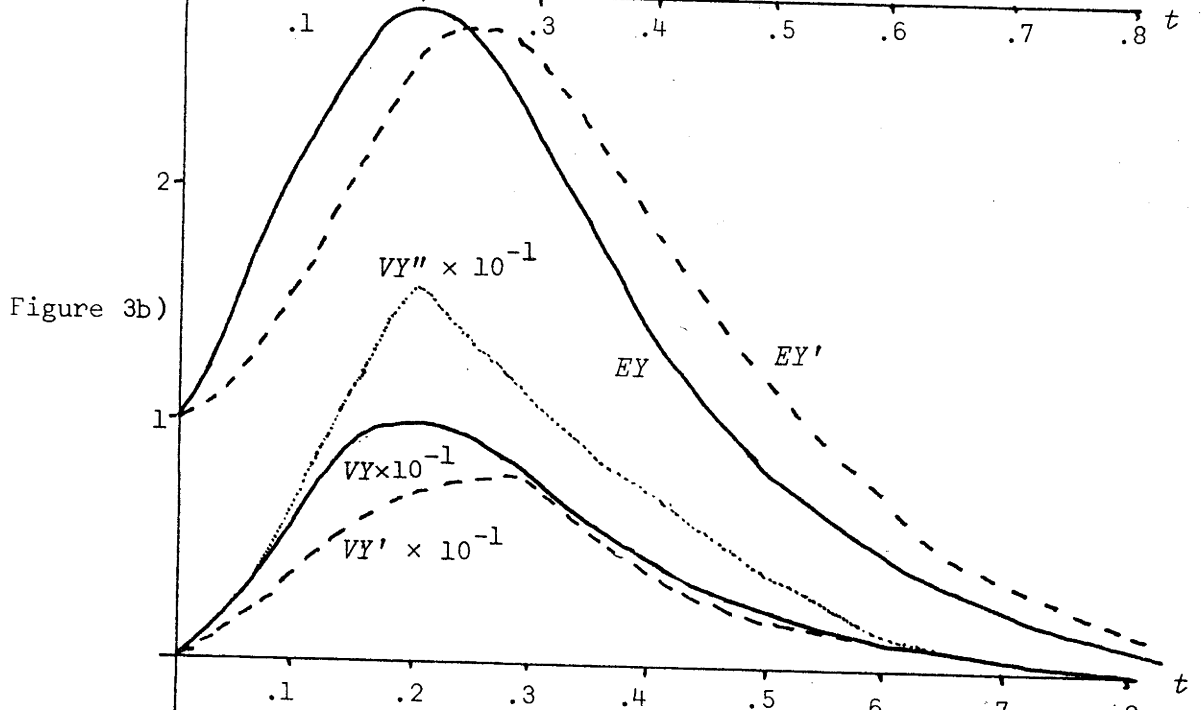
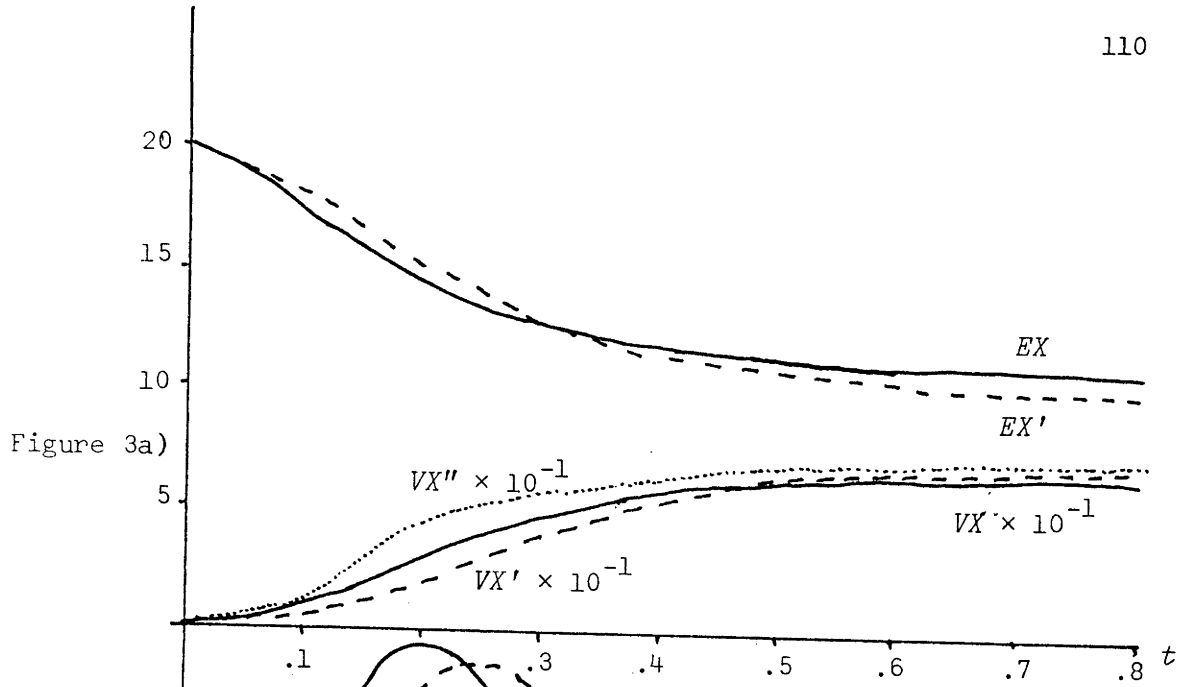


$$(n, a) = (5, 1), \quad \rho = 9$$



$(n, \alpha) = (10, 1), \rho = 9$





$$\underline{(n, a) = (20, 1), \quad \rho = 9}$$

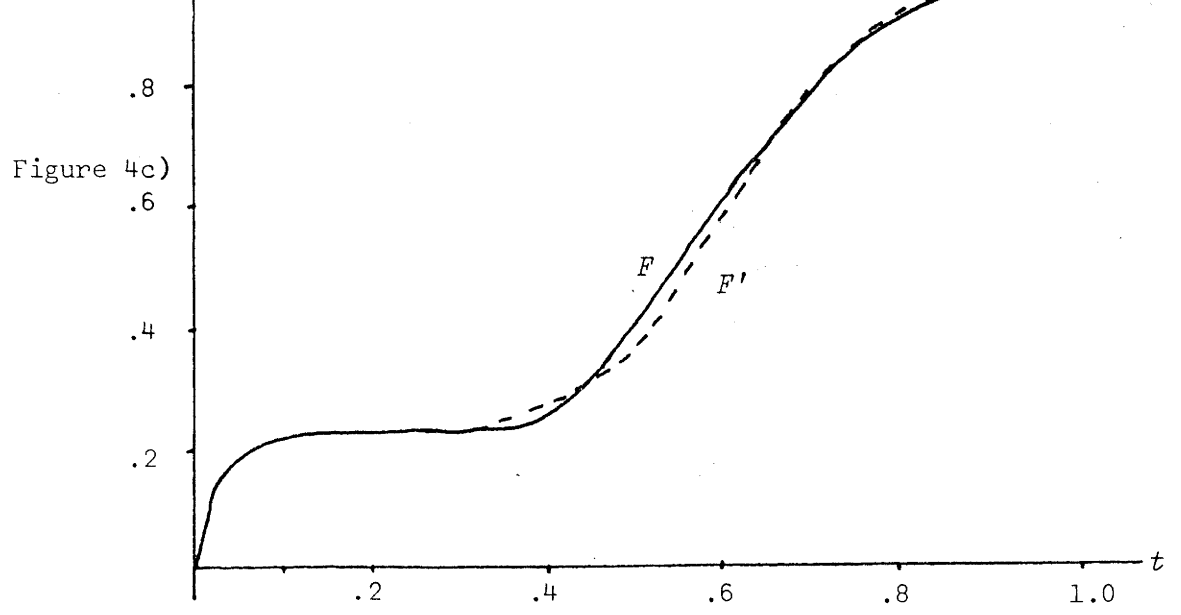
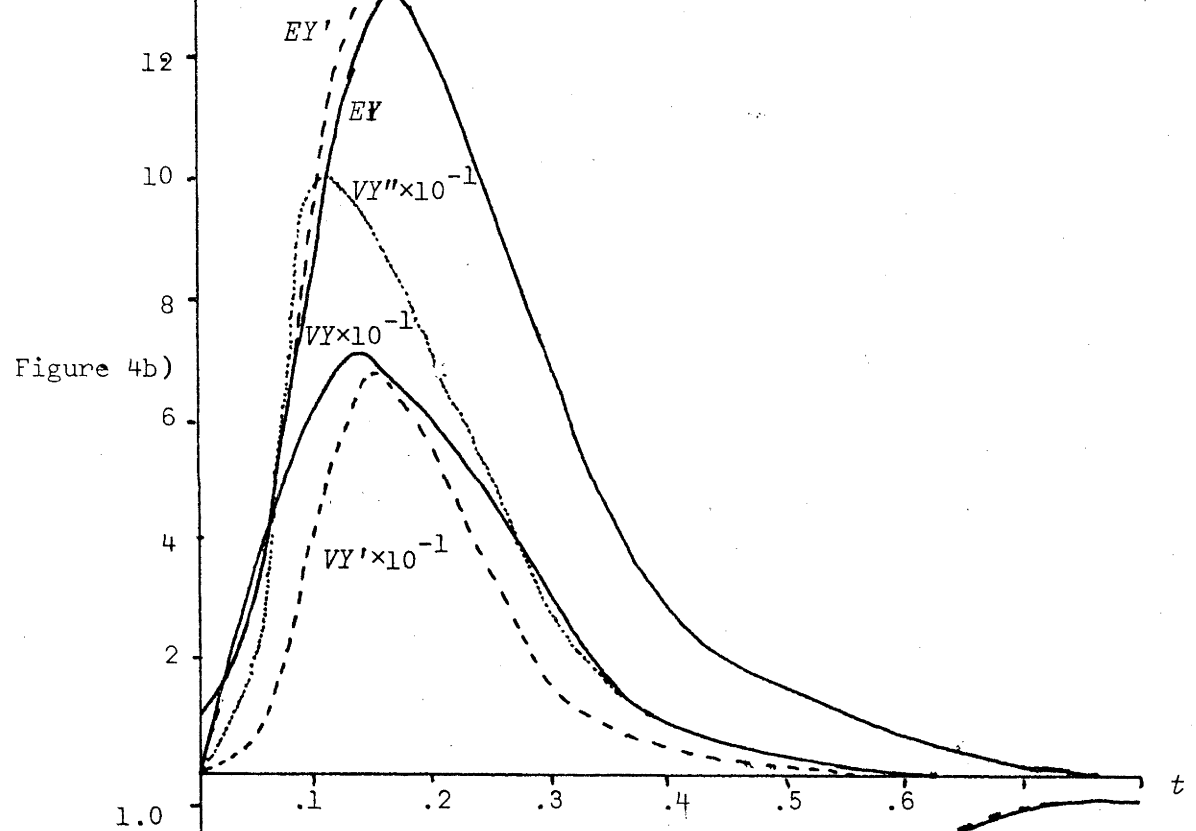
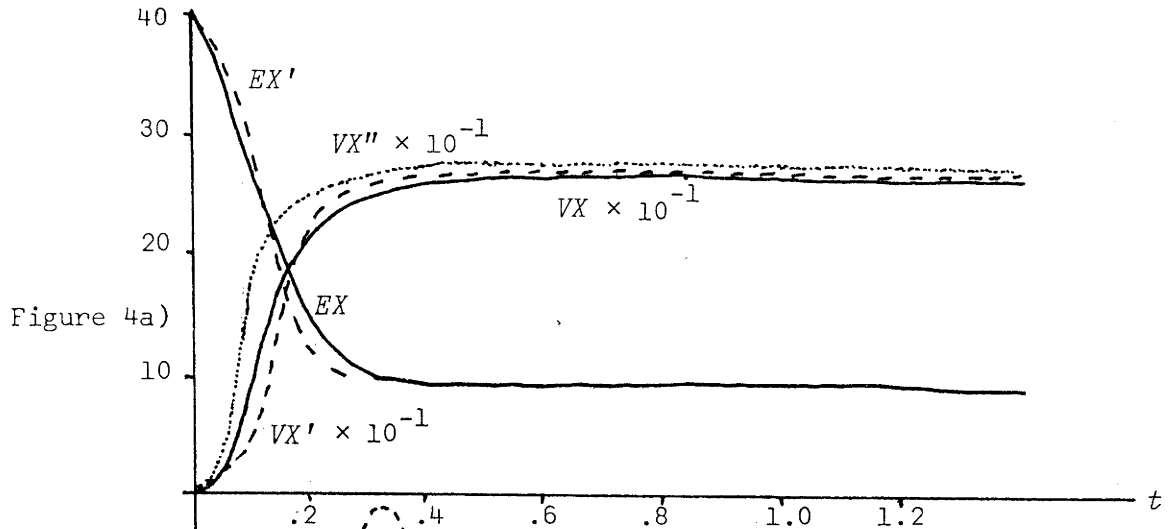


Figure 5a)

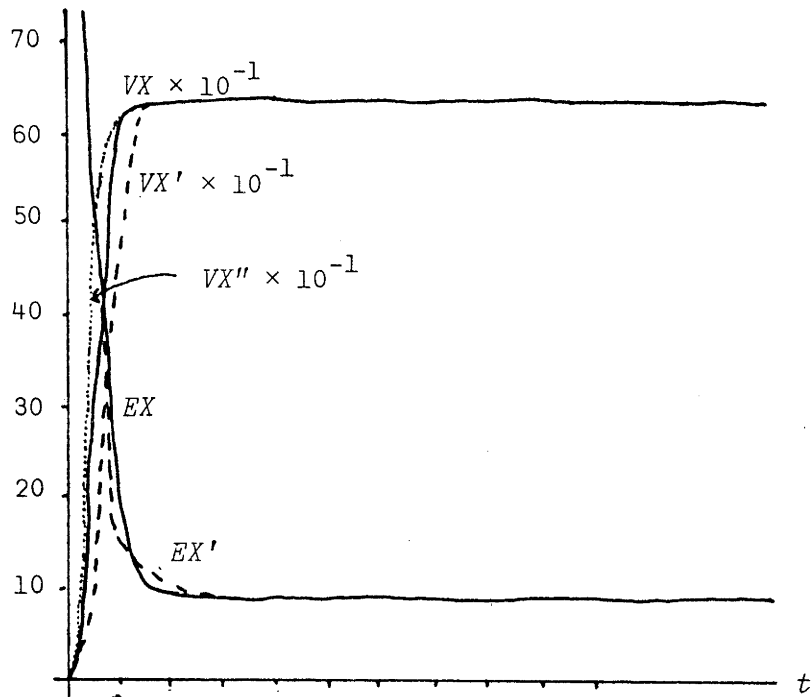


Figure 5b)

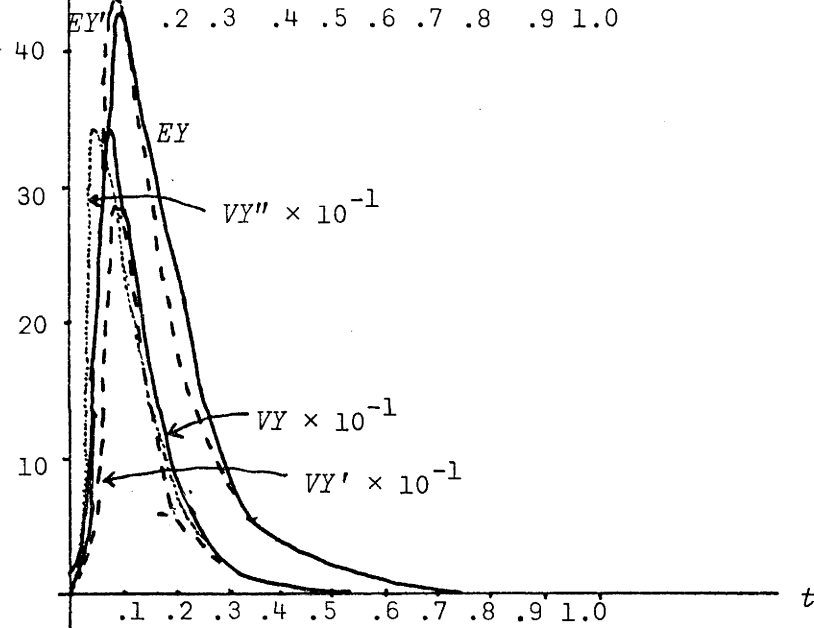
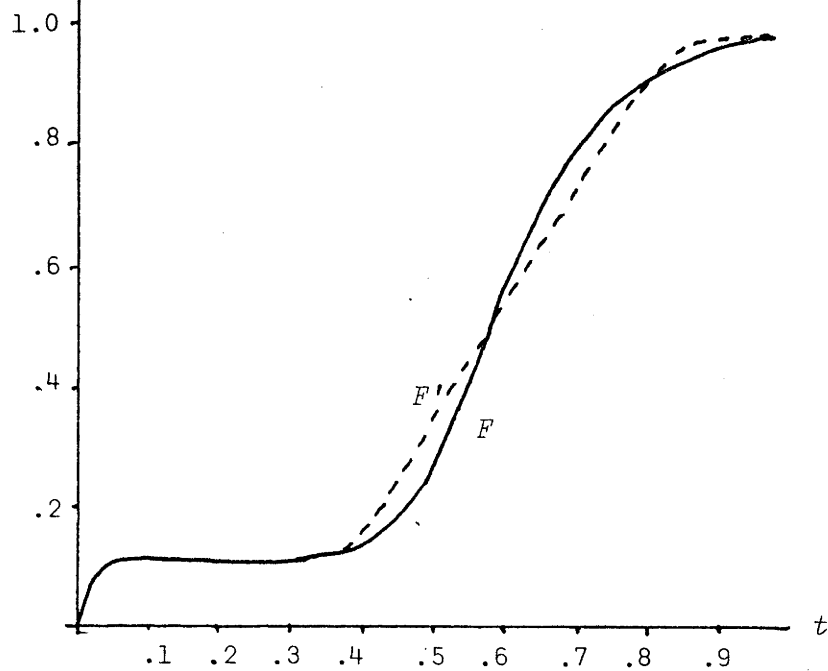
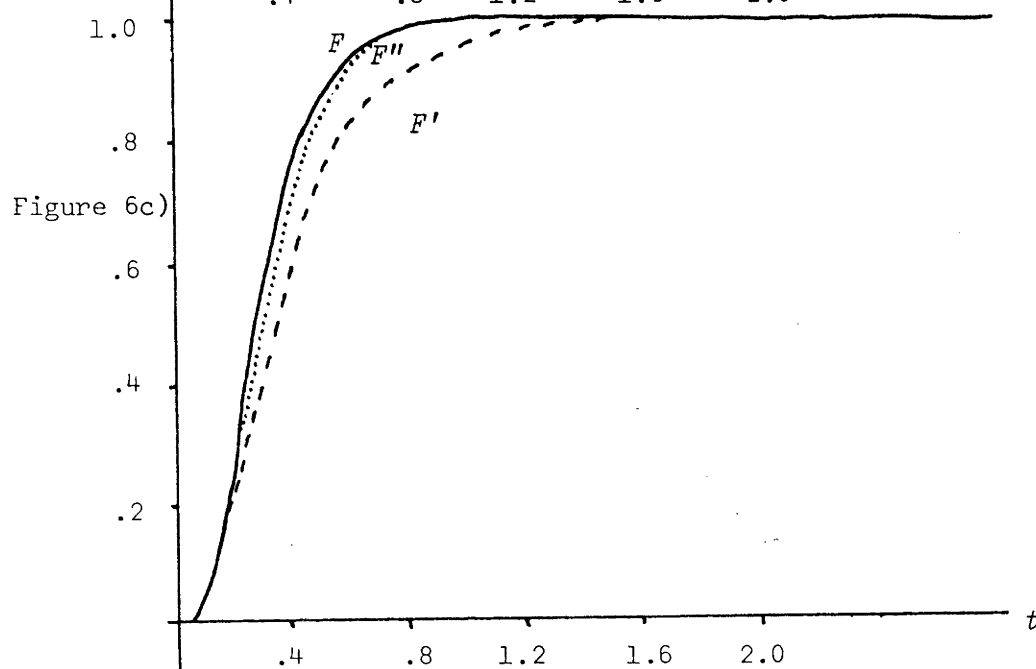
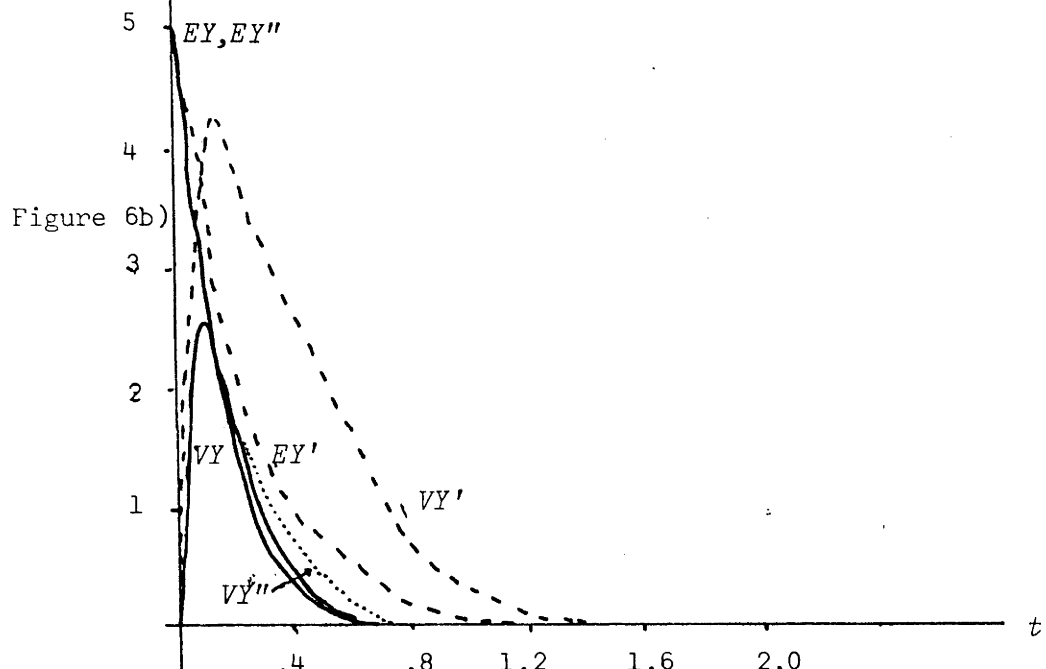
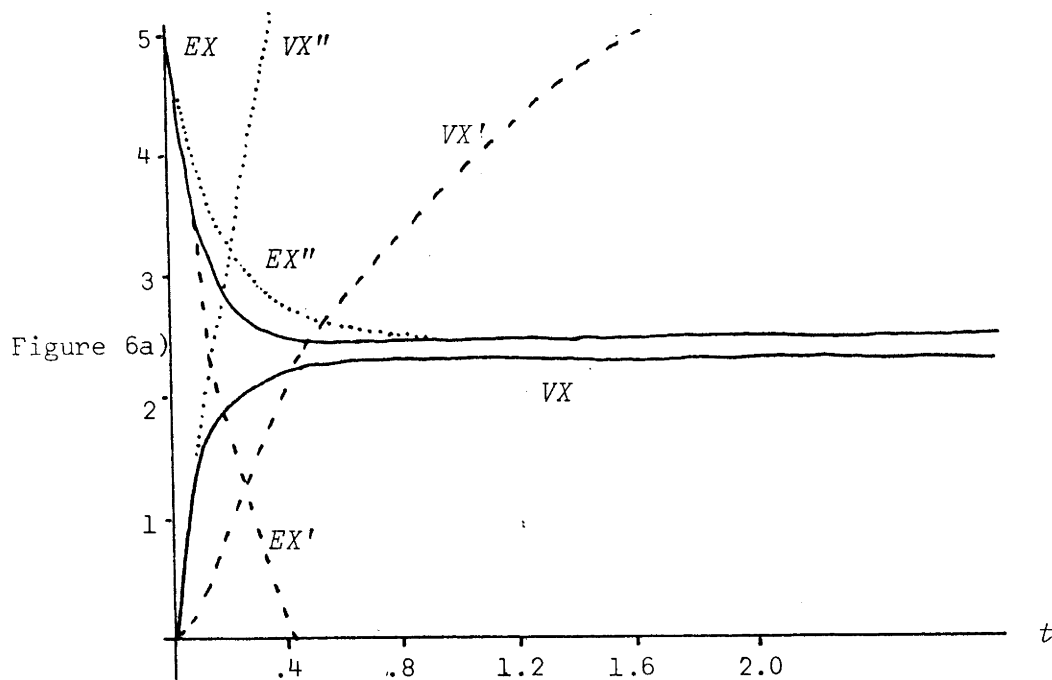
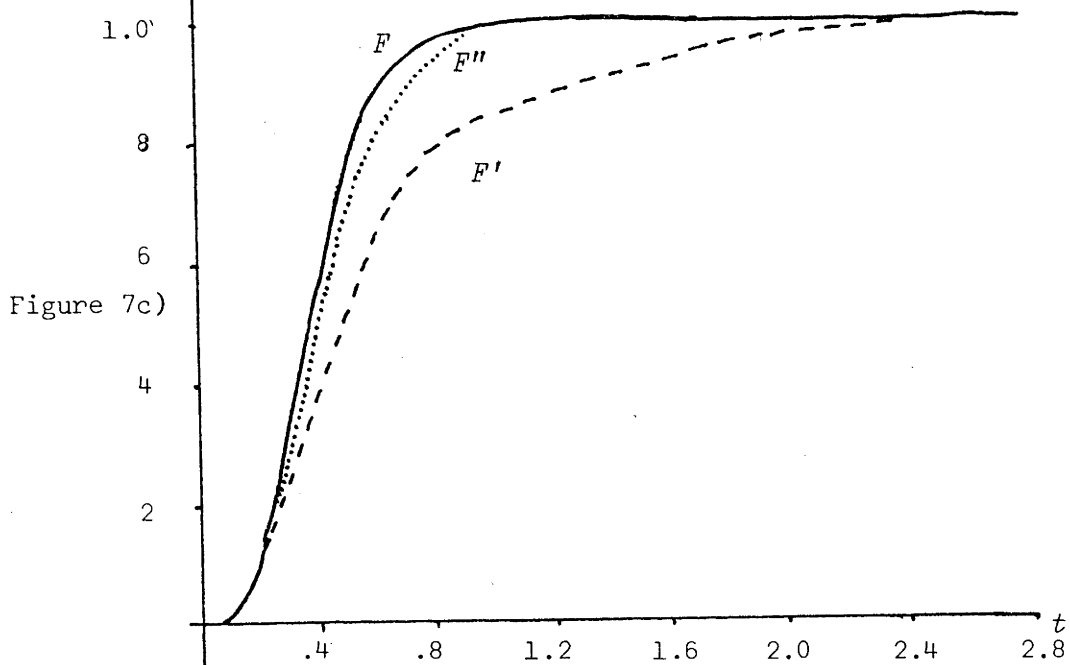
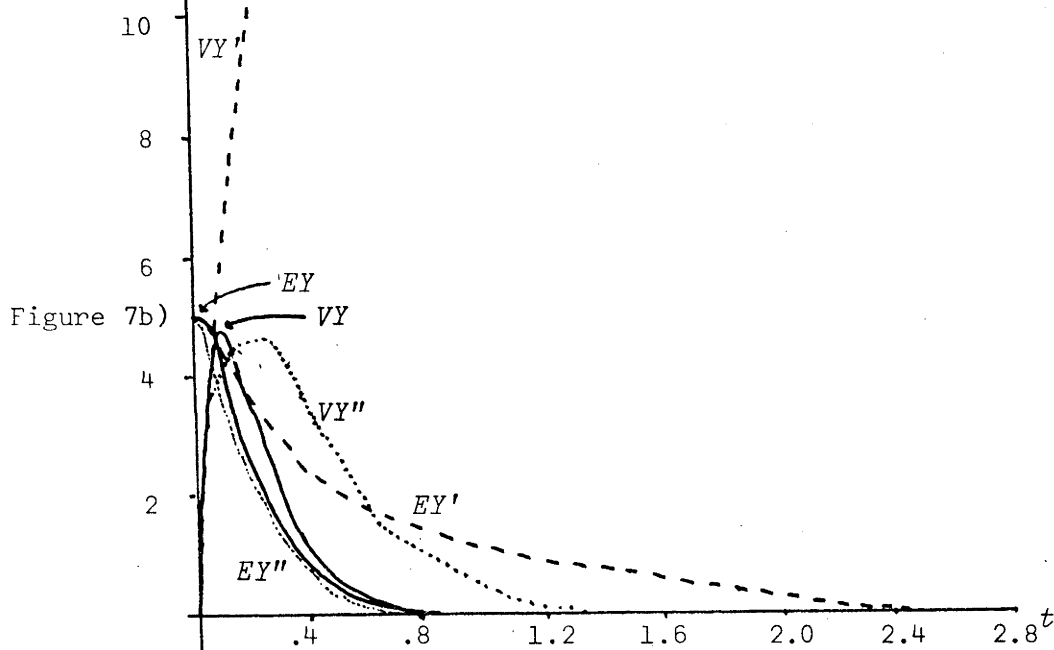
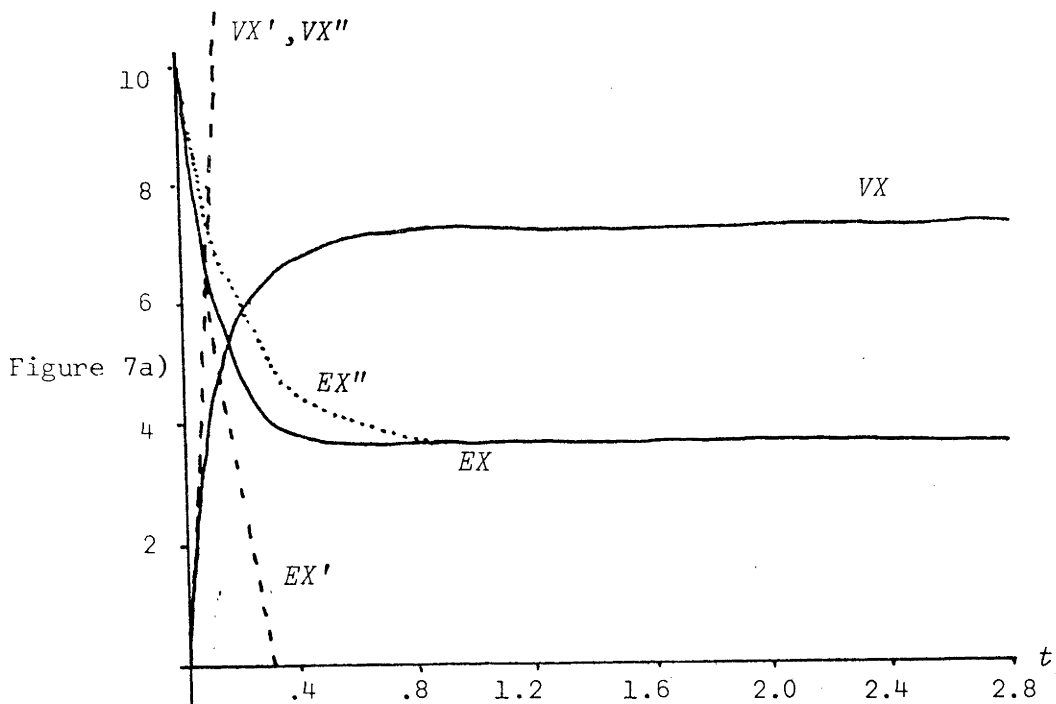


Figure 5c)

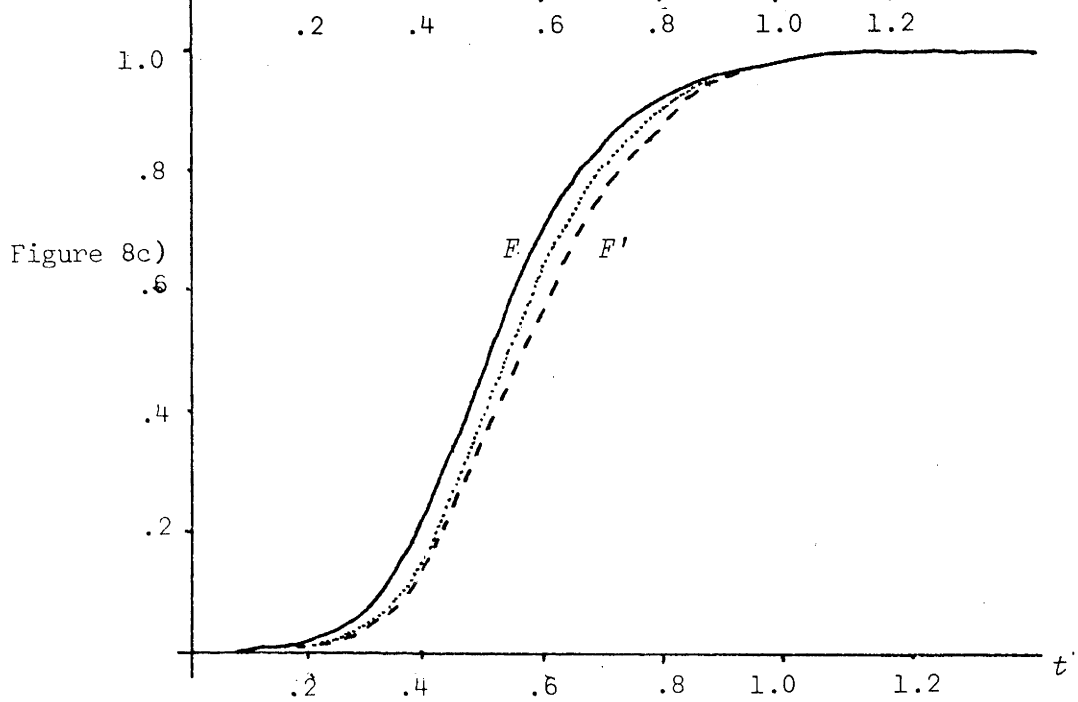
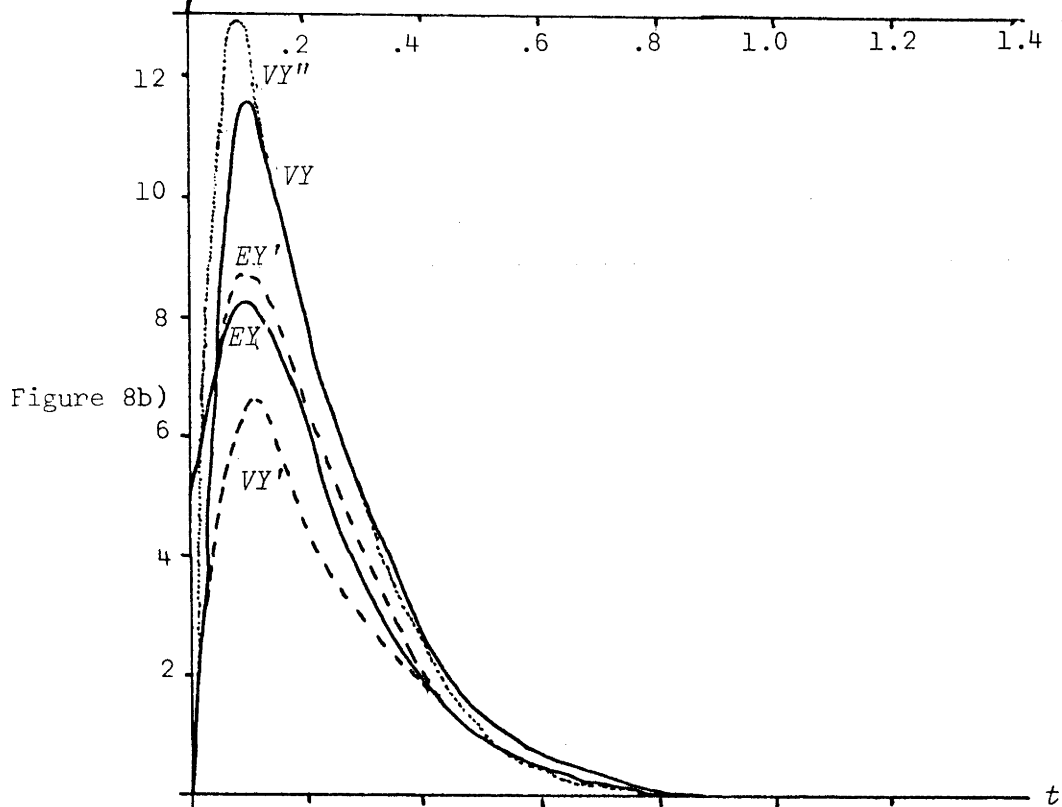
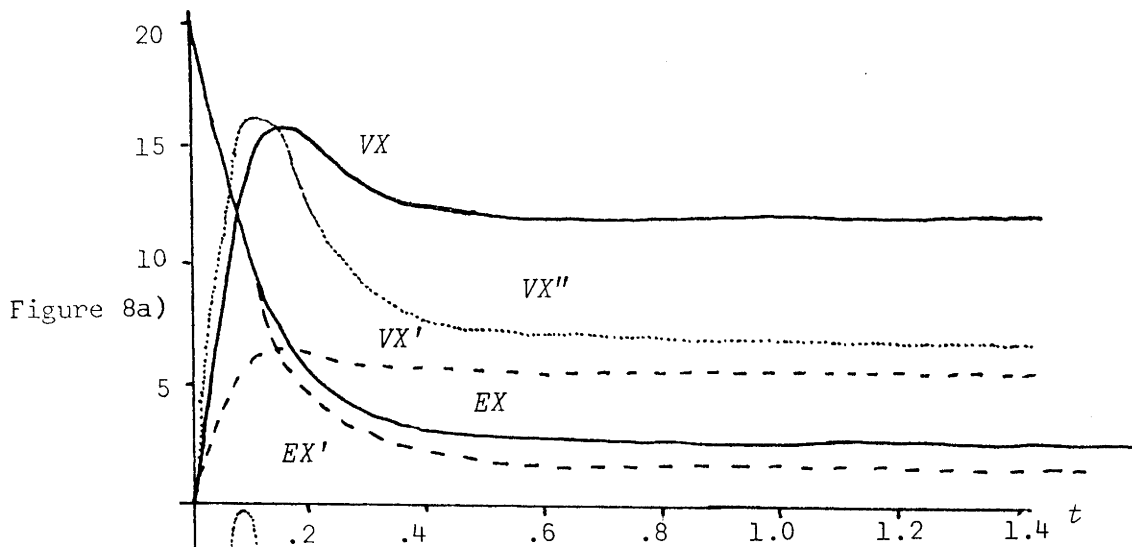


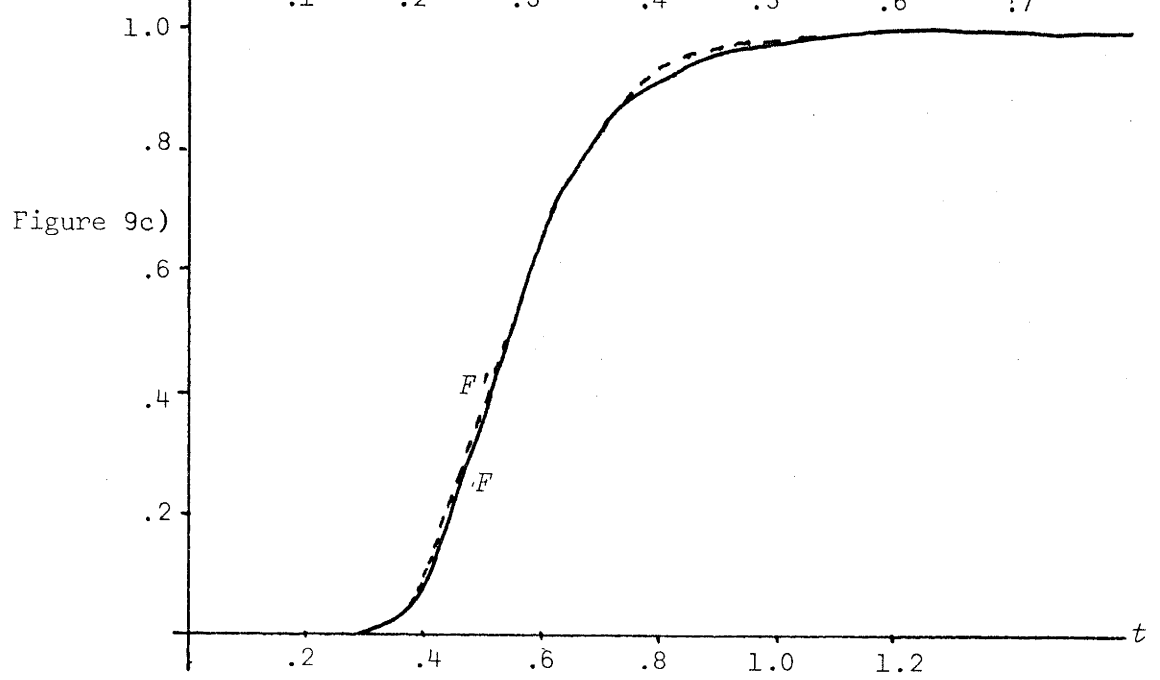
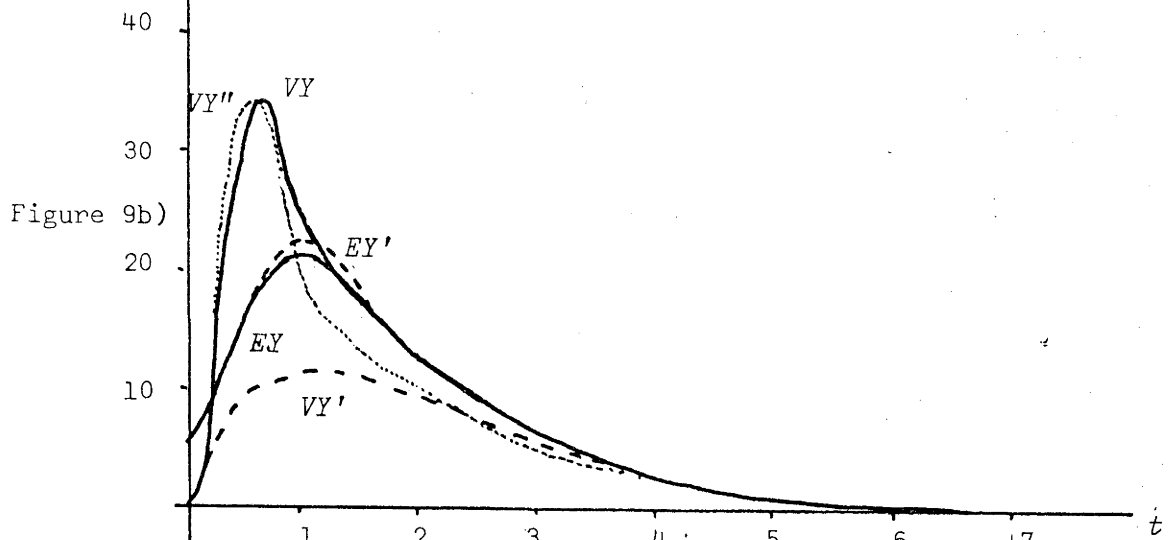
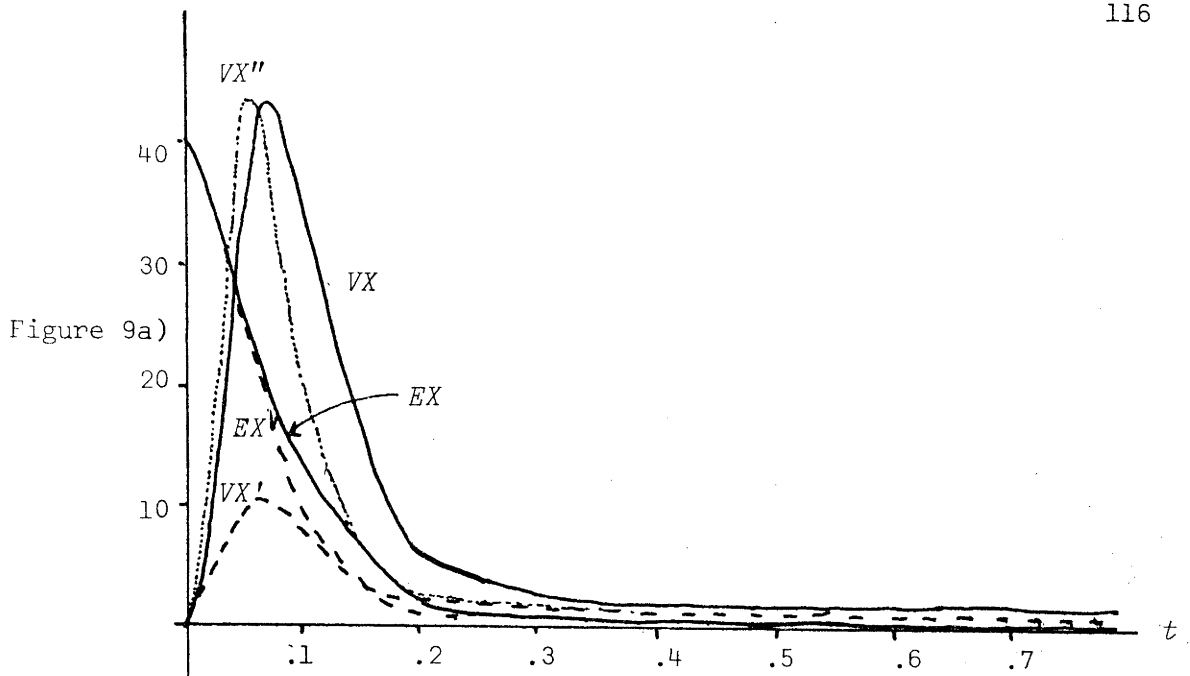


$(n, a) = (5, 5), \rho = 9$



$(n, \alpha) = (10, 5), \rho = 9$





$(n, a) = (40, 5), \rho = 9$

Figure 10a)

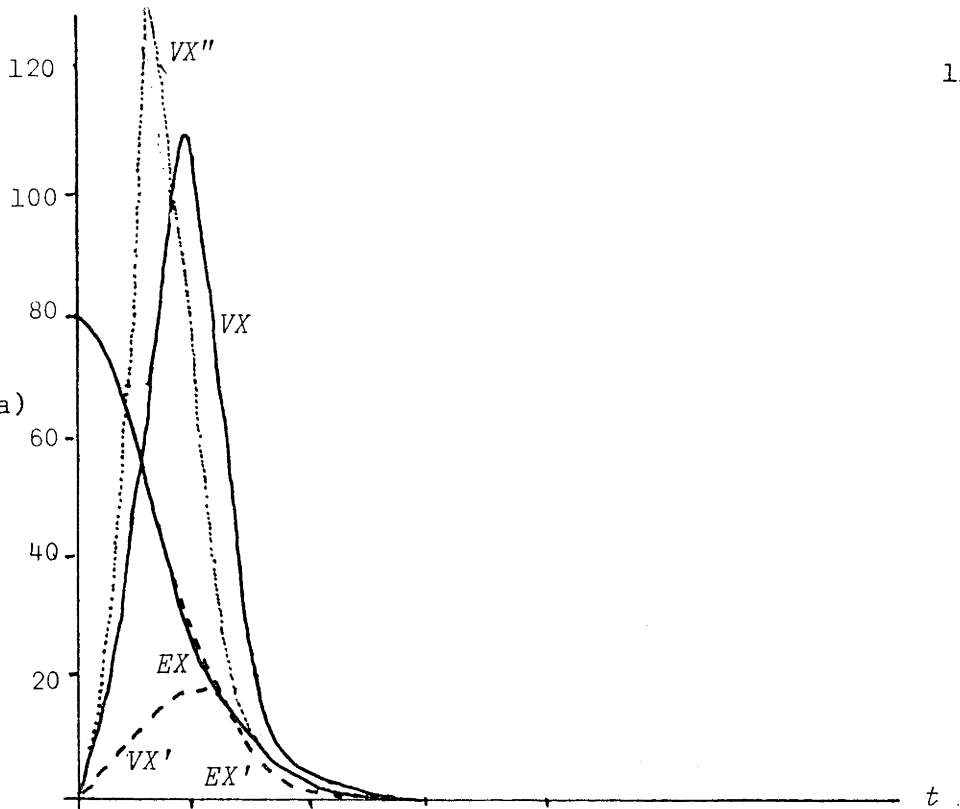


Figure 10b)

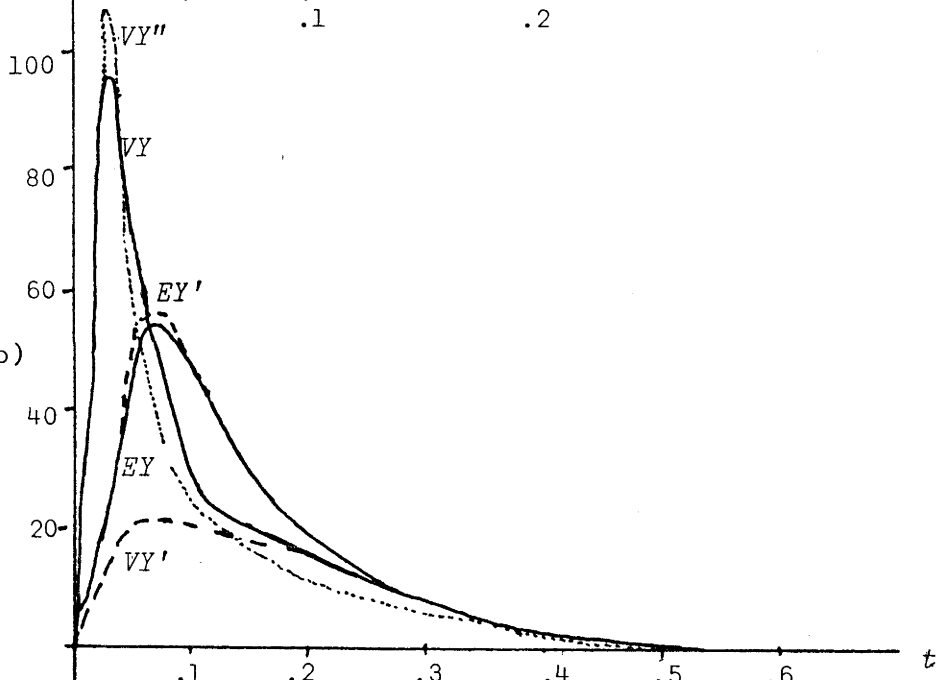
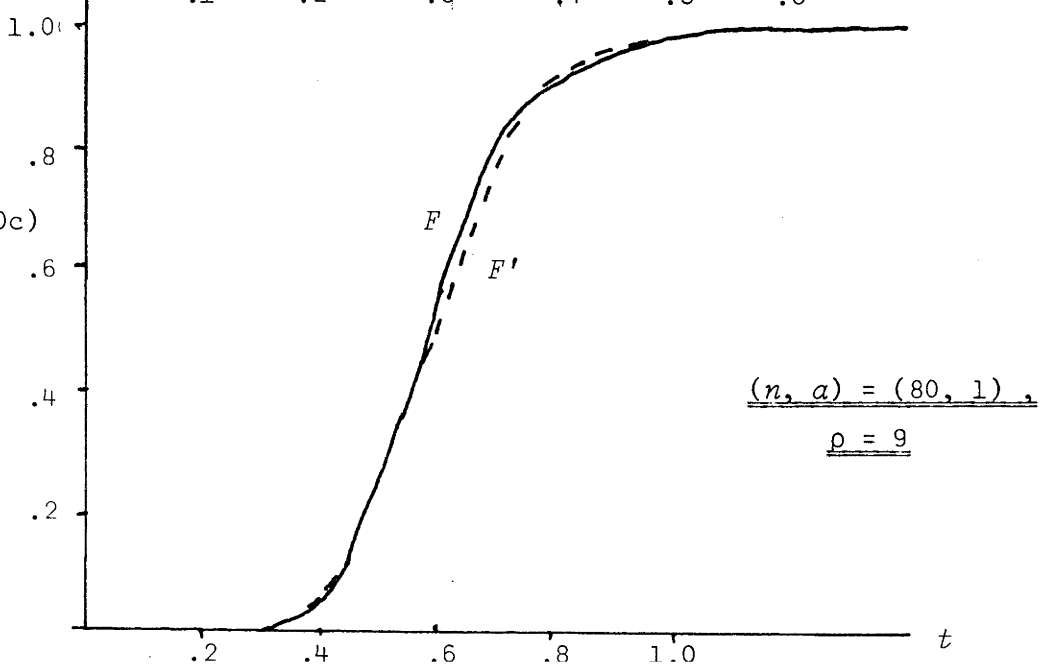
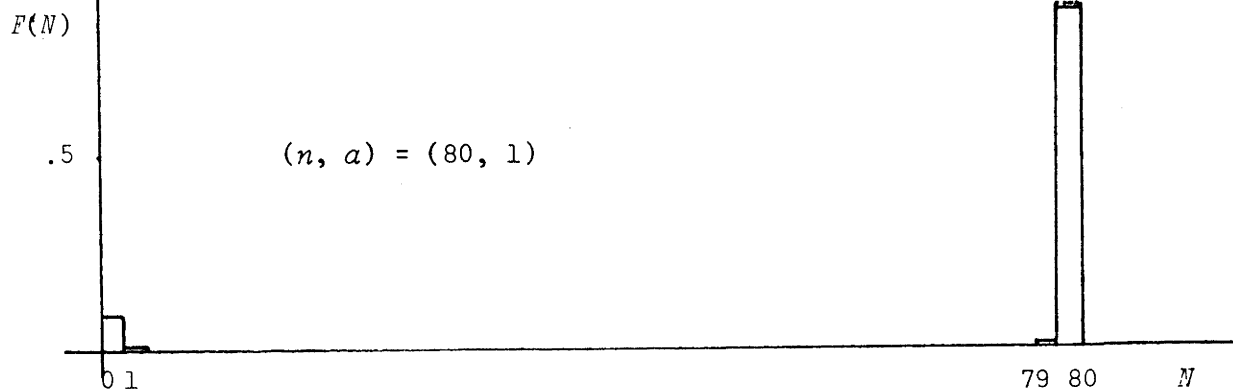
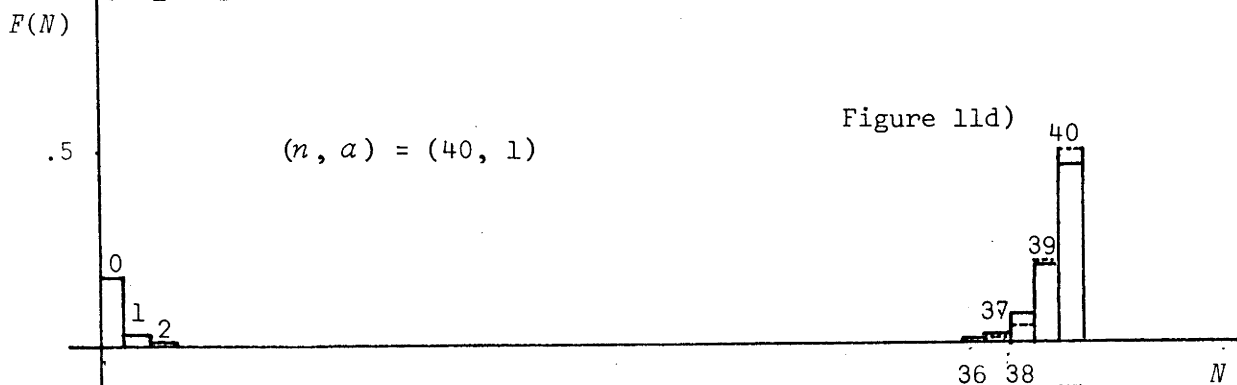
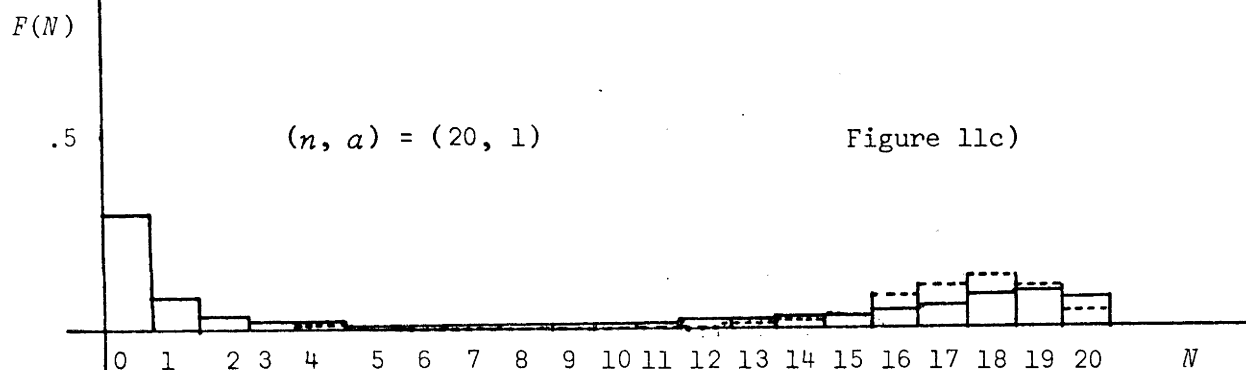
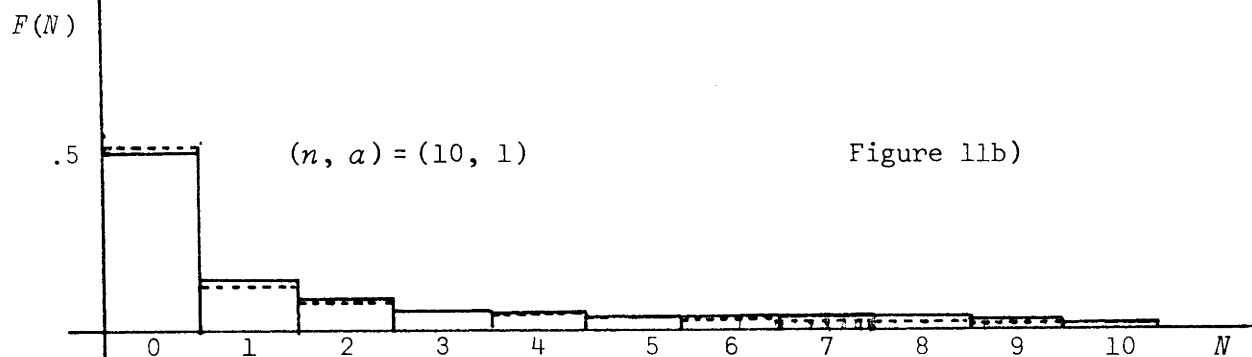
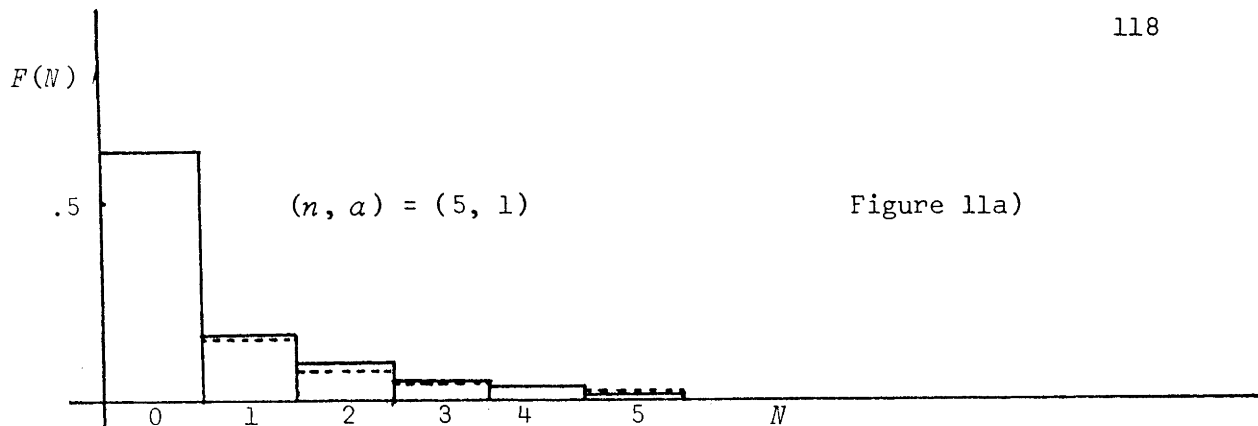
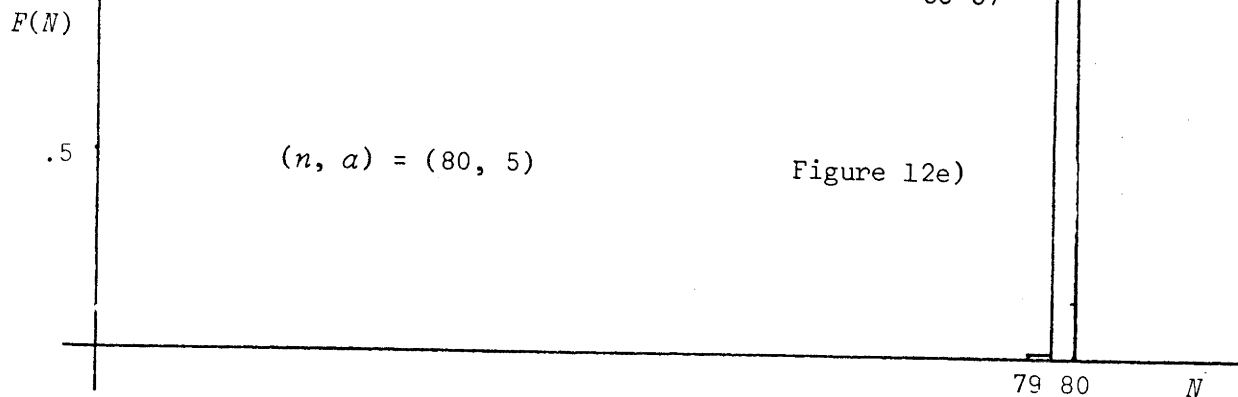
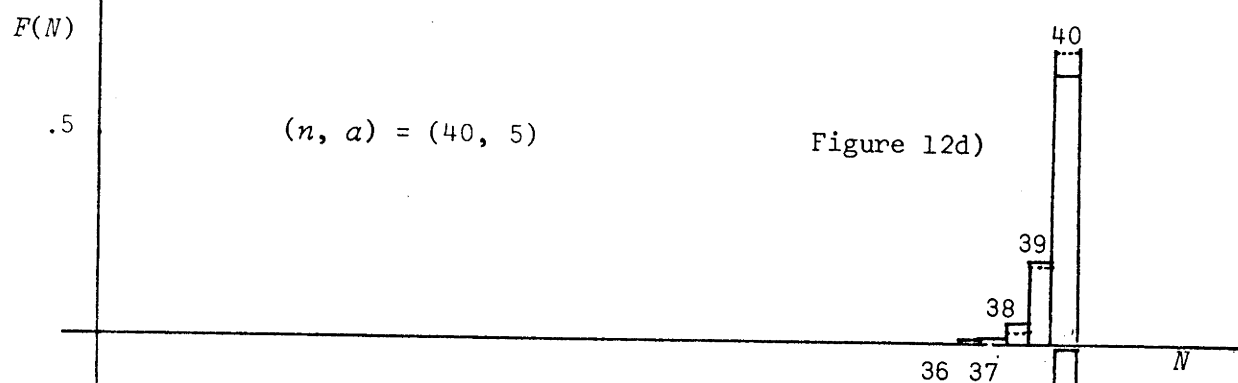
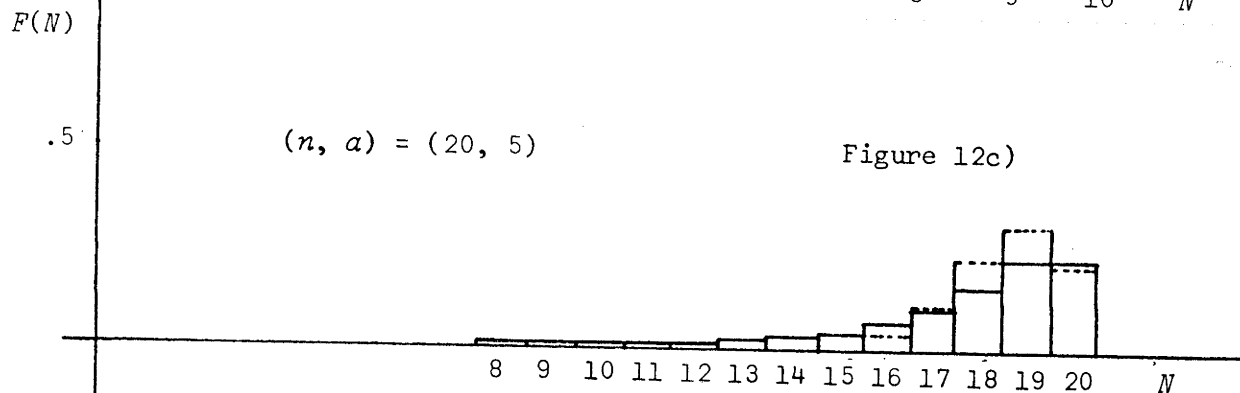
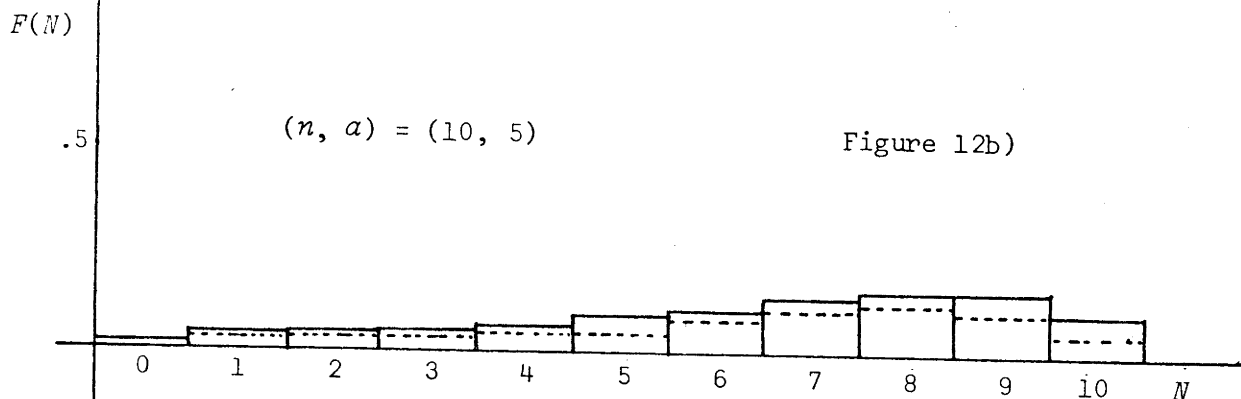
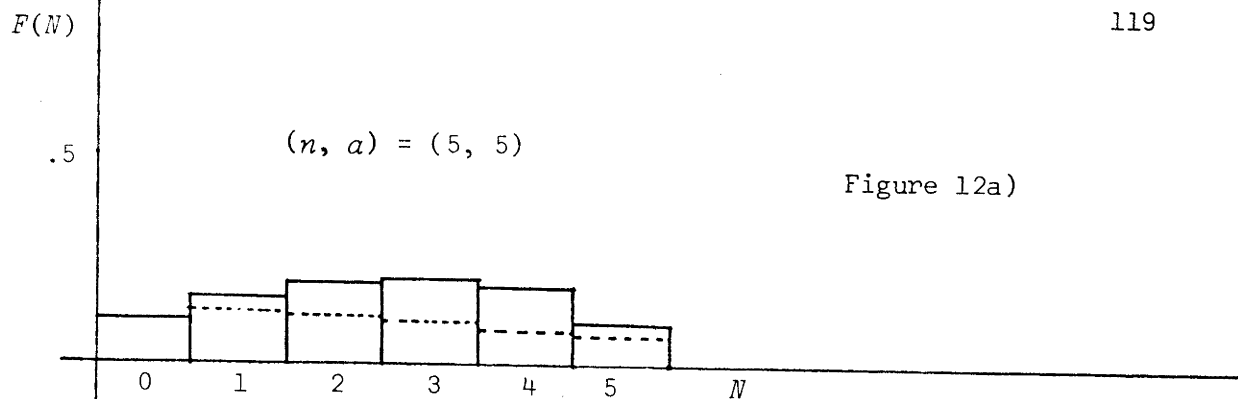


Figure 10c)









## APPENDIX C

APPLICATION OF THE QUASI-DETERMINISTIC APPROXIMATION  
TO THE PREDATOR-PREY MODEL

## THE MODEL

The predator-prey model is well-known (see e.g. Bharucha-Reid (1960)). We shall define the model here for the sake of convenience.

Let  $X_1$  and  $X_2$  be the number of prey and predators respectively at time  $t$ . The infinitesimal transition probability rates are given by

$$(X_1, X_2) \rightarrow \begin{cases} (X_1+1, X_2) & \text{with rate } \mu_1 X_1, \\ (X_1-1, X_2) & \text{with rate } \gamma_1 X_1 X_2, \\ (X_1, X_2+1) & \text{with rate } \mu_2 X_1 X_2, \\ (X_1, X_2-1) & \text{with rate } \gamma_2 X_2, \end{cases}$$

and the initial conditions are  $(X_1(0), X_2(0)) = (n_1, n_2)$ .

The deterministic model corresponding to this stochastic one is defined by the equations

$$\text{C.1a)} \quad \dot{x}_1 = x_1(\mu_1 - \gamma_1 x_2),$$

$$\text{C.1b)} \quad \dot{x}_2 = x_2(\mu_2 x_1 - \gamma_2).$$

where  $(x_1(0), x_2(0)) = (n_1, n_2)$ .

Because of the nonlinear probability rates the stochastic model (like that of the general epidemic) has been found to be mathematically intractable. (In fact the predator-prey model is even more intractable because there is no hierarchical structure i.e. apart from those states

corresponding to extinction of a population, all states may be revisited.)

### THE QUASI-DETERMINISTIC APPROXIMATION

We remove the non-linearity in the probability rates by replacing some of the stochastic variables by deterministic variables. The approximating model is defined by the transitions

$$(X'_1, X'_2) \rightarrow \begin{cases} (X'_1+1, X'_2) & \text{with rate } \mu_1 X'_1, \\ (X'_1-1, X'_2) & \text{with rate } \gamma_1 x_2 X'_1, \\ (X'_1, X'_2+1) & \text{with rate } \mu_2 x_1 X'_2, \\ (X'_1, X'_2-1) & \text{with rate } \gamma_2 X'_2, \end{cases}$$

where initially  $(X'_1(0), X'_2(0)) = (n_1, n_2)$ .

Now  $X'_1$  and  $X'_2$  are independent and each is a generalised birth and death process, the first having birth rate  $\mu_1$  and death rate  $\gamma_1 x_2$  and the second having birth rate  $\mu_2 x_1$  and death rate  $\gamma_2$ . The generalised birth and death process was studied by Kendall (1948).

Letting  $P_1(z, t)$  and  $P_2(z, t)$  be the p.g.f.'s of  $X_1$  and  $X_2$  respectively, we find from Kendall's results that

$$P_i(z, t) = \left[ \frac{\xi_i + (1 - \xi_i - \eta_i)z}{1 - \eta_i z} \right]^{n_i}, \quad i = 1, 2,$$

where

$$\xi_i = 1 - \frac{e^{-\rho_i}}{W_i}, \quad i = 1, 2,$$

and

$$\eta_i = 1 - \frac{1}{W_i}, \quad i = 1, 2,$$

and where

$$W_1 = 1 + e^{-\rho_1(t)} \int_0^t \mu_1 e^{\rho_1(\tau)} d\tau,$$

$$W_2 = e^{-\rho_2(t)} \left[ 1 + \int_0^t \gamma_2 e^{\rho_2(\tau)} d\tau \right],$$

and

$$\rho_1(t) = \int_0^t [\gamma_1 x_2(\tau) - \mu_1] d\tau,$$

$$\rho_2(t) = \int_0^t [\gamma_2 - \mu_2 x_1(\tau)] d\tau.$$

From equations C.1 we see that

$$\rho_i(t) = \ln \frac{n_i}{x_i(t)}, \quad i = 1, 2.$$

The first two moments may be shown to be

$$EX'_1 = x_1,$$

$$EX'_2 = x_2,$$

$$\text{Var } X'_1 = x_1 \left\{ 1 - \frac{x_1}{n_1} \left[ 1 - 2\mu_1 n_1 \int_0^t \frac{d\tau}{x_1(\tau)} \right] \right\},$$

and

$$\text{Var } X'_2 = x_2 \left\{ -1 + \frac{x_2}{n_2} \left[ 1 + 2\gamma_2 n_2 \int_0^t \frac{d\tau}{x_2(\tau)} \right] \right\}.$$

The distributions of the time to extinction,  $F'_i(t) = P_i(0, t)$ ,

$i = 1, 2$ , are given by

$$F'_1(t) = \left[ 1 - \frac{x_1}{n_1} \left( 1 + \mu_1 n_1 \int_0^t \frac{d\tau}{x_1(\tau)} \right)^{-1} \right]^{n_1},$$

and

$$F'_2(t) = \left[ 1 - \left( 1 + \gamma_2 n_2 \int_0^t \frac{d\tau}{x_2(\tau)} \right)^{-1} \right]^{n_2}.$$

## RESULTS

Figure C.1 shows a comparison of real values of  $EX_1$ ,  $\text{Var } X_1$ ,  $EX_2$ ,  $\text{Var } X_2$  and  $F_1(t)$ , calculated from 100 simulations, with corresponding functions from the quasi-deterministic approximation. The parameter values were  $n_1 = 100$ ,  $n_2 = 10$ ,  $\mu_1 = .01$ ,  $\gamma_1 = .001$ ,  $\mu_2 = .001$  and  $\gamma_2 = .01$ . The 100 simulations took 17.0 seconds on the Univac 1100/42 whereas the approximation took 4.2 seconds.

We note that for the range of time shown, the approximations  $EX'_1$  and  $EX'_2$  are very close to the true values. However, although  $EX'_1$  and  $EX'_2$  become very small, they never reach zero and in fact are cyclic functions with period approximately 1400. On the other hand  $EX_1$  and  $EX_2$  once close to zero tend rapidly to it. This is because of the more stochastic nature of the real model. The value of  $EX_1$  becomes so small that extinction is almost certain.

Agreement between  $F_1(t)$  and  $F'_1(t)$  is quite good. We note that  $F_2(t)$  and  $F'_2(t)$  are not shown because both are zero for this range of time.

There is very poor agreement between the real and approximate variances. It is difficult to think of a simple explanation for this, especially in the case of the predator population where  $\text{Var } X'_2$  is an order of magnitude larger than  $\text{Var } X_2$ . Perhaps we could conjecture that  $X_2$  is to some extent "self-correcting" and that this property is lost in the approximating process.

Figure C.1a)

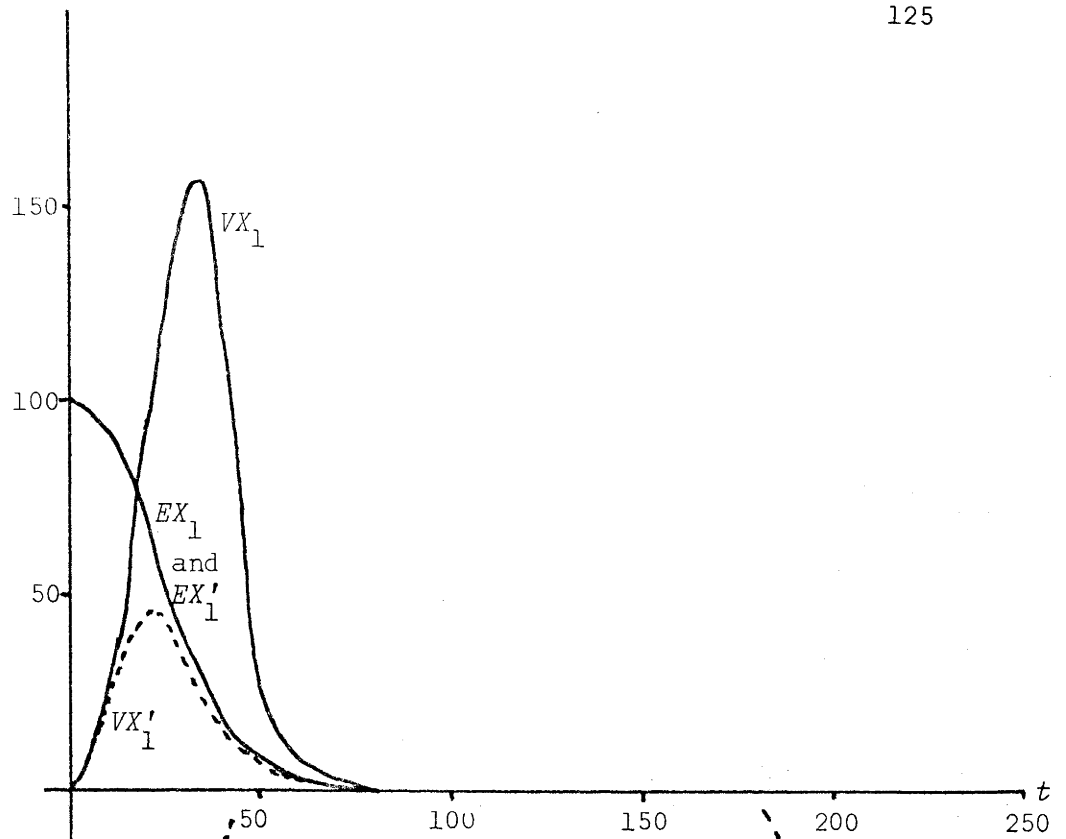


Figure C.1b)

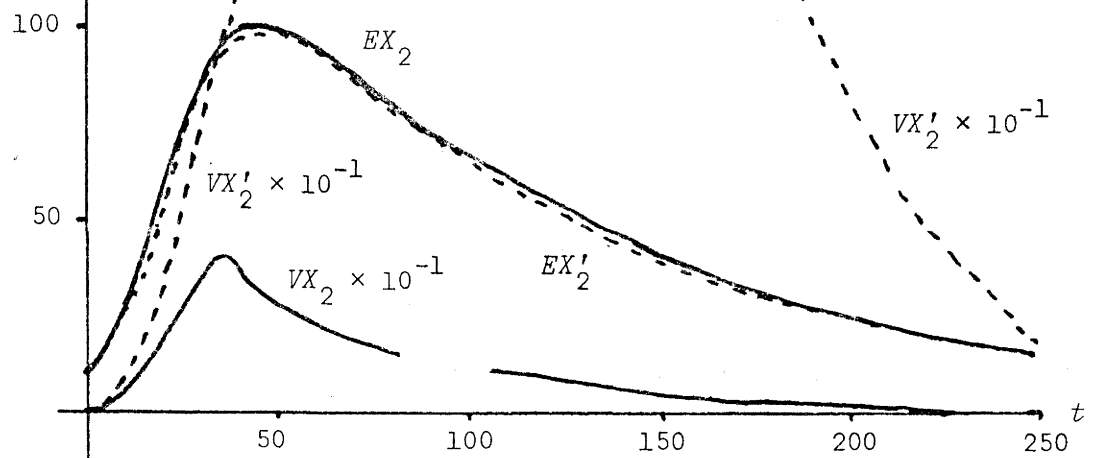
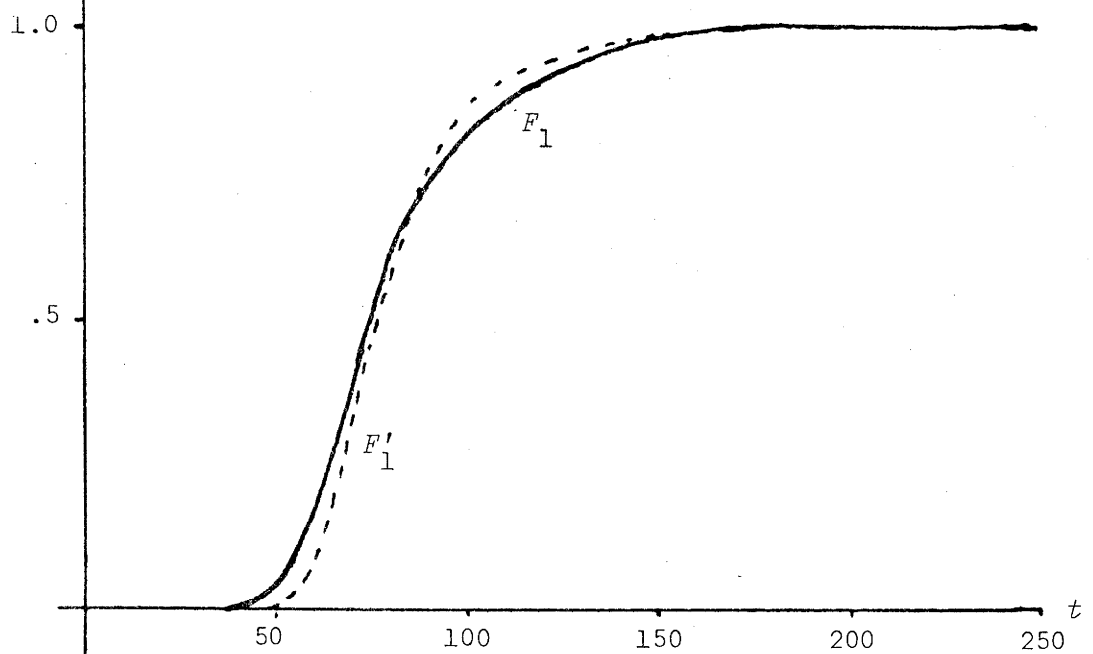


Figure C.1c)





## APPENDIX D

THE JOINT p.g.f. OF THE NUMBER OF BIRTHS IN EACH SUBPOPULATION  
IN A LINEAR MULTIVARIATE BIRTH AND DEATH PROCESS

Let  $Y_i(t)$ ,  $i = 1, \dots, m$ , be the number of members of the  $i$ th subpopulation at time  $t$ . (In general the  $t$  shall be suppressed.) Further, let  $Y$  denote the vector  $(Y_1, \dots, Y_m)$ . In the time interval  $(t, t+\delta t)$  the possible transitions are

$$Y \rightarrow \begin{cases} Y + e_i & \text{with probability } \alpha_i^T \cdot Y \delta t + o(\delta t), \\ Y - e_i & \text{with probability } \beta_i Y_i \delta t + o(\delta t), \end{cases} \quad i = 1, \dots, m,$$

as  $\delta t \rightarrow 0$ , where  $e_i$  is the  $i$ th row of the identity matrix and  $\alpha_i$  is the  $i$ th column of the matrix  $A = \{\alpha_{ji}\}$ ,

It is well-known (see e.g. Griffiths (1973)) that the necessary and sufficient condition for the extinction of  $Y$  with probability 1 is that the characteristic roots of the matrix  $A - B$  have negative real parts, where

$$B = \{\beta_{ji}\},$$

and

$$\beta_{ji} = \begin{cases} \beta_i & \text{if } i = j, \\ 0 & \text{if } i \neq j. \end{cases}$$

Assuming that this condition is satisfied we shall find the joint p.g.f. of the total number of births in each subpopulation at the time of

the extinction of the process.

Let  $W_i$  be the final number of births in population  $i$ ,

$i = 1, \dots, m$ , and

$$P_{\mathbf{a}}(y_1, \dots, y_m) = E \left\{ y_1^{W_1} \dots y_m^{W_m} \mid (Y_1(0), \dots, Y_m(0)) = \mathbf{a} \right\},$$

where  $\mathbf{a} = (a_1, \dots, a_m)$ .

Since each initial member of each subpopulation acts independently we have

$$W_i = I_1^{i1} + \dots + I_{a_1}^{i1} + \dots + I_1^{im} + \dots + I_{a_m}^{im}, \quad i = 1, \dots, m,$$

where  $I_k^{ij}$ ,  $k = 1, \dots, a_j$ , is the final number of births in population

$i$  that originated from the  $k$ th initial member of population  $j$ , and

where the  $I_k^{ij}$  are independent random variables. Therefore,

$$\begin{aligned} \text{D.1 } P_{\mathbf{a}}(y_1, \dots, y_m) &= \prod_{j=1}^m \prod_{k=1}^{a_j} E \left\{ y_1^{I_k^{ij}} \dots y_m^{I_k^{mj}} \mid (Y_1(0), \dots, Y_m(0)) = \mathbf{e}_j \right\} \\ &= \prod_{j=1}^m [P_{\mathbf{e}_j}(y_1, \dots, y_m)]^{a_j}. \end{aligned}$$

The usual renewal argument, together with D.1 gives

$$\text{D.2 } P_{\mathbf{e}_i}(y_1, \dots, y_m)$$

$$= \left[ \beta_i + \sum_{j=1}^m \alpha_{ji} \right]^{-1} \left\{ \beta_i + \sum_{j=1}^m y_j \alpha_{ji} P_{\mathbf{e}_i}(y_1, \dots, y_m) P_{\mathbf{e}_j}(y_1, \dots, y_m) \right\},$$

$i = 1, \dots, m$ .

Equation D.2 gives a system of equations which determine the

$$P_{e_i}(y_1, \dots, y_m) .$$

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